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GenCore version 4.5
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 protein search, using sw model OM protein January 29, 2002, 11:00:40 ; Search time 34.94 Seconds (without alignments) 47.963 Million cell updates/sec Run on:

US-09-763-397A-25

108 1 MKFLVNVALVFMVVYISYIYAD 22 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

ES	Description	melittin, major, p	immunodominant pro	hypothetical prote	hypothetical prote		core antigen - her	NADH dehydrogenase	sapecin B precurso	NADH dehydrogenase	preprotein translo	· preprotein translo	conserved hypothet	hypothetical prote	_		hypothetical prote	calcium receptor (calcium/polyvalent	Ca(2+)-sensing rec	calcium receptor (conserved hypothet	sapC protein homol	hypothetical prote	hypothetical prote		membrane transport	membrane transport	hypothetical prote	membrane protein M
SUMMARIES	QI	MPHB1	140841	H69453	н86742	D70105	NKVLHH	S44136	S66287	S62703	VXECSE	E86089	669513	T26259	T28208	T15959	T23576	A56715	159362	S40476	B56715	B69934	C64134	T16529	T23523	T28725	T41407	T40296	T19005	T10253
	DB	-	7	7	7	7	7	7	7	7	7	~	7	~	7	7	7	7	7	7	~	7	~	N	~	7	7	7	~	~
	Query Match Length DB	70	209	227	352	133	305	40	88	117	127	127	213	320	331	425	206	1078	1079	1085	1088	218	295	373	492	580	576	580	217	569
ď	Query Match	94.4	48.1	47.2	46.8	45.4	45.4	44.4	44.4	44.4	43.5	43.5	43.5	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	40.7	40.7	40.7	40.7	40.7	40.3	40.3	39.8	39.8
	Score	102	. 52	21	50.5	49	49	48	48	48	47	47	47	45	45	45	45	45	45	45	45	44		44	44	44		43.5	43	43
	Result No.		7	æ	4	ហ	ø	7	œ	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

oligopeptide ABC t hypothetical prote	probable mannosylt ammonium transport	NADH dehydrogenase NADH dehydrogenase	hypothetical prote conserved hypothet	probable membrane hypothetical prote	probable sigma fac Na+/H+-exchanging	hypothetical prote probable RING zinc	hypothetical prote
D82242 T19816	T39616 C82985 B71083	F71839 H64678	E86843	S54478 T15639	H71352 C40204	T28410 H84852	T32639
77	000	9 77 79	77	7 7	77	0 0	7
300	372	512 512 512	667	953 360	715	63	259
39.8 39.8	39.8 39.8	9.66	39.8	39.8 39.4	39.4	38.9 38.9	38.9
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30 31		# 15 VO	37 38	39 40	41 42	4 4 4	45

ALIGNMENTS

melittin, major, precursor [validated] - honeybee
N;Contains: melittin F
C;Species: Apis melittera (honeybee)
C;Species: Apis melittera (honeybee)
C;Dete: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 15-Sep-2000
C;Accession: A91133; A91640; B61285; S23131; A01761; A18880
C;Accession: A91133; A91640; B61285; S23131; A01761; A18880
R;Vlasak, R.; Unger-Ullmann, C; Kreil, G.; Frischauf, A.M.
Eur. J. Blochem. 135, 123-126, 1983
A;Title: Nucleotide sequence of cloned cDNA coding for honeybee prepromelittin.
A;Reference number: A91133; MUID:83287387
A;Mocession: A91133
A;Mocession: A91133
A;Mocession: A91133
A;Mocession: A91133
A;Coss-references: GB:X02007; NID:95621; PIDN:CAA26038.1; PID:95622
R;Habermann, E.; Jentsch, J.
Hoppe-Seyler's Z. Physiol. Chem. 348, 37-50, 1967
A;Title: Sequenzanalyse des Melittins aus den tryptischen und peptischen Spaltstuecke

A; Accession: A91640 A; Molecule type: protein A; Residues: 44-69 <HB> R; Gauldie, J; Hanson, J.M.; Shipolini, R.A.; Vernon, C.A. Eur. J. Blochem. 83, 405-410, 1978 A; Title: The Structures of some peptides from bec venom. A; Reference number: A91253; MUID: 78126868

A;Accession: B61285
A;Aolecule type: protein
A;Molecule type: protein
A;Residues: 51-69 <GAU>
R;Ramalingam, K.; Bello, J.
Biochem. J. 284, 663-665, 1992
A;Title: Effect of permethylation on the haemolytic activity of melittin.
A;Reference number: \$231313; MUID:92321983

A. Status: preliminary
A. Residues: 44-69 cRAM>
B. Schroeder, E.; Luebhae, K.; Lehmann, M.; Beetz, I.
Experientia 27, 764-765, 1971
A. Title: Haemolytic activity and action on the surface tension of aqueous solutions of A. Reference number: A91266; MUID: 72098668
A. Contents: annotation; synthesis
A. Note: the structure of melittin was confirmed by synthesis of a peptide with full h
R. Krell, G.; Krell-Kiss, G.
Biochem. Biophys. Res. Commun. 27, 275-280, 1967
A. Title: The isolation of N-formylglycine from a polypeptide present in bee venom.
A. Reference number: A90165; MUID: 67248282

A; Contents: annotation

A;Note: about 10% of melittin is formylated at the amino end R;Luebke, K; Matthes, S; Kloss, G. Experientia 27, 765-767, 1971 Experientia 27, 765-767, 1971 A;Title: Isolation and Structure of N(alpha)-formyl melittin.

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2 KFLVNVALVEMVV---YISYIYA 21
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Best Local Similarity 42.9
Matches 9; Conservative
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Best Local Similarity
Matches 10; Conserv
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H86742
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A; Reference number: A91267; MUID:72098669
A; Contents: annotation; synthesis
A; Note: N-formyl-melittin major was isolated from the venom and its structure was confil
A; Note: N-formyl-melittin major was isolated from the venom and its structure was confil
A; Note: N-formyl-melittin major was isolated from the venom and its structure was confil
A; Aritle: Cleavage of honoghoe prepromelittin by an endoprotease from rat liver microsome A; Title: Cleavage of honoghoe prepromelittin by an endoprotease from rat liver microsome A; Teather, D.; Gribskov, M.; Terwilliger, T. C.
REisenberg, D.; Gribskov, M.; Terwilliger, T. C.
Submitted to the Brookhaven Protein Data Bank, October 1990
A; Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 44-69
A; Contents: annotation; X-ray crystallography, 2.0 angstroms and partial refinement.
A; Terwilliger, T. C.; Elsenberg, D.
J. Biol. Chem. 257, 6010-6015, 1982
A; Terwilliger, T. C.; Elsenberg, D.
A; Terwilliger, T. C.; Elsenberg, D.
A; Tattle: The structure of melittin. I. Interpretation of the structure.
A; Title: The structure of melittin major
C; Meyborda: annotation; X-ray crystallography, 2.0 angstroms
A; Contents: annotation; X-ray crystallography, 2.0 angstroms
C; Meperfamily: melittin major estatus experimental <AND>
A; Title: The structure of melittin major of the structure.
F; 1-21/Domain: signal sequence estatus experimental <AND>
F; 1-21/Domain: signal sequence estatus experimental <AND>
F; 1-21/Domain: signal sequence estatus experimental <AND>
F; 1-69/Product: melittin F **status experimental corm (Gln) (amide in mature form from following 91)*
F; 69/Modified site: formyladed amino end (Gln) (amide in mature form from following 91)*
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immunodominant protein - heartwater rickettsia)
(Species: Cowdria ruminantium (heartwater rickettsia)
(Species: Cowdria ruminantium (heartwater rickettsia)
(Species: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 29-Sep-1999
(Species: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 29-Sep-1999
(Species: 140841; MCIS) Semu, S.M.; Bowie, M.V.; Jongejan, F.; Rurangirwa, F.R.;
Richahan, S.M.; McGuire, T.C.; Semu, S.M.; Bowie, M.V.; Jongejan, F.; Rurangirwa, F.R.;
A. Title: Molecular cloning of a gene encoding the immunogenic 21kDa protein of Cowdria
A. Recession: 140841
A. Accession: I40841
A. Status: preliminary; translated from GB/EMBL/DDBJ
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Hyp4A3
Hypthetical protein AF1633 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
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A; Residues: 1.209 <RES>
A; Cross-references: GB:L07385; NID:9289922; PIDN:AAA50280.1; PID:9289923
C; Superfamily: immunodominant protein
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GB:AE000783; NID:g2687921; PIDN:AAC66442.1; PID:g268
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C:Accession: H69453
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod R; Klenk, H.P.; Clayton, R.D.; Quackenbush, J. Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A. Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, A.; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, A.; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, A.; Accession: H69453
A; Reference number: A69250; MuID:98049343
A; Accession: H69453
A; Accession: H69453
A; Residues: problamary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Mesidues: 1-227 < KLE>
A; Residues: 1-227 < KLE>
A; Cross-references: GB:AE000989; GB:AE000782; NID:g2689312; PIDN:AAB89618.1; PID:g264
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R.Fraser, C. M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; I son. D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Sowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, I. Nature 390, 580-586, 1997
A. Authors: Smith, H.O.; Venter, J.C.
A.; Authors: Smith, H.O.; Venter, J.C.
A.; Attle: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi. A.; Reference number: A70100; MUID: 98065943
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C; Accession: H86742
R; Bolottin, A; Y wincker, P; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, R; Bichordin, A; Wincker, P; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, A; Fittle: The complete genome sequence of the lactic acid bacterium.
A; Reference number: A86625
A; Accession: H86742
A; Attatus: preliminary
A; Molecule type: DNA
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A;Cross-references: GB:AE005176; NID:g12723881; PIDN:AAK05042.1; GSPDB:GN00146
A;Experimental source: strain IL1403
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C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 28-Jul-2000
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Pred. No. 2.5;
6; Mismatches
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15:23:47 2002

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Mon Feb

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C,Accession: $62703
R,Kessler, U.; Zetsche, K.
Plant Mol. Biol. 29, 1081-1086, 1995
A;Title: Physical map and gene organization of the mitochondrial genome from the unic A;Reference number: $62702; MUID:96145517
A;Accession: $62703
A;Accession: $62703
A;Accession: $62703
A;Actus: nucleic acid sequence not shown; translation not shown
A;Residues: 1-117 <KES>
          C;Accession: S66287; S32323; Ju0224
R;Lee, S.R.; Kurata, S.; Matori, S.
FEBS Lett. 368, 485-487, 1995
A;Title: Molecular cloning of cDNA for sapecin B, an antibacterial protein of Sarcoph A; Accession: S66287; MUID:95361929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Genome: mitochondrion
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 3
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - Platymonas subcordiformis mito
C;Species: mitochondrion Platymonas subcordiformis
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 11-Jun-1999
                                                                                                                                                                                                                                                                                                two novel sapecin homol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL;247795; NID:g633584; PIDN:CAA87750.1; PID:g633586
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preprotein translocase secE chain - Escherichia coli
C;Species: Escherichia coli
C;Dacte: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C;Accession: A33139; A32873; H65204
R;Downing, W.L.; Sullivan, S.L.; Gottesman, M.E.; Dennis, P.P.
  C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
                                                                                                                                                                    A; Wolecule type: mRNA
A; Residues: 1-88 CLEE>
A; Cross-references: GB.580571; NID:g1245698; PIDN:AAB35004.1; PID:g1245699
R; Yamada, K.; Natori, S.
Biochem J. 291, 275-279, 1993
A; Title: Purification, sequence and antibacterial activity of two novel sala, A; Reference number: S32323; MUID:93228618
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A,Molecule type: protein
A,Residues: 55-88 <AMA>
C,Superfamily: sapecin precursor
C,Superfamily: sapecin precursor
C;Keywords: antibacterial; disulfide bond
F;124/Domain: signal sequence #status predicted <SIG>F;25-4/Domain: propeptide #status predicted <PRO>F;55-88/Product: sapecin B #status experimental <AMAT>F;57-78,64-84,68-86/Disulfide bonds: #status experimental
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Pred. No. 3.9;
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6; Mismatches
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Matches 7; Conservative
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Matches 9; Conserva
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C;Species: mitochondrion Candida parapsilosis
C,Date: 06-Feb-1995 #sequence_revision 26-Jul-1996 #text_change 07-Dec-1999
C;Accession: S44136
R;Nosek, J.
                                                                                                                                                                                                                                                                                                                                                           Cispecies: heron hepatitis virus, HHBV
A;Note: host Ardea cinerea (gray heron)
C;Species: all orsep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C;Accession: C30082
R;Sprengel, R.; Kalleta, E.F.; Will, H.
A;Virol. 62, 3832-3839, 1988
A;Title: Isolation and characterization of a hepatitis B virus endemic in herons.
A;Reference number: A93037; MUID:88333160
A;Accession: C30082
A;Residues: 1-305 <SPR>
A;Cross-references: GB:M22056; NID:9325452; PIDN:AAA45737.1; PID:g325453
C;Superfamily: hepatitis B virus core antigen
C;Superfamily: core protein
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A;Residues: 1-40 <NOS>
A;Cross-references: EMBL:X75676; NID:g473032; PIDN:CAA53373.1; PID:g996061
C;Genetics:
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C; Superfamily: Borrelia burgdorferi hypothetical protein BB0044
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                                                                            Length 133
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C;Species: Sarcophaga peregrina
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A;Reference number: S44135
A;Accession: S44136
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Pred. No. 6.1;
2; Mismatches
                                                                         Score 49; DB 2
Pred. No. 3.1;
6; Mismatches
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44.4%; Score 48; DB
Best Local Similarity 35.0%; Pred. No. 1.6;
Matches 7; Conservative 7; Mismatches
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A;Genome: mitochondrion
A;Genetic code: SGC3
C;Keywords: mitochondrion; NAD; oxidoreductase
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26 FLVTVPLVCTIVYDSCLYMD 45
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                                                                                                                                                                                                12 FLISVFLIFIVSGITYFYS 30
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                                                                    Query Match
Best Local Similarity 47.49
Matches 9; Conservative
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Matches 11; Conservative
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Similarity 41.2%;
7; Conservative
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Best Local Similarity
Matches 11; Conserv
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Best Local S
Matches 7
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-127 <STO>
A;Residues: 1-127 <STO>
A;Coss-references: GB:AE005174; NID:q12518903; PIDN:AAG59177.1; GSPDB:GN00145; UWGP:Z55
A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Dimalanta, E.; Potamousis, K.; Apodaca, 11ler, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Mature 409, 529-533, 2001
A; Pitle: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-127 <SCH>
B; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617
A; Accession: H65204
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C;Comment: This integral inner membrane protein is an essential component of the protein C;Genetics:
                                                                                                              A; Cross-references: GB:M30610; NID:9147798; PIDN:AAA24621.1; PID:9147800
R; Schatz, P.J.; Riggs, P.D.; Jacq, A.; Fath, M.J.; Beckwith, J.
Genes Dev. 3, 1035-1044, 1989
A; Title: The secE gene encodes an integral membrane protein required for protein export
A; Reference number: A32873; MUID:89378734
A; Accession: A32873
     J. Bacteriol. 172, 1621-1627, 1990
Affilie. Sequence and transcriptional pattern of the essential Escherichia coli secE-nus Affilie. Sequence number: A35139; MUID:90170882
A;Acference number: A35139; A150-170882
A;Accession: A35139.
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C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C;Accession: E86089
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Pred. No. E
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C; Superfamily: protein-export protein secE
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C,Superfamily: protein-export protein secE
C,Keywords: inner membrane; protein export
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MKWVVVVALLLVAIVGNYLYRD 38
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172, 1621-1627, 1990
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Best Local Similarity 40.5%
Local Similarity 40.5%
Local Similarity
Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                               A; Molecule type: DNA
A; Residues: 1-127 <DOW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Genetics:
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conserved hypothetical protein AF2111 - Archaeoglobus fulgidus conserved hypothetical protein AF2111 - Archaeoglobus fulgidus cispercies: Archaeoglobus fulgidus ful
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A; Residues: 1-213 <KLE>
A; Residues: 1-213 <KLE>
A; Cross-references: GB:AE000958; GB:AE000782; NID:g2689281; PIDN:AAB89138.1; PID:g264
C; Superfamily: conserved hypothetical protein MJ1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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A;Ablcoule type: DNA
A;Residues: 1.320 <WIL>
A;Residues: 1.320 <WIL>
A;Cross-references: EMBL:Z82075; PIDN:CAB04930.1; GSPDB:GN00023; CESP:W07A8.1
A;Experimental source: clone W07A8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein ORF47 - Melanoplus sanguinipes entomopoxvirus hypothetical protein ORF47 - Melanoplus sanguinipes entomopoxvirus C;Species: Melanoplus sanguinipes entomopoxvirus C;Dete: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000 G;Accession: T28200 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000 G;Accession: T2820 #s. Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L. J. Virol. 73, 533-552, 1999 A;Virol. 73, 533-552, 1999 A;Virol. 73, 533-552, 1999 A;Virol. 73, Free genome of Melanoplus sanguinipes entomopoxvirus. A;Reference number: Z20484; MUID:99102612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein W07A8.1 - Caenorhabditis elegans caenorhabditis elegans cispecies: caenorhabditis elegans cispecies: caenorhabditis elegans cispecies: caenorhabditis elegans cispecies: caenorhabditis elegans cispacies: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000 cispacesion: T26259
R:Basham, V. the EMBL Data Library, November 1996 submitted to the EMBL Data Library, November 1996 A;Reference number: 220184
A;Reference number: 220184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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A;Introns: 83/1; 141/3; 256/3
C;Superfamily: Caenorhabditis elegans hypothetical protein W07A8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 320;
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Pred. No. 24;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 47; DB 2;
pred. No. 8.8;
6; Mismatches
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A; Status: preliminary; translated from GB/EMBL/DDBJ

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Sympleted to the EMBL Data Library, April 1996
A; Description: The sequence of C. elegans cosmid F02E8.
A; Reference number: 218436
A; Accession: T15959
A; Accession: T15959
A; Accession: T425 AIL>
A; Residues: 1-425 AIL>
A; Cross-references: EMBL: U33340; NID: 91255859; PID: 91255863; PIDN: AAA96209.1; GSPDB: GNOG A; Experimental source: strain Bristol N2; clone F02E8
C; Genetics: A; Genetics: A; Genetics: A; Aimap position: X
A; Introns: 29/3; 69/2; 102/3; 153/1; 214/3; 273/1; 338/1; 379/1
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A;Molecule type: DNA
A;Residues: 1-331 <AFO>
A;Residues: 1-331 <AFO>
A;Cross-references: EMBL:AF063866; NID:g4049647; PIDN:AAC97829.1; PID:g4049869
A;Experimental source: isolate Tuscon
C;Genetics:
A;Note: MSV047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F02E8.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C;Accession: T15959
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                                                                                                                                                                                                                Query Match
41.7%; Score 45; DB 2; Length 331;
Best Local Similarity 31.6%; Pred. No. 25;
Matches 6; Conservative 8; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45; DB 2; Length 425;
Pred. No. 31;
2; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 50.0%;
Matches 9; Conservative 7
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                                                                                                                                                                                                                                                                                                                           4 LVNVALVFMVVXISYIYAD 22
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January 29, 2002, 11:16:20 ; Search time 20.36 Seconds (without alignments) 39.618 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                         OM protein - protein search, using sw model
                                                                                                                                            Run on:
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US-09-763-397A-25 108 1 MKFLVNVALVFMVVYISYIYAD 22 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 Total number of hits satisfying chosen parameters:

100059 seqs, 36664827 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	P01501 apis mellif	028640 archaeoglob				_	-	O28169 archaeoglob			_	P48442 rattus norv	_				Q03516 saccharomyc	P26434 rattus norv	028739 archaeoglob		Q9z706 chlamydia p	P93766 hordeum vul	_	_	Q60336 methanococc	Q57965 methanococc	P56626 trichosanth	P19580 bacillus an	000476 homo sapien	_	P45082 haemophilus	013009 sus scrofa
		21	1																															
SUMMARIES		ID	MEL_APIME	YG33_ARCFU	Y044 BORBU	CORA_HPBHE	SAPB_SARPE	NU3M_PLASU	SECE_ECOLI	YL11_ARCFU	SP87_DICDI	CASR_HUMAN	CASR_MOUSE	CASR_RAT	CASR_BOVIN	YPDC_BACSU	Y223_AQUAE	SAPC_HAEIN	YM8G_YEAST	NAH4_RAT	YF33_ARCFU	THT1_HUMAN	MRAY_CHLPN	MLO_HORVU	NUOA_MYCTU	LSPA_MYCGE	Y027_METJA	Y545_METJA	RIP1_TRIAN	CAPB_BACAN	NPT4_HUMAN	INR2_BOVIN	CYDD_HAEIN	GUAU_PIG
		DB	7	Н	1	7	Н	Н	-		-	-	-	-	-	H	-	-	н	-	-	Н	~							-	-	7	-	-
		Match Length	70	227	133	305	88	117	127	213	677	1078	1079	1079	1085	218	271	295	953	717	278	497	349	533	128	181	184	251	294	397	401	530	586	113
,	Ouery	Match	94.4	47.2	45.4	45.4	44.4	44.4		43.5	42.6	41.7	41.7	41.7	41.7	40.7	40.7	40.7	39.8	39.4	38.9	38.9	38.4	37.5	37.0	37.0	37.0	37.0	37.0	37.0	37.0	37.0	37.0	36.6
		Score	102	51	49	49	48	48	47	47	46	45	45	45	45	44	44	44	43	42.5	42	42	41.5	40.5	40	40	40	40	40	40			4	39.2
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096799 skeletonema		P12983 vibrio algi		Q37626 prototheca	P25871 nicotiana t	P41852 aeromonas h	Q37371 acanthamoeb	Q95840 magnaporthe	P03154 duck hepati	Q09206 caenorhabdi	Q9npb9 homo sapien
YC47_SKECO	DEF1_STOCA	ATPZ_VIBAL	NSG2_MOUSE	NU6M_PROWI	OLPA_TOBAC	GSPN_AERHY	NU6M_ACACA	COX3_MAGGR	CORA_HPBDU	SRA4_CAEEL	CKRB_HUMAN
-		-	-	-	-	-	-	٦	Н	~	-
69	79	129	171	207	251	252	260	269	305	329	350
36.1	36.1	36.1	36.1	36.1	36.1	36.1	36.1	36.1	36.1	36.1	36.1
39	33	39	39	39	38	38	39	39	39	39	39
34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT MEL_APINE MELL MELL MELL MELL MELL MELL MELL ME
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REVIEW.

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                                                                                                                                                                                                                                                                                                     MEDILNE=98049343: PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Kletchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Richardson D.L., Nerlavage A.R., Graham D.E., Kyrpides N.C.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Richarson S., Reich C.I., McKell L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Wasson T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of the hyperthermophilic, sulphate-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 390:364-370(1997).
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STRAIN-ARCC 55210 / B31;
MEDIINS-98065943;
Praser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
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42.9%; Pred. No. 2;
tive 6; Mismatches 6; Indels
                                                                                                                                                                                    Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 109 128 POTENTIAL.
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Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
NCBL_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                    20-AuG-2001 (Rel. 40, Created)
20-AuG-2001 (Rel. 40, Last sequence update)
20-AuG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL PROTEIN AF1633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128
192
                                                                                                                                                       Archaeoglobus fulgidus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
es 9; Conserv
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                      Archaeoglobus.
NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y044_BORBU
O51073;
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                                                                                                                                                                                    Archaea;
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7044_BORBU
1D 47044_BORBU
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GN 8000
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Matches
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0
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PIR; A01762; MEHB1.
PIR; A01762; MEHBC1.
PDB; 2MLT; 15-7UL-92.
PDB; 1BH1; 16-FEB-99.
PPB; 1BH1; 17-10-10; Melittin.
Pfam; PF01372; Melittin; 1.
PeroDon; PP014636; Melittin; 1.
Hemolysis; Toxin; Venom; Amidation; Formylation; Signal; 3D-structure;
                                                                                                                                                                                                                                                            FORMYLATION (ABOUT 10% OF THE MOLECULES). AMIDATION (G-70 PROVIDE AMIDE GROUP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RQQG -> KRQQ (IN MELITIIN 2; POSSIBLY AN ARTEFACT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISCELLANEOUS: N-FORMYL-MELITTIN MAJOR HAS 80% OF THE ACTIVITY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                SPECIES-A.mellifera; Barnham K.J., Hewish D., Werkmeister J., Curtain C., Kirkpatrick A., Bartone N., Norton R., Rivett D.; Submitted (JUN-1998) to the PDB data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE-Issue 12 of July 2001;
WWW-"http://www.expasy.org/spotlight/articles/sptlt012.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IN MELITIN 2; POSSIBLY AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        607F52C091C23BB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 102; DB 1; 1
Pred. No. 7.6e-08;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARTEFACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DATABASE: NAME-Protein Spotlight;
Biol. Chem. 257:6016-6022(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                       MEDLINE-90254148; PubMed-2187536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.4%; S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53
54
68
7585 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X02007; CAA26038.1; -.
                                                  STRUCTURE BY NMR OF 44-69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21; Conservative
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69
69
69
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Best Local Similarity
Matches 21; Conserv
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444
69
44
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Allergen. SIGNAL

PROPEP

MOD_RES

VARIANT

HELIX

MOD_RES

SEQUENCE

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YG33_ARCFU

YG33_ARCFU ID YG33_A

ò QQ us-09-763-397a-25.rsp

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Gaps

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Indels

Mismatches

5.

22

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3 FLVNVALVEMVVYISYIYAD
                                             26 FLVTVPLVCTIVYDSCLYMD
       Conservative
      11;
                                                                                                                   SAPB_SARPE
P31529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEPTIDE
DISULFID
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                                                                                         SAPB_SARPE
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      Matches
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                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey B.K., Gwinn M., Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M., van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fulji C., Cotton M.D., Horst K., Roberts K., Hatch B., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sprengel R., Kaleta E.F., Will H.; "Isolation and characterization of a hepatitis B virus endemic in
                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heron hepatitis b virus.
Viruses. Retroid viruses; Hepadnaviridae; Avihepadnavirus.
NCBI_TaxID=28300;
                                                                                                                                                                                                                                                                                                                                 Length 133
                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                Hypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 11 31 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2B228EF44162CB06 CRC64;
                                                                                                                                                                                                                                                                                          133 AA; 16052 MW; A57686EA30F1959B CRC64;
                                                                                                                                                                                                                                                                                                                                Score 49; DB 1;
Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last Sequence update)
01-APR-1990 (Rel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       305 AA
                                                                                                                                                                                                                                                                                                                                                          6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interPro; IPR002006; Hepatitis_core.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-88333160; PubMed-3418788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00906; Hepatitis_core; 1.
                                                                                                                                                                                                                                          EMBL; AE001118; AAC66442.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 AA; 34925 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Virol. 62:3832-3839(1988).
                                                                                                                                                                                                                                                                                                                                45.48;
                                                                                                                                                                                                                                                                                                                                                                                3 FLVNVALVEMVVYISYIYA 21
                                                                                                                                                                                                                                                                                                                                                                                                       12 FLISVFLIFIVSGITYFYS 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M22056; AAA45737.1;
                                                                                                                 Nature 390:580-586(1997).
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 47.4
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C30082; NKVLHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Core protein.
SEQUENCE 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORE ANTIGEN
                                                                                                     burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORA_HPBHE
P13845;
                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           herons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORA_HPBHE
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m IIGR}
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Length 305;

DB 1; 4.9;

Score 49; Pred. No.

45.4%;

Query Match Best Local Similarity

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                                                                                                                                                              Sarcophaga peregrina (Flesh fly) (Boettcherisca peregrina).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Sarcophagidae; Sarcophaga.
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=95361929; PubMed=7635204;
Lee S.-R., Kurata S., Natori S.;
"Molecular cloning of cDNA for sapecin B, an antibacterial protein of Sarcophaga, and its detection in larval brain.";
FEBS Lett. 368:485-487(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-93228618; PubMed-8471044; Yamada K., Natori S.; Purification, sequence and antibacterial activity of two novel sapecin homologues from Sarcophaga embryonic cells: similarity of sapecin B to charybdotoxin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insect immunity; Antibiotic; Cleavage on pair of basic residues;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. J. 291:275-279(1993).
-!- FUNCTION: SAPECINS, WHICH ARE POTENT BACTERICIDAL PROTEINS,
ARE PRODUCED IN RESPONSE TO INJURY. SAPECIN B IS CYTOTOXIC
GRAM-POSITIVE BACTERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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-!- INDUCTION: BY INJURY TO THE LARVAL CELL WALL.
-!- SIMILARITY: BELONGS TO THE ARTHROPOD DEFENSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001542; Arthro_defensin.
Pfam; PF01097; Arthro_defensin; 1.
PROSITE; PS00425; ARTHROPOD_DEFENSINS; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.4%; Score 48; DB 1;
47.4%; Pred. No. 2.5;
Live 6; Mismatches
                                                     01-JUL-1993 (Rel. 26, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
SAPECIN B PRECURSOR.
88 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86
10041 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; S80571; AAB35004.1; -.
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  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 55-88, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
..hes 9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S32323; S32323
PIR; JU0224; JU0224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1
25
57
57
64
88 AA;
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SEQUENCE FROM N.A.
MEDLINE=89378734; Pubmed=2673920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           secretion machinery
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  [5]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translocase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNITS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                      Kessler U., Zetsche K.;
"Physical map and gene organization of the mitochondrial genome from the unicellular green alga Platymonas (Tetraselmis) subcordiformis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. When the property of the second of the essential Escherichia "Sequence and transcriptional pattern of the essential Escherichia Coll secEnusco peron."; Battern of the essential Escherichia University of the essential Escherichia Sequence.
                                                                                                                                                                                                       Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae; Platymonas.
NCBL_TaxID=3161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-A02.00 (Rel. 15, Created)
01-A0G-1990 (Rel. 15, Last sequence update)
01-A0G-2091 (Rel. 40, Last annotation update)
20-A0G-2001 (Rel. 40, Last annotation update)
20-A0G-2001 (Rel. 40, Last annotation update)
SECE OR PREPROFOR B3981 OR 25554 OR ECS4904.
Escherichia coli, and
Escherichia coli 0157:H7.
Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                      (Prasinophyceae).";
Plant Mol. Biol. 29:1081-1086(1995).
-!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
-!- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 3 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.4%; Score 48; DB 1; Length 117; 36.8%; Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Ubiquinone; Mitochondrion.
13668 MW; 11634AEF4742F694 CRC64;
                                                                                                     15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NADH-UBIQUINONE OXIDOREDUCTAŠE CHAIN 3 (EC 1.6.5.3).
                                                                         117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 127 AA
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                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z47795; CAA87750.1; -- interPro; IPRO0040; Oxidored_q4. Pfam; PF00507; oxidored_q4; I. oxidoreductase; NAD; ubiquinone; M
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE~96145517; Pubmed~8555450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 FLVNVALVFMVVYISYIYA 21
1 MKFLTSLLLLFVVVMVSAV 19
                                                                                                                                                                               Platymonas subcordiformis. Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 AA;
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P16920;
                                                                                                                                                                   ND3 OR NAD3
                                                                        NU3M_PLASU
Q36518;
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                                          RESULT 6
NU3M_PLASU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
SECE_ECOLI
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à QQ

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SECUROR FROM N.T. RIMD 0509952;
MEDLINE-21156231; PUDMEd=112588796;
MEDLINE-21156231; PUDMEd=112588796;
MEDLINE-21156231; PUDMEd=112588796;
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Ilda T., Takanh H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kubara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterchemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-95196752; PubMed-7889938; Flower A.M., Osborne R.S., Silhavy T.J.; The allele-specific synthetic lethality of prIA-prIG double mutants predicts interactive domains of SecY and SecE."; EMBO J. 14:884-893(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schatz P.J., Bieker K.L., Ottemann K.M., Silhavy T.J., Beckwith J., "One of three transmembrane stretches is sufficient for the functioning of the SecE protein, a membrane component of the E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-0157:H7 / EDE933 / ATCC 700927;
MEDLINE-21074935; PubMed-1120551;
MEDLINE-21074935; PubMed-1120551;
Rose D.J. Mayhew G.F. Brains P.S., Gregor J., Kirkpetrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpetrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., J. Boutin A., Shao Y., Miller L.,
Grotbeck E.J. Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
Mature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Manting E.H., van Der Does C., Remigy H., Engel A., Driessen A.J., "SecYEG assembles into a tetramer to form the active protein translocation channel.":
                                                                                                                                                                                                                                                                                                                               Daniels D.L.; "Analysis of the Escherichia coli genome. IV. DNA sequence of the region from 89.2 to 92.8 minutes."; Nucleic Acids Res. 21:5408-5417(1993).
Schatz P.J., Riggs P.D., Jacq A., Fath M.J., Beckwith J.; 
"The secg gene encodes an integral membrane protein required i 
protein export in Escherichia coli."; 
Genes bev. 3:1035-1044(1989).
                                                                                                                                                                              SEQUENCE FROM N.A.
STRALN-KI2 / MG165;
STRALN-S4089392; PubMed-8265357;
Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Evaluating the oligomeric state of SecYEG in preprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20402345; Pubmed=10944122; Yahr T.L., Wickner W.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20164453; PubMed=10698927;
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EMBO J. 19:852-861(2000).
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SP87_DICDI
P54643;
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MEDLINE-98049343; PubMed-9389475;
MEDLINE-98049343; PubMed-9389475;
MEDLINE-98049343; PubMed-9389475;
MEDCHOUM K.A., Dodson R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Richardson D.L., Merlavage A.R., McReney K., Adams M.D., Loftus B.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Nature 390:364-370(1997).
                                                                                                                                                                                                                         Pfam; PF00584; SecE; 1.
PROSITE; PS01067; SECE_SEC61G; 1.
Protein transport; Translocation; Transmembrane; Inner membrane;
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                                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB 1; Length 127; Pred. No. 4.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                      6; Indels
 -!- SIMILARITY: BELONGS TO THE SECE/SEC61-GAMMA FAMILY.
                                                                                                                                                                                                                                                                                                                                                PERIPLASMIC (PROBABLE).
94D37280522875CE CRC64;
                                                                                                                                                                                                                                                                      CYTOPLASMIC (PROBABLE). PROBABLE.
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15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 AA
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EMBL: AE005629; AAG59177.1; --
EMBL: AP002567; BAB38327.1; --
PIR: A35139; VXECSE.
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40.9%;
                                                                                                                   EMBL; M30610; AAA24621.1; -. EMBL; U00006; AAC43079.1; -.
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                                                                                                                                                                                                Ecocene; EG10939; secE.
InterPro; IPR001901; SecE.
Pfam; PF00584; SecE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                               Complete proteome
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028169;
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                                                                                                                                                                                                                                                                                     TRANSMEM
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                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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1. SUBSECLULAR LOCATION: ACCUMULATES SPECIFICALLY IN REGULATED SECRETORY VESICLES OF PRESPORE CELLS (PRESPORE VESICLES). THE PROTEIN LATER ACCUMULATES EXTRACELLULARLY IN THE SPORE COAT.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 47; DB 1; Length 213;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5B193379E5BC7278 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCY-1997 (Rel. 35, Last annotation update)
SPORE COAT PROTEIN SP87 PRECURSOR (PL3 PROTEIN).
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MEDLINE=94229358; PubMed=8174787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 MKLLVVLSAALVYSIVRLSHIYS 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKFLV--NVALVFMVVYISYIYA 21
                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000958; AAB89138.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23062 MW:
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Pfam; PF01914; UPF0056; 1.
Hypothetical protein; Transmen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 47.8
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 2
213 AA;
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SEQUENCE FROM N.A.
                         SEQUENCE FROM N.A.
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                                                SPORE COAT PROTEIN SP87.
PRESPORE MOTIF 1.
PRESPORE MOTIF 2.
PRESPORE MOTIF 3.
PRESPORE MOTIF 4.
PRESPORE MOTIF 5.
PRESPORE MOTIF 6.
PRESPORE MOTIF 6.
PRESPORE MOTIF 9.
PRESPORE MOTIF 9.
PRESPORE MOTIF 10.
PRESPORE MOTIF 10.
PRESPORE MOTIF 11.
S. X. 9 AA REPEATS OF G-G-S-S-G-G-T-S.
                                                                                                                                                                                                                                                                                                                                                                                        CASR_HUMAN STANDARD; PRT; 1078 AA.
PH180: 013912; 016379; 016108; 016109; 016110;
01-FEB-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-NOG-2001 (Rel. 40, Last annotation update)
EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR).
HOMO SAPIERS (HUMAN).
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                            LINKED (GLCNAC. . .) (POTENTIAL).
EF6E29CFF57E78D5 CRC64;
                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                             1-4 (APPROXIMATE),
1-5 (APPROXIMATE),
3 x 40 AA APPROXIMATE REPEATS.
                                                                                                                                                                                             2-3.
8 x 26 AA APPROXIMATE REPEATS.
                                                                                                                                                                                                                                                                                                                    Score 46; DB 1; Length 677;
Pred. No. 24;
H: Mismatches 8; Indels
                                                                                                                                                                                                                                                            GLY/SER/THR-RICH.
GLY/SER/THR-RICH.
GLY/SER/THR-RICH.
                                       Sporulation; Signal.
                                                                                                                                                                                                                                                                                       POLY-PRO.
                                                                                                                                                                                                                                                                                 POLY-SER.
                                                                                                                                                                                    1 MKFLVNVALVFMVVYISYIYA 21
                                                                                                                                                                                                                                                                                                                                                      Query Match 42.6%;
Best Local Similarity 42.9%;
Matches 9; Conservative
                Dictybb; DD02054; pspb.
InterPro; IPR003645; Foln.
SMART; SM00274; FOLN; 5.
Glycoprotein; Repeat; Spor
     EMBL; U25144; AAA73515.1;
HSSP; P06620; 1INA.
                                                                                                                                                                                                                                                                                                  677 AA;
                                      Glycoprotein;
SIGNAL
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CARBOHYD
SEQUENCE
                                                   CHAIN
REPEAT
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CASR_HUMAN
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PROGNEC FROM NA.

12)

13. Submitted (DEC-1994) to the EMBL/Genbank/DDBJ databases.

14. Submitted (DEC-1994) to the EMBL/Genbank/DDBJ databases.

15. Submitted (DEC-1994) to the EMBL/Genbank/DDBJ databases.

16. Submitted (DEC-1994) to the EMBL/Genbank/DDBJ databases.

17. SEQUENCE FROM NA.

18. Submitted (DEC-1994) to the EMBL/Genbank/DDBJ databases.

18. The Company of Company of

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20-MUG-2001 (Rel. 40, Last sequence update)
20-MUG-2001 (Rel. 40, Last annotation update)
EXTRACELLUIAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CALL CALCIUM-SENSING RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR CALCIUM-SENSING RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
STRAIN=C57BL/6; TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                 receptor; Transmembrane; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL)
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
VII (POTENTIAL).
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Q9QY95; Q9QZU8; Q9R1D6; Q9R1Y2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
II (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (
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                                                                                                                                                           Pfam; PF00003; 7tm 3; 1.
Pfam; PF01094; ANE_receptor; 1.
PRINTS; PR00548; GPCRMGR.
PRINTS; PR00548; GPCRMGR.
PROSITE; P800979; G_PROTEIN_RECEP_F3_1; 1.
PROSITE; P800980; G_PROTEIN_RECEP_F3_2; 1.
PROSITE; P800980; G_PROTEIN_RECEP_F3_2; 1.
PROSITE; P800980; G_PROTEIN_RECEP_F3_2; 1.
PROSITE; P800559; G_PROTEIN_RECEP_F3_3; 1.
PROSITE; P850059; G_PROTEIN_RECEP_F3_4; 1.
PROSITE; P850059; G_PROTEIN_RECEP_F3_4; 1.
PROSITE; P850059; G_PROTEIN_RECEP_F3_4; 1.
PROSITE; P850059; G_PROTEIN_RECEP_F3_4; 1.
PROSITE; P8500799; G_PROTEIN_RECEP_F3_4; 1.
PROSITE; P850099; G_PROTEIN_RECEP_F3_4; 1.
PROTEIN_RECEP_F3_4; 1.
PROSITE; P850099; G_PROTEIN_RECEP_F3_4; 1.
PROSITE; P850099; G_PROTEIN_RECEP_F3_4; 1.
PROSITE; P850099; G_PROTEIN_RECEP_F3_4; 1.
PROSITE PROSITE PROTEIN_RECEP_F3_4; 1.
PROSITE PROSITE PROTEIN_RECEP_F3_4; 1.
PROSITE PROSITE PROSITE PROTE
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Pred. No.
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                                                                                                                    InterPro; IPR001828; ANF_receptor InterPro; IPR000337; GPCR_Mgr.
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090Y96; 008968; 088519; 090Y95;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequents)
20-AUG-2001 (Rel. 40, Last sequents)
                                                                                                                                          GPCR_Mgr.
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Best Local Similarity
Matches 9; Conserv
              GCR 2697:
                                          MIM; 601199; -.
MIM; 145980; -.
MIM; 601198; -.
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CHAIR SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

ALTERNATIVE PRODUCTS: 2 ISOFORMS SEEM TO BE PRODUCED BY ALTERNATIVE PRODUCTS: 2 ISOFORMS SEEM TO BE PRODUCED BY ALTERNATIVE SPLICING.

CHAIR STATE AND ALTERNATIVE BUT NOT IN BRAIN, LUNG, LIVER, HEART, SKELETAL MUSCLE, OR PLACENTA.

HYPERCALCEMIA (FHI) AND NEONDATAL SEVERE HYPERPARATHYROIDISM (NSHPT), TWO INHERITED CONDITIONS CHARACTERIZED BY ALTERED CALCIUM (NSHPT), TWO INHERITED CONDITIONS REDUCE THE ACTIVITY OF THE RECEPTOR.

CHARACTERIZED INDIVIDUALS EXHBIT MILD OR MODEST HYPERCALCEMIA, CONTRAST, NSHPT IS A RARE AUTOSOMAL RECESSIVE LIFE-THREATENING

CONTRAST, NSHPT IS A RARE AUTOSOMAL RECESSIVE LIFE-THREATENING

CONTRAST, NSHPT IS A RARE AUTOSOMAL RECESSIVE LIFE-THREATENING

CONTRAST, NSHPT HAS BEEN DEMONSTRATED TO BE THE HOMOZYGOUS FORM OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISEASE: DEFECTS IN PCARI ARE ALSO THE CAUSE OF AUTOSOMAL DOMINANT HYPOPARATHYROIDISM (ADHP). ADHP IS CHARACTERIZED BY HYPOCALCEMIA AND HYPERPHOSPHATEMIA DUE TO INADEQUATE SECRETION OF PARATHYROID HORMONE. SYMPTOMS ARE SEIZURES, TETANY AND CRAMES. SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
                                                           Calcium-sensing receptor mutations in familial benign hypercalcemia and neonatal hyperparathyroidism."; J. Clin. Invest. 96:2683-2692(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                            Ward B.K., Stuckey B.G.A., Gutteridge D.H., Laing N.G., Pullan P.T.,
Ratajczak T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A novel mutation (L174R) in the Ca2+-sensing receptor gene associated with familial hypocalciuric hypercalcemia."; Hum. Mutat. 10:233-235(1997).
                                                                                                                                                                    VARÍANTS ADHP THR-116; HIS-681 AND SER-806, AND VARIANT SER-851 MEDLING-9631154; PUDMed-873126; Baron J., Winer K.K., Yanoveki J.A., Cunningham A.W., Laue L., Zimmerman D., Cutler G.B. Jr.; "Mutations in the Ca(2+)-sensing receptor gene cause autosomal dominant and sporadic hypoparathyroidism."; Hum. Mol. Genet. 5:601-606(1996).
Grant D.B., Heath D.A., Hughes I.A., Paterson C.R., Whyte M.P.,
Thakker R.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB29413.2; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                         VARIANT FHH ARG-174.
MEDLINE-97442275; PubMed-9298824;
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S68036; AAB29415.1;
S81755; AAD14370.1;
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GCR_1874;
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Length 1078; Indels

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Oda Y., Tu C.-L., Chang W., Crumrine D., Koemueves L., Mauro T., Elias P.M., Bixle D.D.; Harbe calcium sensing receptor and its alternatively spliced form in murine epidermal differentiation.";

GCR_2013; GCR_2696;

GCRDb; GCRDb; GCRDb; GCRDb;

GCR_2012

GCRDb;

EMBL;

EMBL; EMBL; EMBL; EMBL; EMBL; EMBL;

EMBL;

MEDLINE=20092890; PubMed=10625662;

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RE REBL, AF110179; AAD28371.1; . .

REBL, AF128442; AAD28371.1; . .

REBL; AF12843; AAD40838.1; . .

REBL; AF008200; AAC19388.1; . .

REBL; AF008214; AAC50252.1; . .

REMEL; AF15965; AAF00193.1; . .

REMEL; AF15965; AAF00193.1; . .

REMEL; AF15965; AAF00193.1; . .

RICAFPC: IPRO1083; GPCR_Mgr.

RICAFPC: IPRO1083; GPCR_Mgr.

REMEL; AF00037; GPCR_Mgr.

REMEL; AF00037; GPCR_MGr.

REMEL; AF00037; GPCR_MGr.

REMEL; AF00039; GPCR_MGr.

REMEL; AF00099; GPCR_MGR.

REMEL; AF00099; GPROTEIN_RECEP_F3_1; 1.

REMEL; PS00999; G_PROTEIN_RECEP_F3_3; 1.
                                                                                                                                                                                                                                                                           TISSUE-Epiphyseal cartilage;
MEDLINE-20043955;
Chang W., Tu C., Chen T.-H., Komuves L., Oda Y., Pratt S.A.,
Miller S., Shoback D.;
"Expression and signal transduction of calcium-sensing receptors in
cartilage and bone."
Endocrinology 140:5883-5893(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-1- ALTERNATIVE PRODUCTS: 2 ISOFONNS; A (SHOWN HERE) AND B; ARE
--- PRODUCED BY ALTERNATIVE SPLICING.
--- TISSUE SPECIFICITY: EPIDERMIS, KIDNEY AND CARTILAGE.
--- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 646-799 FROM N.A., AND TISSUE SPECIFICITY.

MEDIATE-97231187; PubMed-9076582;

MEDIATES L.D., Hartle J.E. II, Sidhanti S.R., Guo R., Hinson T.K.;

"A distinct cation-sensing mechanism in MC373-E1 osteoblasts
functionally related to the catioum receptor.";
J. Bone Miner. Res. 12:393-402(1997).

-I. FUNCTION: SENSES CHANGES IN THE EXTRACELLULAR CONCENTRATION OF CALCIUM INOS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A
G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
MESSENGER SYSTEM.
                                                                                                                                                                                                                                                          SEQUENCE OF 256-600 FROM N.A. (ISOFORM A), AND TISSUE SPECIFICITY
                                           SEQUENCE FROM N.A. (ISOFORM A), AND TISSUE SPECIFICITY.
STRAIN-BLACK SWISS X 129/5VU; TISSUE-Kidney;
MEDILINE-20119379; PubMed=10652312;
Pi M., Garner S.C., Flannery P., Spurney R.F., Quarles L.D.;
"Sensing of extracellular cations in CasR-deficient osteoblasts.
Evidence for a novel cation-sensing mechanism.";
J. Biol. Chem. 275:3256-3263(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=NWRI; TISSUE=Brain;
Hildenbrand J., Ammon H.P.T., Wahl M.A.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Kidney;
Moawad T.I., Riccardi D.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 507-582 FROM N.A. (ISOFORM A).
Biol. Chem. 275:1183-1190(2000)
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O'I-FEB-1996 (Rel. 33, Created)
10-FEB-1996 (Rel. 33, Last sequence update)
20-AuG-2001 (Rel. 40, Last annotation update)
EXTRACELIULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID EXTRACELIULAR CALCIUM-SENSING RECEPTOR).
CASR OR GPRCZA OR PCAR1.
Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
EXTRACELLULAR CALCIUM-SENSING RECEPTOR.
EXTRACELLULAR (POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
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ilarity 45.0%; Pred. No. 47;
Conservative 5; Mismatches 6; Indels
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II (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                            IV (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
VI (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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N-LINKED (GLCNAC...) (PO N-LINKED (GLCNAC...)) (PO N-LINKED (GLCNAC...) (PO N-LINKED (GLCNAC...)) (PO N-LINKED (GLCNAC...) (PO N-LINKED (GLCNAC...)) (PO 
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CYTOPLASMIC (POTENTIAL).
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L -> D (IN REF 3).
C -> D (IN REF 2).
V -> A (IN REF 2).
Y -> H (IN REF 2).
Y -> H (IN REF 5).
F -> L (IN REF 5).
T -> I (IN REF 5).
T -> I (IN REF 2).
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889 889
906 909
1057 1057
1064 1064
1076 1076
1079 AA, 120839 M
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Matches 9; Conserv
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SEQUENCE FROM N.A.
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805 KFITFSMLIFFIVWISFIPA 824
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                                                                   CASR_BOVIN
                                                       RESULT
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                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                 Ruat M., Snowman A.M., Snyder S.H.;
"Calcium sensing receptor: molecular cloning in rat and localization
to nerve terminals.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR CALCIUM-SENSING RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                              -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 92:3161-3165(1995).
-!- FUNCTION: SENSE CHANGES IN THE EXTRACELLULAR CONCENTRATION OF CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
PROSITE: PS00980; G_PROTEIN_RECEP_F3_2; 1.
PROSITE: PS00981; G_PROTEIN_RECEP_F3_3; 1.
PROSITE: PS50259; G_PROTEIN_RECEP_F3_4; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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N-LINKED (GLCNAC. . .) (
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N-LINKED (GLCNAC.
Proc. Natl. Acad. Sci. U.S.A. 92:131-135(1995).
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InterPro; IPR001828; ANF_receptor.
InterPro; IPR00037; GPCR_Mgr.
Pfam; PF00003; 7tm_3; 1.
Pfam; PF01094; ANF_receptor; 1.
PRINTS; PR00248; GPCRMGR.
PRINTS; PR00592; CASENSINGR.
                                                    MEDLINE-95241465; PubMed-7724534;
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                                                                                                                                                                                                                                                                                                                                      EMBL; U10354; AAC52149.1; -
                          SEQUENCE OF 1-294 FROM N.A.
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488
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                                                                                                                                                                                                           01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 40, Last annotation update)
EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR CALCIUM-SENSING RECEPTOR. EXTRACELLULAR (POTENTIAL). (POTENTIAL). CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R EMBL; S67307; AAB29171.1; -.

R PIR; S40476.

R GCRDb; GCR_0900; -.

R InterPro; IPR001828; ANF_receptor.

R InterPro; IPR001828; ANF_receptor.

R InterPro; IPR001828; ANF_receptor.

R Pfam; PF01094; ANF_receptor; 1.

R Pfam; PF01094; ANF_receptor; 1.

R PRINTS; PR00592; CASENSINGR.

R PROSITE; PS00999; G_PROTEIN_RECEP_F3_1; 1.

R PROSITE; PS00981; G_PROTEIN_RECEP_F3_2; 1.

R PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.

R PROSITE; PS00981; G_PROTEIN_RECEP_F3_4; 1.

R G_PCOTEIN_COUPLED_F3_4; 1.
                                                                                                                                                                                                                                                                                                                                                                    -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                     CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDY LINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
                                                                                                             Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
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CYTOPLASMIC (POTENTIAL).
IV (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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VI (POTENTIAL).
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VII (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (PC
 PRT; 1085 AA
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                                                                                   CELL CALCIUM-SENSING RECEPTOR).
  STANDARD;
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                     NCBI_TaxID=9913;
CASR_BOVIN
P35384;
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Gaps

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Indels

Score 45; DB 1; Length 1079;

Pred. No. 47;

41.78;

Conservative

Query Match Best Local Similarity Matches 9; Conserv

37 FFLGVVLVFPIMFIQYV 53

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         N-LINKED (GLCNAC...) (POTENTIAL).
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STRAIN-168 / MARBURG;
STRAINE-96349105; Pubbwed-8760912;
SOIOKin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,
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01-0CT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 24.7 KDA PROTEIN IN RECQ-CMK INTERGENIC REGION.
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Pred. No. 18;
; Mismatches 5; Indels
                                                                                                                                                                            DB 1; Length 1085; 47;
                                                                                                                                                                                                          6; Indels
                                                                                                                                          5D66DE8C9CD13E47 CRC64;
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88556D50863E14BC CRC64;
(POTENTIAL)
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 CYTOPLASMIC
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Pred. No.
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Subtilist; BG11438; ypdC.
Hypothetical protein; Transme
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Best Local Similarity 41.2
Matches 7; Conservative
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218 AA;
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Best Local Similarity
Matches 9; Conserv
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299116;
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P50738;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way monfified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                         MEDIARE-98196666; PubbMed-9537320;
MEDIARE-98196666; PubbMed-9537320;
Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
Fridman R.A., Short J.M., Olson G.J., Swanson R.V.;
arph complete genome of the hyperthermophilic bacterium Aquifex aeolicus."
                                                                                                                                                                                                                                                                                                                            Nature 392:353-358(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Transmembrane; Plasmid; Complete proteome.
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                                                                    (Rel. 39, Last sequence update) (Rel. 40, Last annotation update)
                                                                                                                                                     Bacteria; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxID=63363;
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                         271 AA
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209 PC
238 PC
31365 MW;
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                                                         30-MAY-2000 (Rel. 39, Created)
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Best Local Similarity 27.33
Matches 6; Conservative
                                                                                                  HYPOTHETICAL PROTEIN AA23
                            STANDARD;
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189 2
218
271 AA;
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                                                                                                                                   Aquifex aeolicus.
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                            YZ23_AQUAE
066414;
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January 29, 2002, 10:59:20 ; Search time 66.28 Seconds (without alignments) 24.587 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Honey bee melittin	Recombinant vaccin	Human VEGF-X prote	Human VEGF-X prote	Glutathione-S-tran	Infections salmon	Melittin signal pe	Human GIL-19/AE289	Cytomegalovirus US	Honey bee melittin	Honey bee melittin
SUMMARIES	ID	AAY70301	AAY70278	AAB10640	AAB10641	AAW47008	AAE05128	AAB72437	AAB36293	AAY97249	AAR99533	AAW87499
	DB	21	21	21	21	19	22	22	21	21	17	20
	Ouery Match Length DB ID	22	350	354	354	1189	386	21	49	177	21	21
æ	Query	100.0	100.0	100.0	100.0	100.0	96.3	94.4	94.4	94.4	89.8	89.8
	Score	108	108	108	108	108	104	102	102	102	46	97
	Result No.	-	7	e	4	S	9	7	60	6	10	11

O)	molec	Secretion signal a	æ	Ehrlichia canis MA		Ehrlichia chaffeen	Ehrlichia chaffeen	Major antigenic pr	Cowdria ruminatium	. B. burgdorferi ant	Heron hepatitis B	Human O-fucosyltra	H. pylori flagella	Human secreted pro	Human CaR transmem	G protein-coupled	Human calcium sens	Human calcium sens	Human calcium sens	Dogfish shark kidn	Amino acid sequenc	Chicken calcium-se	Parathyroid calciu	Human parathyroid	Human parathyroid	Human calcium rece	Human parathyroid	Human parathyroid	Human calclum rece	Human wild type ca	Cynomolgous monkey	Protein encoded by	Rat kidney calcium
AAW64613	AAW61590	AAW85766	AAW51098	AAB36192	AAU04202	AAW51099	AAB36193	AAU04203	AAB36194	AAY19802	AAY 29763	AAW80573	AAW20456	AAY02715	AAY49110	AAU03853	AAY45001	AAY45000	AAY44999	AAW32059	AAW25762	AAU00508	AAW11889	AAW54846	AAW38274	AAY 28840	AAY41780	AAW89565	AAY51827	AAY70325	AAU02195	AAB74391	AAW54847
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AAY70301 standard; peptide; 22 AA. AAY70301; AAY70301 RESULT

ALIGNMENTS

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Honey bee melittin signal peptide. (first entry) 06-JUN-2000

Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; T-cell epitope; tetanus toxoid; antiganic epitope; treatment; circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175; BSA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody; melittin; honey bee.

Apis sp.

WO200011179-A1.

99WO-US18869. 19-AUG-1999; 02-MAR-2000.

98US-0097703. 21-AUG-1998;

(NAIM-) NAT INST IMMUNOLOGY. (USSH) US DEPT HEALTH & HUMAN SERVICES.

Shi YP, Hasnain SE; Lal AA, (NAIM-) NAT INST IMMUNOLOGY. (USSH) US DEPT HEALTH & HUMAN SERVICES.

WPI; 2000-237654/20. N-PSDB; AAZ51336.

Shi YP,

Lal AA,

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                                                                                                                                        honey bee. It is used in the construction of recombinant protein concrine. The recombinant protein construction of recombinant protein concrine. The recombinant protein comprises, melitth signal peptide, vaccine. The recombinant protein comprises, melitth signal peptide, this) fag, T-cell epitope from tetanus toxoid and 21 antigenic epitopes from circumsporozoite protein (CSP), sporozoite surface protein-2 (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), merozoite surface protein-1 (MSP-1), merozoite surface protein-1 specific antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of P. falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting P. falciparum in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; T-cell epitope; tetanus toxoid; antigenic epitope; treatment; SSP-2; circumsporozoite protein; CSP; sporozoite surface protein-1; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; MSP-2; apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                   Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Recombinant multivalent malarial vaccine"
                                                                                                                            The present sequence is the melittin secretory signal peptide from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 22;
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100.0%; Pred. No. 1.6e-10;
ive 0; Mismatches 0;
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/label= Melittin_signal_peptide
/note= "Derived from Honey bee"
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/label- Mature_CDC/NIIMALVAC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant vaccine CDC/NIIMALVAC-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY70278 standard; Protein; 350 AA.
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                                                                                                 Claim 2; Page 16; 52pp; English
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Chimeric - Clostridium tetani
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Best Local Similarity
Matches 22; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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The present sequence is that of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melittin signal peptide, (His)6 tag, T-cell epitope protein comprises, melittin signal peptide, (His)6 tag, T-cell epitope from tetanus toxoid and 21 antigenic epitopes from circumsporczoite cfrom tetanus toxoid and 21 antigenic protein. (SSP-2), liver stage cantigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical compared antigenil (MAM-1), erythrocyte binding antigenily (FBA-175), reportry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of plasmodium falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumaticid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human VEGF-X protein for expression in Baculovirus/insect cell systems.
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                                                                                                                                Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle
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100.0%; Pred. No. 2.8e-09;
ive 0; Mismatches 0;
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                                                                                                                                                                                                         Claim 3; Page 43-44; 52pp; English.
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99US-0124967.
99US-0164131.
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Best Local Similarity 100
Matches 22; Conservative
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08-NOV-1999;
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AAB10640
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Homo sapiens.
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06-MAY-1997;
09-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
AAW47008
 δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiantitic, antiporiatic and antidiabletic activity and acts as an angiogenesis and vascularization antidiabletic activity and acts as an angiogenesis and vascularization or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vascularisation including formation and proliferation of new blood and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic uncers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair, proliferation of new blood vessels, tissue regeneration. This sequence represents a human VEGF-X protein which can be expressed in Baculovirus/insect cell systems and which is
                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; andiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
                                                            New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Goslewska A;
                                                                                                                                                                                                                                                                                                                                                                                                               Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human VEGF-X protein for expression in E. coli systems.
                                                                                                                                                                                                                                                                                                                                                                                                               DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 108; DB 21;
100.0%; Pred. No. 2.9e-09;
ive 0; Mismatches 0;
                                                                                                                Disclosure; Fig 20; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB10641 standard; Protein; 354 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKFLVNVALVFMVVYISYIYAD 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0164131,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0124967.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98GB-0028377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (JANC ) JANSSEN PHARM NV.
                      WPI; 2000-442669/38.
Dhanaraj SN, Xu J;
                                                                                                                                                                                                                                                                                                                                                                          354 AA;
                                    N-PSDB; AAA71984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200037641-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                             sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB10641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB10641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
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(VEGE-X) protein (13) and its encoding polynucleotide [13] which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidabetic activity and acts as an angiogenesis and vasculatic and regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic cretinopathy by inhibiting angiogenic activity or inappropriate cascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ at tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents a human VEGE-X protein which can be expressed in E. coli systems and which is described in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                       preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -              
                                                                                                                                                                                    New vascular endothelial growth factor protein, useful for treating or
                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel vascular endothelial growth factor-X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prògnosis; cell proliferation; cancer; ageing; ribonucleoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22..23
/note= "enterokinase cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 108; DB 21;
100.0%; Pred. No. 2.9e-09;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW47008 standard; Protein; 1189 AA
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                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 21; 127pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKFLVNVALVFMVVYISYIYAD 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    960S-0724643.
970S-0844419.
970S-0846017.
970S-0851843.
970S-0854050.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
                                                                     2000-442669/38
Dhanaraj SN, Xu J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 22
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                                                                                                           N-PSDB; AAA71985
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The present invention relates to vaccine for prevention and/or prophylaxis of infectious salmon anaemia in fish. The invention prophylaxis of infectious salmon anaemia in fish. The invention provides for nucleic acid sequence encoding viral proteins of infectious salmon anaemia virus (ISAV) as well as the isolated protein. Nucleic acids encoding viral protein is useful for the manufacture of a DNA vaccine for diagnosis, treatment and/or prophylaxis of infectious salmon anaemia in fish, and viral protein can be used for the manufacture of antibodies that are specific for ISAV. The present sequence is infectious salmon anaemia virus 92-M fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UGGT; UDP-glucose:glycoprotein glucosyltransferase; enzyme; honeybee; melittin signal peptide.
                                                                                                                                                                                                                                                                                                                                  Novel vaccine for treatment and/or prevention of infectious salmon anemia in fish {\mbox{-}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 104; DB 22; Length 38
Pred. No. 1.3e-08;
1; Mismatches 0; Indels
    /note= "Mature ISAV 92-M protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bergeron JJM,
                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Page 39-41; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB72437 standard; Peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CANA ) NAT RES COUNCIL CANADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-JUL-2000; 2000WO-CA00883.
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                                                                                                                  03-JAN-2001; 2001WO-EP00046.
                                                                                                                                                     07-JAN-2000; 2000EP-0200054.
29-FEB-2000; 2000EP-0200700.
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Best Local Similarity 95.59
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dignard D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Melittin signal peptide
                                                                                                                                                                                                                                               Biering E, Krossoy B;
                                                                                                                                                                                                              (ALKU ) AKZO NOBEL NV.
                                                                                                                                                                                                                                                                                       WPI; 2001-441845/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-218358/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       386 AA;
                                                                                                                                                                                                                                                                                                       N-PSDB; AAD09875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200112845-A1.
                                         WO200149712-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-AUG-1999;
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                                                                             12-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB72437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
AAB72437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δλ
                                                                                                                                                                                                                                                                                                                The present sequence represents a fusion protein from an example of the present invention which describes human telomerase reverse transcriptase (hTRT). The present invention also describes the transcriptase (hTRT). The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTRT, by detecting the change in hTRT recombinant protein or polynuclectide, on administration of the compound; protein or polynuclectide, on administration of the compound; protein or protein in a sample by binding a relevant of the hTRT RNA or protein in a sample by binding a relevant of the hTRT RNA or protein in a sample by binding a relevant of the hTRT RNA or protein in a sample by binding a relevant of the sample and detecting the complex formed or in the case of RNA detection, amplification product with presence of hTRT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTRT expression; and (B) the use of an agent that causes an increase in cell vertebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hTRT and the polynuclectide encoding hTRT can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of tellomerase activity can be used to treat conditions that are associated with high tellomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               salmon anaemia vírus; ISAV; 9Z-M clone; vaccine; prophylaxis; salmon anaemia; therapy; fusion protein; antianaemic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                          Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 108; DB 19; Length 1189;
Pred. No. 1e-08;
Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Infectious salmon anaemia virus (ISAV) 92-M fusion protein.
                                                                                                                  Lingner J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1..21
/label= Mellitin_signal_peptide
22..26
/label= Linker_peptide
27..386
                                                                                                                  Harley C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Infectious salmon anaemia virus.
Unidentified.
                                                                                                                                                                                                                                                                                Example 6; Page 234-235; 387pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE05128 standard; Protein; 386 AA.
                                                                                                                  Chapman KB,
Harley CB;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                        (GERO-) GERON CORP.
(UYTE-) UNIV TECHNOLOGY CORP.
    97US-0911312.
97US-0912951.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0
Best Local Similarity 100.0
Matches 22; Conservative
                                                                                                              , Cech TR,
Nakamura T,
                                                                                                                                                                      WPI; 1998-171633/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1189 AA;
14-AUG-1997;
14-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric -
Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infectious
                                                                                                                                   Morin GB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sednence
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                                                                                                                  Andrews
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Gaps

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Length 386;

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interleukin-10 (IL-10) and is assumed to be a cytokine. It can be used in the regulation of cell proliferation and differentiation, haematopoiesis, immune stimulation or suppression, tissue growth and tumour inhibition. In addition, it also has uses in the treatment of inflammation and in nutrition.
                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                AAY97249
                                                                                                                                                                                                                                                                                                                  RESULT
   888888
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                                                                                                                                              The present invention relates to a method for determining the effect of a test sample on UDP-glucose:glycoprotein glucosyltransferase (UGGT) activity. The method comprises exposing an acceptor substrate for UGGT to a labelled donor in the presence of the test sample and UGGT. The method is useful for determining UGGT activity. In particular, the method is useful for determining UGGT activity. In particular, the method is useful in glucosyltransferase assay and kinetics measurement for reticulum which catalyses the addition of a glucose residue onto asparagine-linked oligosaccharides, which are present on incorrectly folded glycoproteins. The present sequence is the honeybee melittin signal peptide. This sequence was used in the construction of an expression vector for rat UGGT (see AAF60732 and AAB72436).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences for the novel human GIL-19/AE289 protein. The protein shows homology to
                              Determining the effect of a test sample on UDP-glucose.glycoprotein glucosyltransferase (UGGT), useful for measuring UGGT activity, comprises exposing an acceptor substrate for UGGT to a labeled donor the presence of UGGT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (interleukin)-10, useful in upregulation of humoral immune responses, as an antlinflammatory agent and as a modulator of immune responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human GIL-19 protein that shows a high degree of homology to IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, GIL-19/AE289; IL-10; interleukin-10; nutrition;
cell proliferation; immune stimulation; immune suppression;
haematopolesis regulation; tissue growth; inflammation; cancer.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human GIL-19/AE289 protein sequence FLAG epitope tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 102; DB 22;
Pred. No. 1.3e-09;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xuan D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB36293 standard; Protein; 49 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                       94...
100.08; F1.
                                                                                                                 Example 1; F1g 8; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; Page 50; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKFLVNVALVFMVVYISYIYA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-APR-2000; 2000WO-US11479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0131473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          associated with injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fouser L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-687325/67.
                                                                                                                                                                                                                                                                                                                                                                                 21 AA;
N-PSDB; AAF60733.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200065027-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jacobs K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB36293;
                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                             US2; hCMV; major histocompatibility complex; MHC; class I; class II; antigen presentation; inhibition; CD8-positive; CD4-positive; T cell; transplant; gene therapy; immunosuppressive; fusion; DL6.
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibiting recognition of cellular tissue by {\rm CD8+} and {\rm CD4+} T cells, treat or prevent autoimmune diseases, and to improve gene therapy, comprises introducing human cytomegalovirus US2 protein into cells
                             .;
0
  Length 49;
                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                     1..21
/label= Bee_mellitin_signal_peptide
  94.4%; Score 102; DB 21; 100.0%; Pred. No. 3.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Single glycine spacer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hegde NR;
                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Soluble_US2_protein
                             Mismatches
                                                                                                                                                                                                                                     Cytomegalovirus US2t-DL6 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= DL6_epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 12; Page 49; 53pp; English.
                                                                                                                                                      AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boname J,
                                                                                                                                                                                                                                                                                                                   Chimeric - Human cytomegalovirus.
Chimeric - Apis sp.
Chimeric - Homo sapiens.
Chimeric - Synthetic.
                                                                                                                                                    AAY97249 standard; Protein; 177
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                                                                    1 MKFLVNVALVFMVVYISYIYA
                                                                                                                                                                                                           (first entry)
Query Match 94.4
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159..177
                                                                                                                                                                                                                                                                                                                                                                                                                               22..157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-506069/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200046361-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-AUG-2000
                                                                                                                                                                               AAY97249;
                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
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The present sequence is the honey bee (Apis melifica) melittin excretion peptide. It may be used in the Aedes aegypti Densonucleosis virus (AeDNV) based vectors of the invention to aid vector propagation, isolation and subcloning. AeDNV based vectors, esp. confg. the p61, p0.5 and p7 promoters are useful for targeting heterologous proteins to the
chains, and optionally DM-alpha chains. US2 has a double inhibitory chains, on the MHC class II pathway, inhibiting recognition of cellular tissue by CDB-positive and CD4-positive T cells. US2 or its soluble variants, can be used to reduce inappropriate immune responses. The US2 protein can be used to improve the persistence of a virus. Vectors encoding soluble US2 protein (residues 28-143) can be used to improve the persistence of a virus. Vectors autoimmune disease, especially where it is mediated by MHC II molecules. The vector can also be used to improve gene therapy, and preferably also contains a sequence encoding a therapeutic product. The protein is exogenously supplied or expressed from a recombinant cell, and may also be used to inhibit CD4-positive mediated immune responses, transplant immune responses and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression system; promoter; p61; p0.5; p7; heterologous protein; production; vector; cassette.
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gene expression system in insect cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carlson JO, Higgins DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.4%; Score 102; DB 21;
100.0%; Pred. No. 1.2e-08;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (RESE ) RESEARCH CORP TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Honey bee melittin excretion peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR99533 standard; peptide; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKFLVNVALVFMVVYISYIYA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95WO-US14170.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Afanasiev BN, Beaty B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-251772/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 21, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                    immune responses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apis melifica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9614423-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR99533;
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AAR99533
AAR99533
AC AAR9
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The invention relates to the use of a Aedes aegypti densonucleosis virus (AeDNV) as a heterologous gene expression system. A recombinant protein using the vectors of the invention can be produced by a method that comprises (1) transfecting an insect cell that stably expresses AeDNV comprises (1) transfecting an insect cell that stably expresses AeDNV structural proteins vpl and vp2 with an expression comprising the comprising an AeDNV promoter linked to a sequence coding for the protein comprising an AeDNV promoter linked to a sequence coding for the protein and with an expression vector comprising the AeDNV nonstructural proteins NSI and NS2 encoding genes; (2) obtaining infectious virions from the transfected cell; (3) infecting a second insect cell with the virions; culturing the second cell under conditions such that the protein is expressed, and (4) recovering the protein from the second cell under conditions from the second cell. Aedes albopictus Cépás cells can be transfected with AeDNV vectors without allocations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytopathic effects. The present sequence represents a honey bee cytopathic effects. This signal peptide can be used in the AeDNV mellitin excretion peptide. This signal peptide can be used in the AeDNV expression vectors for secretion or nuclear localisation.
                                                                                                                                                                                                                                                      AeDNV; Aedes DNV; densonucleosis virus; gene expression; recombinant; structural protein; VP1; VP2; promoter; nonstructural protein; NS1; NS2; virion; transfection; cytopathic; honey bee; excretion peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant protein production in mosquito cells - using Aedes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 97; DB 20; Length 21
Pred. No. 7.9e-09;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Higgins DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (RESE ) RESEARCH CORP TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Afanasiev BN, Beaty BJ, Carlson JO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       densonucleosis virus expression system
                                                                                                                                                                                                                             Honey bee melittin excretion peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Column 6; 23pp; English.
                                                                                                                       AAW87499 standard; peptide; 21 AA.
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95US-0485341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0485341.
94US-0334669.
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Matches 20; Conserv
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Gaps

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Indels

Length 177;

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Thibault KJ;

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Gaps

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89.8%; Score 97; DB 17; L4 95.2%; Pred. No. 7.9e-09; iive 1; Mismatches 0;

Conservative

Query Match Best Local Similarity Matches 20; Conserv

Length 21;

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colitis; pneumonia; cystic fibrosis.
                                                                                                                                                                           WPI; 1998-399067/34.
N-PSDB; AAV45274.
                                                                                                                                                                                                                                                                                                                                                                                                                  26 AA;
                                            W09830592-A1
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                                                                                        09-JAN-1998;
                                                                                                             10-JAN-1997;
                                                                                                                                                       Fitchen JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-APR-1999.
                                                                  16-JUL-1998
                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                              fibrosis
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                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a secretion signal from the plasmid pMelBac which is used in a method involving the construction of a target molecule from human J chain protein fragments. This construct is used in a method to target imaging agents to epithelial surfaces at which they may remain or undergo transeptthelial transport via transcytosis. At least one imaging agent is linked to the targeting molecule comprising a polypeptide that (a) forms a closed covalent loop, (b) contains at least 3, preferably 4, peptide domains having beta-sheet character separated by domains lacking beta-sheet character and (c) is not full length dimeric 19A. The imaging agents are useful in the diagnosis of disease. The target molecule is also capable of specifically binding to a basolateral factor associated with an epithelial surface to cause internalisation of a biological agent linked to the target molecule.
                                                                                                 Target; imaging agent; epithelium; transepithelial transport; diagnosis;
transcytosis; disease; basolateral; internalisation; J chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J chain; targeting molecule; epithelial; beta-sheet; asthma; cancer; inflammatory disorder; autoimmune disorder; celiac disease;
                                                                                                                                                                                                                                                                                                                        New epithelial tissue targeting agent - used to deliver imaging agents to an epithelial surface for internalisation; useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Targeting molecule secretion signal and multiple cloning site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 93.5; DB 19;
Pred. No. 3.5e-08;
); Mismatches 0;
                                                                           pMelBac secretion signal peptide motif.
                                                                                                                                                                                                                                                                                                                                                                     Example 1c; Page 89; 118pp; English.
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         AAW64613 standard; Protein; 26 AA
                                                                                                                                                                                                                                                                   Hiatt AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKFLVNVALVFMVVYISYIYAD 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.6%;
95.5%;
                                                                                                                                                                                                 98WO-US00339
                                                                                                                                                                                                                      97US-0782480
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                                                     03-NOV-1998 (first entry)
                                                                                                                                                                                                                                            (EPIC-) EPICYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                 Fitchen JH, Hein MB,
                                                                                                                                                                                                                                                                                        WPI; 1998-399066/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 AA;
                                                                                                                                                                                                                                                                                                  N-PSDB; AAV49671
                                                                                                                                                     WO9830591-A1
                                                                                                                                                                                                                      .0-JAN-1997;
                                                                                                                                                                                                 09-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-0CT-1998
                                                                                                                                                                           16-JUL-1998
                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                               diagnosis
                               AAW64613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW61590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW61590
AAW64613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
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The secretion signal and multiple cloning site are used in the assembly of a targeting molecule (TM). The TMs are used to target biological agents to epithelial surfaces at which they can be internalised. The TMs comprise a polypeptide that: (a) forms a closed covalent loop; (b) contains at least 3, preferably 4, peptide domains having beta-sheet character separated by domains lacking beta-sheet character; and (c) is not full length dimeric IgA. The TMs are useful to prevent and/or treat diseases associated with epithelial surfaces, e.g. asthma, cancer, (myco)bacterial, viral or fungal infection, inflammatory disorders, autoimmune disorders, celiac disease, colitis, pneumonia and cystic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epithelial cell; cancer; treatment; therapy;
non-small cell lung carcinoma; breast carcinoma;
ovarian carcinoma; prostate carcinoma; endometriosis;
viral infection; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Targeting molecule; J chain; immunoglobulin; IgM; IgA; substrate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 26;
                                                                                                                                                                                                                                                                                                                                    New epithelial tissue targeting agent - used to deliver biologically active compounds to an epithelial surface for internalisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.6%; Score 93.5; DB 19; 95.5%; Pred. No. 3.5e-08; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Secretion signal and multiple cloning site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 44; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW85766 standard; Peptide; 26 AA.
                                                                                                                                                                                            Hiatt AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKFLVNVALVFMVVXISYIYAD 22
98WO-US00542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US22304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                           (EPIC-) EPICYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 95.5'
                                                                                                                                                                                            Hein MB,
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ï

McGuire TC;

Ganta RR, Mahan SM,

Burridge MJ,

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MAP2; major antigenic protein 2; rickettsia; DNA vaccine.
                                                                                                                                                                                                                                                                                Ehrlichia canis major antigenic protein 2 (MAP2).
                                                                                                                                                                                                                                                     AAW51098 standard; Protein; 205 AA.
                                                                                                                                                                                                                   1 MKFLVNVALVFMVVYISYIYAD 22
                                                                                                                                                                                                                         1 mkflvnval-fmvvyisyiyad 21
                                                                                                                                                                                                 Query Match
Best Local Similarity 95.5
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                     (UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                                      Ehrlichia canis.
                                                                                                                                                                                                                                                                                                               WO9816554-A1.
                                                                                                                                                                                                                                                                                                                                            17-0CT-1996;
                                                                                                                                                                                                                                                                                                                                  17-0CT-1997;
                                                                                                                                                                                                                                                                         14-SEP-1998
                                                                                                                                                                                                                                                                                                                         23-APR-1998,
                                                                                                                                                                                                                                                               AAW51098;
                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                  AAW51098
                                                                                                                                                                                                                                              RESULT
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Gaps ;;

Indels

Mismatches

96US-0733230.

(first entry)

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This polypeptide comprises the major antigen protein 2 gene (MAP2) of Ehrlichia canis. It is encoded by the MAP2 gene (see AAV07181). A claimed composition comprises a nucleic acid (see AAV07184). encoding a polypeptide (see AMV87188-99) that elicits a protective immune response against a rickettsial pathogen. The nucleic acid is used, in human or veterinary medicine, in vaccines to protect against Rickettsia, Ehrlichia, Anaplasma and Cowdria species. The nucleic acid dose not replicate in the host but remains episomal and capable of expressing polypeptide for at least 19 mth. The Ehrlichia antigenic polypeptides can also be used diagnostically to detect antibodies associated with Ehrlichia infection (claimed).
                                                                                                                                                                         Composition containing nucleic acid encoding rickettsial antigen useful for, e.g. stimulating protective immune response in humans or
                                                                                                                                                                                                                                                                                                            Claim 3; Fig 3A; 39pp; English.
                         Barbet AF, Burridge MJ
Nyika A, Rurangirwa FR;
                                                                                                          WPI; 1998-251232/22.
                                                                                                                                      N-PSDB; AAV07181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                animals
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                          cells, particularly for delivery of enzymes, binding agents, inhibitors, nucleic acids, carbohydrates and lipids, is new.

The targeting agent comprises a polypeptide which forms a closed covalent loop and contains a least three peptide domains having covalent loop and contains. The targeting molecule preferably lacking beta-sheet character. The targeting molecule preferably comprises all or a portion of a native J chain sequence. J chain comprises all or a portion of a native J chain sequence. J chain comprises all or a portion of a native J chain sequence. J chain comprises all or a portion of an entire J chain sequence. J chain composition of at least one biological agent which is capable of entering and the propolarised epithelial cell. The targeting molecule may be linked to the biological agent by a substrate for an intracellular or extracellular enzyme which is associated with or intracellular encounted by the non-polarised target cell. The targeting molecule can be used in a pharmaceutical composition for treating a patient carlinoma and endometricals composition for treating a patient carlinoma and endometricals, viral infection or inflammatory carcinoma, continummatory construction of target molecules described.

Construction of target molecules described.
                                                                                                                                                                                                                                                                          Targeting molecule useful in drug delivery for treating cancer, viral infection or inflammatory disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 93.5; DB 20;
Pred. No. 3.5e-08;
0: Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 43; 102pp; English
                                                                                                                                         Hiatt AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.68;
                  97US-0954211
                                                                              (EPIC-) EPICYTE PHARM INC.
                                                                                                                                             Hein MB,
                                                                                                                                                                                                  WPI; 1999-288174/24.
N-PSDB; AAX08824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 AA;
                            20-0CT-1997;
                                                                                                                                             Fitchen JH,
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50.9%; Score 55; DB 19; Length 205; 40.0%; Pred. No. 0.31; tive 7; Mismatches 5; Indels
                                                                                                                                                                                                          Search completed: January 29, 2002, 10:59:20 Job time: 2244 sec
                                                                                                                    4 ikfilnvcllfaaiflgysy 23
                                                                                            1 MKFLVNVALVFMVVYISYIY
             Query Match
Best Local Similarity 40.0
Matches 8; Conservative
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; 0

Gaps

; 0

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Search time 1760.55 Seconds (without alignments) 55.199 Million cell updates/sec
                                                                                                                                                                      1923
1 MKFLVNVALVFMVVXISYIY......DFFGISYYEKVLAKYKDDLE 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /ptcdata/2/paa/US097_COMB.pep:*/ptcdata/2/paa/US098_COMB.pep:*/ptcdata/2/paa/US099_COMB.pep:*/ptcdata/2/paa/US099_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/2/paa/US095_COMB.pep:*
/cgn2_6/ptodata/2/paa/US096_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                               3148936 seqs, 277657034 residues
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                                                                                            ٠.
                                                                                         January 29, 2002, 10:16:04
                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                         Pending_Patents_AA_Main:*
                                                                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                       US-09-763-397A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/1
                                                                                                                                                                                                                   BLOSUM62
                                                                                                                                                                    Perfect score:
                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
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                                                                                                                                                                                                                                                               Searched:
                                                                                         Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Sequence 2, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 18, Appl	Sequence 1, Appli	Sequence 2, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 8, Appli
SUMMARIES			ID	US-09-763-397A-2	US-07-677-539B-6	US-07-727-636-6	US-08-948-885-18	US-08-932-929A-1	US-07-842-694-2	US-09-125-031-8	US-09-125-031A-8	US-09-134-333-8
			DB	21	٣	m	13	13	m	12	12	15
			Length	350	412	412	412	423	424	127	127	127
	æ	Query	e Match Length DB ID	100.0	11.2	11.2	11.2	10.9	10.9	10.9	10.9	10.9
			Score	1923	215.5	215.5	215.5	210.5	210.5	210	210	210
		Result	NO.	-4	7	m	4	'n	9	7	80	6

5, A 31, 3,	, , , , , , , , , , , , , , , , , , ,	Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli	, , , , , , , , , , , , , , , , , , ,	Sequence 9, Appli Sequence 12, Appl Sequence 10, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli
677-539B- 727-636-5- 820-843A- 760-797- 932-929-	55	15 US-09-101-316-2 15 US-09-125-0318-2 15 US-09-125-0318-2 15 US-09-134-333-2 15 US-09-125-0318-10 15 US-09-125-0318-10 15 US-09-125-0318-10 15 US-09-124-333-10	US-09-12 US-09-12 US-09-12 US-09-13 US-09-13 US-09-12	15 US-09-1.75-683B-9 15 US-09-1.75-683-1.2 15 US-09-1.75-683B-1.0 17 US-09-311-817-2 19 US-09-500-376-8 9 US-08-593-006-2 15 US-09-117-415-2
3388 3388 4224 4224	4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	10000000000000000000000000000000000000	116 116 116 127 127 355	355 361 376 384 594
10.8 10.8 10.8 10.8	100.0 100.7 100.6 100.6	10.3	100.333333	7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.
208.5 208.5 207.5 207.5 207.5	207.200.5 206.5 206.5 200.5 200.5 200.5	198.5 198.5 198.5 198.5 198.5	198.5 198.5 198.5 196.5 196.5	196.5 196.5 196.5 196.5 196.5
. 112	18 118 20 20 30 30	2 2 2 2 2 4 3 3 2 9 8 4 3 3 9 9 8 4 3 9 9 8 4 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	. 3 3 3 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5	8 4 4 4 4 4 9 0 4 5 6 7 8 9 8

ALIGNMENTS

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Sequence 2, Application US/09763397A
GENERAL Introdument of the United States of America, as represented by the APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the Department of Health and Human Services, Centers for APPLICANT: Control and Prevention
APPLICANT: Control and Prevention
APPLICANT: Altaf A.
APPLICANT: Ping Shi, Ya
APPLICANT: Hasain, Seyed E.
TILE REFERENCE: 6395-57049
CURRENT APPLICANTON NUMBER: US/09/763, 397A
CURRENT PAPLICATION NUMBER: US/09/097, 703
PRIOR PRILING DATE: 1999-08-19
PRIOR PLILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
CORPHARE: Patentin Version 3.1
SOFTWARE: Patentin Version 3.1
CRGANISM: Artificial Sequence
FEATURE:
PEATURE:
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29 KH-----KKLKQPGDGNPWSPCSVTCG-------KPKDELDYENDIEKKICKME 70
                                                                                                                                                                                                                     Sequence 6. Application US/07727636
GENERAL INFORMATION:
APPLICANT: LALTAF A.
APPLICANT: GOLDMAN, IRA F.
TITLE OF INVENTION: CIRCUMSPOROZOITE PROTEIN OF PLASMODIUM
TITLE OF INVENTION: REICHENOWI AND VACCINE FOR HUMAN MALARIA
NUMBER OF SEQUENCES: 54
CORRESPONDENCE S:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.2%; Score 215.5; DB 3; Length 412; ilarity 62.2%; Pred. No. 2.8e-10; Conservative 2; Mismatches 7; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18, Application US/08948885
GENERAL INFORMATION:
APPLICANT: Jessell, Thomas M. and Avihu Klar
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
TITLE OF INVENTION: OVUEL SECRETED PROTEIN, F-SPONDIN
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER KEAUADLE. Floppy disk
COMPUTER: TBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
FILING DATE: 19910710
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REPERSONCE/DOCKET NUMBER: 5683/91540
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
FENCTH: 412 amino acids
                                                                                                                                                                                                                                                                                                                                               STREET: 1615 L STREET, N.W. CITY: WASHINGTON
KH-----KKLKQPGDGNPWSPCSVTCG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ss: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide US-07-727-636-6
                                                                                                       388 KCSSVFNVVNSSIG 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11111111111 1 1 388 KCSSVFNVVNSSIG 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                             71 KCSSVFNVVNSNSG 84
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Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
US-08-948-885-18
                                                                                                                                                                                    RESULT 3
US-07-727-636-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                QΩ
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                                                                                                                                                                                                       61 DIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLLEDSGSNGKKITCECTKPDSKP 120
                                                                                                                            61 DIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLLEDSGSNGKKITCECTKPDSKP 120
                                                                                                                                                                               121 IVQYDNFNANPNANPNANPDGNCEDIPHVNEFSAIDLGNAEKYDKMDEPQHYGKSLTPLE 180
                                                                                                                                                                                                                                                                 ELYKPNDKSLYQYIKANSKFIGITELSNTFINNAGQHGHMHGNEREDERTLTKEYEDIVL 240
                                                                                                                                                                                                                                                                                         241 KEFTYMINFGRGONYWEHPYQKSDQPKQYEQHLTDYEKIKEGKPLDKFGNIYDYHYEHSS 300
                                                                                                                                                                                                                                                                                                                                                                           1 MKFLVNVALVFMVYISYIYADHHHHHHHKKKKKQPGDGNPWSPCSVTCGKPKDELDYEN 60
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                     1 MKFLVNVALVFMVVISYIYADHHHHHHHKHKKLKQPGDGNPWSPCSVTCGKPKDELDYEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2

US-07-677-539B-6

Sequence 6, Application US/07677539B

GENERAL INFORMATION:

APPLICANT: LAL, ALTAF A.

APPLICANT: GOLDAN, IRA F.

TITLE OF INVENTION: REICHENOWI AND VACCINE FOR HUMAN MALARIA NUMBER OF SEQUENCES: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 215.5; DB 3; Length 412;
Pred. No. 2.8e-10;
2; Mismatches 7; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 PSSTKSSSPSNVKSASLATRLMKKFKAEIRDFFGISYYEKVLAKYKDDLE 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:

ZIP:
ZOUNTRY:
ZOUGE
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppd disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETENTIN Release #1.0, Version #1.25
CURREW APPLICATION DATA:
FILING DATE: 19911205
CLASSIFICATION: 424
ATTORREY/AGENT INFORMATION:
NAME: SCOTT, WATSON T
REGISTRATION NUMBER: 26,581
REFERENDE/COCKET NUMBER: 5683/91540
TELECHONE: 202.861-3067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: OUSHWAN, DARBY & CUSHWAN STREET: 1615 L. STREET, N.W. CITY: WASHINGTON STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.2%;
62.2%;
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AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 11.2
Best Local Similarity 62.2
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: peptide US-07-677-539B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                               181
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COFTWARENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/842,694
FILING DATE: 19920227
CLASSIFTCATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Canter, Carol G.
REGISTRATION NUMBER: 31151
REFERENCE/DOCKET UNBER: 845015
: INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                             10.9%; Score 210.5; DB 1 63.4%; Pred. No. 8.4e-10; tive 1; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cohen, Joseph
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: Malaria Vaccine Antigen
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: SmithKline Beecham Corporation
STREET: P.O. Box 1539 / Corporate Patents
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 KH----KKLKQPGDGNPWSPCSVTCG------
                                                                                                                                                         B45015-1FWC2
                                                    APPLICATION NUMBER: 08/663,371
FILING DATE: 13-JUNE-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
FELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/07842694 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
  18-SEPT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 424 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
COMPUTER: IBM PC COMPA
OPERATING SYSTEM: PC-D
                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 63.4
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                  single
                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 KCSSVFNVVNS 192
                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
US-08-932-929A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 KCSSVFNVVNS 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ANTI-SENSE: NO
US-07-842-694-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
US-07-842-694-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13; Length 412;
                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1. Application US/08932929A

GENERAL INFORMATION:
APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: Hybrid Protein Between CS
TITLE OF INVENTION: Hybrid Protein Between CS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKilne Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2.2...,
Pred. No. 2.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRI.

ZIP: 19406
COMPUTER READABLE FORM:
MEDIUW TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFFWARE: FESTSEE for Windows Version 2.0
                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/313,288
FILING DATE: January 5, 1995
ATORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 11.2%; Score 215.5; Best Local Similarity 62.2%; Pred. No. 2.8 Matches 46; Conservative 2; Mismatches
                  ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 412 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: peptide US-08-948-885-18
                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                          New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                      FILING DATE
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US-08-932-929A-1
                                                                          STATE: No COUNTRY:
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RESULT 9

US-09-134-333-8

Sequence 8. Application US/09134333

Sequence 8. Application US/09134333

Sequence 8. Application US/09134333

APPLICANT: LONGACRE-ANDRE, SHIRLEX

APPLICANT: NATO, FARIDABANO

APPLICANT: BARNWELL, JOHN

APPLICANT: BARNWELL, JOHN

APPLICANT: BARNWELL, JOHN

TITLE OF INVENTION: RECOMBINANT PROFEIN CONTAINING A C-TERMINAL FRAGMENT OF FILE REFERENCE: 0660-0135-0XCIP

FILE REFERENCE: 0660-0135-0XCIP

FILE REFERENCE: 1999-04-18

EARLIER APPLICATION NUMBER: PCT/FR97/00290

EARLIER FILING DATE: 1999-04-14

EARLIER FILING DATE: 1996-02-14

NUMBER OF SEQ ID NOS: 14

SECTION NO 9

LEMANNEL PATENTIN OF TO SET OF T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 ALVFMVVYISYIYADHHHHHHHHHKHKKLKQPGDGNPWSPCSVTCGKPKDELDYENDIEKKIC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 KMEKCSSVFNVNSNSGCFRHLDEREECKCLL------99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 ALVEMVYISYIYADHHHHHHHHKHKKLKQPGDGNPWSPCSVTCGKPKDELDYENDIEKKIC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 ALLELFSFIFFVTKEFNISQHQCVKKQCPEFFN-------ISQHQC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 KMEKCSSVFNVVNSNSGCFRHLDEREECKCLL-------99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 VKKQCP-----ENSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADA 94
                                                                                                                                                                                                                                                                                                                                                                                                                              ; DB 15; Length 127;
1.6e~10;
thes 23; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 33.6%; Pred. No. 1.6e
Matches 49; Conservative 14; Mismatches
PRIOR APPLICATION NUMBER: PCT/FR97/00290
PRIOR FILING DATE: 1997-02-14
PRIOR PELICATION NUMBER: FR96/01822
PRIOR FILING DATE: 1996-02-14
NUMBER OF SEQ ID NOS: 15
SOGTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LIENGTH: 127
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 ----EDSGSNGKKITCECTKPDSKPI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-09-134-333-8
                                                                                                                                                                                                                                                                                                    ; ORGANISM: Plasmodium falciparum
US-09-125-031A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/09125031
Sequence 8, Application US/09125031
GENREAL INFORMATION:
APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: ROTH, CHARLES
APPLICANT: ROTH, CHARLES
TAPLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF TITLE OF INVENTION: PASADOLUM MSP-1
FILE REFERENCE: 0660-0139-0XPCT
CURRENT APPLICATION NUMBER: US/09/125,031
CURRENT APPLICATION NUMBER: PCT/FR97/00290
EARLIER APPLICATION NUMBER: PCT/FR97/00290
EARLIER PILING DATE: 1999-03-10
EARLIER FILING DATE: 1999-02-14
SEALIER FILING DATE: 1996-02-14
SOFTWARE: PALENTIN OFF: 12
SEALIER FILING DATE: 1997-02-14
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GUNERAL INCRMATION:
APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: BARNWELL, OGNIN
APPLICANT: BARNWELL, OGNIN
APPLICANT: MATO, FARINBANO
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: PLASMODIUM MS-1
FILE REFERENCE: 0660-0139-0XRCT
CURRENT APPLICANTON NUMBER: US/09/125,031A
CURRENT FILING DATE: 1999-03-10
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                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                       ---KPKDELDYENDIEKKICKME 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 KMEKCSSVFNVVNSNSGCFRHLDEREECKCLL------------------99
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                                                                                                                                        19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90;
                                                                         Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.9%; Score 210; DB 15; Length 127; Best Local Similarity 33.6%; Pred. No. 1.6e-10; Matches 49; Conservative 14; Mismatches 23; Indels 66
                                                                      Score 210.5; DB 3; Length 4
Pred. No. 8.4e-10;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 ----EDSGSNGKKITCECTKPDSKPI 121
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                                                                                                                                                                                                       29 KH----KKLKQPGDGNPWSPCSVTCG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LENGTH: 127
TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-09-125-031-8
                                                                         Query Match
Best Local Similarity 63.4%;
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                              183 KCSSVFNVVNS 193
                                                                                                                                                                                                                                                                                                                                         71 KCSSVFNVVNS 81
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US-09-125-031A-8
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APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PRO
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REPERENCE: 063915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILIG DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 HHHKHKKLKQPGDGNPWSPCSVTC-----GKPKDELDYENDIEKKICKMEKC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 388;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
          CORPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BALGHIUN Release #1.0, Version #1.25
SOFTWARE PAREILCATION DATA:
APPLICATION NUMBER: US/07/727,636
ATTONEN WATSON TO CLASSIFICATION: 424
ATTONEN PATSON TO TO THE REGISTRATION NUMBER: 26,581
REGISTRATION NUMBER: 26,581
REGISTRATION NUMBER: 26,581
REGISTRATION NUMBER: 26,381
REGISTRATION NUMBER: 26,281
REGISTRATION NUMBER: 20,281
REGISTRATION NUMBER: 20,281
REGISTRATION NUMBER: 20,281
REGISTRATION NUMBER: 20,381
TELEFAX: 20,281
TELEFAX: 20,281
TELEFAX: 20,281
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 208.5; DB 3;
Pred. No. 1.1e-09;
4; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature

CTHER INFORMATION: Circumsporozoite (CS) protein

NAME/KEY: misc_feature

CTHER INFORMATION: gi|4493889

US-09-820-843A-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----GNPWSPCSVTCG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.8%; Score 207.5; DB 2
51.8%; Pred. No. 1.4e-09;
Live 4; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-820-843A-31; Sequence 31, Application US/09820843A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 IEKKICKMEKCSSVFNVVNSNSG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.8%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I Similarity 51.8%;
43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 10.89
Best Local Similarity 58.39
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           sə: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 KHKKLKQPGD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: peptide US-07-727-636-5
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  366 SSVFNVVNSSIG 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 SSVFNVVNSNSG 84
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Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 31
LENGTH: 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
                                                   Sequence 5, Application US/07677539B
GENERAL INFORMATION:
APPLICANT: LAL, ALTAF A.
APPLICANT: GOLDMAN, IRA F.
TITLE OF INVENTION: CIRCUMSPOROZOITE PROTEIN OF PLASMODIUM
TITLE OF INVENTION: REICHENOWI AND VACCINE FOR HUMAN MALARIA
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-727-636-5
Sequence 5, Application US/07727636
Sequence 5, Application US/07727636
Sequence 5, Application:
APPLICANT: LALA ALTAF A.
APPLICANT: GOLDMAN, IRA F.
TITLE OF INVENTION: CIRCUMSPOROZOITE PROTEIN OF PLASMODIUM
TITLE OF INVENTION: REICHENOWI AND VACCINE FOR HUMAN MALARIA
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3; Length 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                              COMPUTE: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: LIBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/07/677,539B
FILING DATE: 19911205
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET UNMBER: 26,581
REFERENCE/DOCKET UNMBER: 26,581
RELEPHONE: 202-861-3067
TELEPHONE: 202-861-3067
TELEPHONE: 202-894
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nes 13;
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Pred. No. 1.1e-
4; Mismatches
                                                                                                                                                                  ...UNKESSEE: CUSHWAN, DARBY & CUSHWAN STREET: 1615 L STREET, N.W. STATE: D.C. COUNTRY: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: CUSHMAN, DARBY & CUSHMAN STREET: 1615 L STREET, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 388 amiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 58.3%;
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
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366 SSVFNVVNSSIG 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20036
                                  US-07-677-539B-5
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APPLICANT: Slaoui, Moncef
APPLICANT: Wijendale, Frans
TITLE OF INVENTION: VACCINE FORMULATIONS CONTAINING
TITLE OF INVENTION: VACCINE FORMULATIONS CONTAINING
TITLE OF INVENTION: 3-O-DEACYLATED MONOPHOSPHORYL LIPID A AND A CARRIER
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SuithKline Beecham Corporation
STREET: 709 swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08932929
GENERAL INFORMATION:
APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION:
TITLE OF INVENTION: PLASMODIUM AND HBAGG
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADERESS:
ADDRESSEE: Smithkline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: PO. BOx 1539 - UW2220
CITY: King of Prussia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS SOFTWARE: FESTSED FOR WINDOWS VERSION 2.0 SOFTWARE: FESTSED FOR WINDOWS VERSION 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/903,084
FILING DATE: 17-JUL-1997
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: 08/741,575
FILING DATE: 30-CCT-1996
APPLICATION NUMBER: 08/303,542
FILING DATE: 09-SEP-1994
FILING DATE: 09-SEP-1994
ATYORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 KHKKLKQPGD------GNPWSPCSVTCG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Kerekes, Zoltan
REGISTRATION NUMBER: 38,938
REFERENCE/DOCKET NUMBER: B451
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 IEKKICKMEKCSSVFNVVNSNSG 84
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                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 424 amino acids amino acid
                                                                                                                                                                                                           STREET: 709 smc...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-903-084-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                          19046
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                                                                                                                                                                                                                                                                                                               COUNTRY:
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US-08-932-929-3
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                                                                                                                                                                                                                                         APPLICANT: De Wilde, Michel
APPLICANT: Chen, Joseph
TITLE OF INVENTION: HYBRID PROTEIN BETWEEN CS FROM
TITLE OF INVENTION: HASMODIUM AND HBSAG
NUMBER OF SEQUENCES:
ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 - UW2220
CITY: King of Prussia
STATE: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Pennsylvania
COUWTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATUS SYGTEM: PC COMPATIBLE
OPERATUS POPULCATION DATA:
APPLICATION UNBER: US/08/760,797
FILING DATE: 17-MAY-1995
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: US 08/244,085
FILING DATE: 17-MAY-1994
CLASSIFICATION WUMBER: B45015C1
FILING DATE: STORTE STORTE
APPLICATION NUMBER: B45015C1
TELECOMMUNICATION HOROMATION:
TELECOMU
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Pred. No. 1.6e-09;
4; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---GNPWSPCSVTCG----
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US-08-903-084-3
Sequence 3, Application US/08903084
SEPLICANT: BRUCK, Claudine
APPLICANT: Francotte, Myriam
APPLICANT: Kummert, Suzanne
                                                                                                                                                      US-08-760-797-3
; Sequence 3, Application US/08760797
; GENERAL INFORMATION:
          363 IEKKICKMEKCSSVFNVVNSSIG 385
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51.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: Si
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Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: ILOPY disk
COMPUTER: ELOPY disk
COMPUTER: ELOPY disk
COMPUTER: IS M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,371
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/663,371
FILING DATE: 21-OCT-1994
ATTORNEY/AGENT INFORMATION:
FILING DATE: 21-OCT-1994
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: B45015-1
TELECOMMUNICATION INPORMATION:
TELEFAX: 610-270-5096
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acid
STRANDEDNESS: 3ingle
TOPOLOGY: linear
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Query Match 10.8%; Score 207.5; DB 13; Length 424; Best Local Similarity 51.8%; Pred. No. 1.6e-09; Matches 43; Conservative 4; Mismatches 9; Indels 27; Gaps

29 KHKKLKQPGD-----KPKDELDYEND 61

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Search completed: January 29, 2002, 10:55:58 Job time: 2394 sec

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Appli Appli Appli Appli Appli Appli Appli

Appl

Sequence

Sequence Seq

us-09-763-397a-25.rai

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APPLICANT: Cech, Thomas R.
APPLICANT: Clayner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBRE OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUMTY: USA ZIP: 94111-3834 COMPUTER READBLE FORM: MEDIUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
FILING APPLICATION NUMBER: US 08/846,017
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION NUMBER: US 08/854,050
FILING DATE: O9-MAY-1997
PRIOR APPLICATION NUMBER: US 08/854,050
FILING DATE: O9-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/974,549A FILING DATE: 19-NOV-1997 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 613, Application US/08974549A; Patent No. 6166178; GENERAL INFORMATION:
   1085
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1297
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4411.7
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37.0
36.1
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US-08-974-549A-613
   800128459786644444
800128459786012845
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Sequence 36, Appl
Sequence 2, Appli
Sequence 2, Appli
                                                                                                                January 29, 2002, 10:59:58 ; Search time 32.24 Seconds (without alignments) 15.356 Million cell updates/sec
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/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-960-190A-36

US-08-314-62

US-08-782-480-43

US-08-953-326-23

US-08-953-326-24

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US-08-953-326-24

US-08-953-326-24

US-08-978-741-6

US-08-378-741-6

US-08-378-741-6

US-08-378-741-6

US-08-378-741-6

US-08-485-588-7

US-08-485-588-7

US-08-485-588-7

US-08-485-58-7

US-08-485-58-7

US-08-481-7198-7

US-08-481-55-8

US-08-353-744-7

US-08-481-58-8

US-08-481-58-8
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Maximum Match 100%
Listing first 45 summaries
                                                                                 OM protein – protein search, using sw model
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1 MKFLVNVALVFMVVYISYIYAD
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Fatent No. 5627048
GENERAL INFORMATION:
APPLICANT: Higgins, David R.
APPLICANT: Aligalis, David R.
APPLICANT: Annasiev, Boris N.
APPLICANT: Carlson, Jonathan O.
APPLICANT: Annasiev, Berry
TITLE OF INVENTION: AEDES AEGYPTI DENSOVIRUS EXPRESSION
ITTLE OF INVENTION: SYSTEM
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
COTTY: Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 94.4%; Score 102; DB 4; Length 21; Best Local Similarity 100.0%; Pred. No. 1e-09; Matches 21; Conservative 0; Mismatches 0; Indels
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COUNTY: United States
ZIP: 11530
COMPUTER READBLE FORM
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
CORPUTER: IBM PC COMPALIBLE
COMPUTER: DATENT PC-DOS/MS-DOS
SOFTWARRE: PatentIn Release #1.0, Version #1.25
SOFTWARRE: PatentIn Release #1.0, Version #1.25
SOFTWARRE: DATENT DATENT
       FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: COLIESS, PETER F
REGISTRATION NUMBER: 33,860
REFREENCE/DOCKET NUMBER: 48002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                    36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKFLVNVALVFMVVYISYIYA 21
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                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-960-190A-36
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                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
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melittin signal sequence and full length
hTRT protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 36, Application US/08960190A
Fatent No. 623246;
GENERAL INFORMATION:
APPLICANT: Acceded, Jorge
APPLICANT: Acceded, Jorge
APPLICANT: Jiao, Jin-an
APPLICANT: WWONTYON: SOLUBLE MHC COMPLEXES AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SOURNCES: 38
CORRESPONDENCE ADDRESS:
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:

REPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17685
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17685
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: APPLE, RANGOLP, Ted
RESISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/COCKET NUMBER: 36,429
REFERENCE/COCKET NUMBER: 36,429
REFERENCE/COCKET NUMBER: 36,429
REFERENCE/COCKET NUMBER: 415,576-0300
INFORMATION FOR SEQ ID NO: 613:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPELEYN: 1189 amino acids
TYPELEYN: 1189 amino acids
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SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,190A
FILING DATE: 29-OCT-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKFLVNVALVFMVVYISYIYAD 22
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Protein
| LOCATION: 1..1189
| COTHER INFORMATION: N
| OTHER INFORMATION: m
| US-08-974-549A-613
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US-08-960-190A-36
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Length 26;
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Patent No. 6251392
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hiatt, Andrew C.
APPLICANT: Fitchen, John H.
TITLE OF INVENTION: NOVEL EPITHELIAL CELL TARGETING AGENT NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
             APPLICANT: Fitchen, John H.
TITLE OF INVENTION: NOVEL EPITHELIAL TISSUE IMAGING AGENT
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seatile
STATE: Washington
                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE: US/08/782,480
FILING DATE: 10-JAN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
TELECOMMUNICATION: NUMBER: 31,098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 93.5; DB 3;
Pred. No. 2.6e-08;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SED ID NO: 43
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.6%;
95.5%;
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 86.6'
Best Local Similarity 95.5'
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 amino acids
Hein, Mich B
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US-08-954-211-43
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                                       Length 21;
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Pred. No. 6e-09;
                                                                              0; Indels
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SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,341A
FILING DATE: June 7, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 94852-I
TELECOMMUNICATION NUMBER: 94852-I
TELEFHONE: (516)742-4346
TELEFHONE: (516)742-4366
TELEFA: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                           APPLICANT: Afanasiev, Boris N.
APPLICANT: Carlson, Jonathan O.
APPLICANT: Beaty, Barry J.
APPLICANT: Highins, David R.
APPLICANT: Thibault, Kelly J.
TITLE OF INVENTION: AEDES AEGYPTI DENSOVIRUS TITLE OF INVENTION: EXPRESSION SYSTEM NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                     Score 97; DB 1;
Pred. No. 6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-782-480-43
Sequence 43. Application US/08782480
Patent No. 6045774.
GENERAL INFORMATION:
APPLICANT: Hiatt, Andrew C.
                                                                                                                                                                                                                                                                    Sequence 2, Application US/08485341A Patent No. 5849523 GENERAL INFORMATION:
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                                                                                                                                            1 MKFLVDVALVFMVVYISYIYA 21
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ilarity 95.2%;
Conservative
                                   Query Match
Best Local Similarity 95.2%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                        1 MKFLVNVALVFMVVYISYIYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 21 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: SI
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-485-341A-2
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APPLICANT: Mahan, Suman M.

TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
TITLE OF INVENTION: Animals and Humans
FILE OF INVENTION: Animals and Humans
FILE POF INVENTION: ANIMALS: US/08/953,326
CURRENT FILING DATE: 1997-10-17
CURRENT FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER FILING DATE: 1996-10-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTION DATE: 1996-10-17
NUMBER OF SEQ ID NOS: 24
LENGTH: 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and
TITLE OF INVENTION: their Derivatives
FILE REFERENCE: SIN-101 4564/66529
CURRENT APPLICATION NUMBER: US/09/248,588
CURRENT APPLICATION NUMBER: US/09/248,588
EARLIER APPLICATION NUMBER: 0/074537
BARLIER FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 113
SEQ ID NOS: 113
SEQ ID NO ID NOS: 113
SEQ ID NO ID NOS: 110 NOS: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.4%; Score 49; DB 4; Length 305; 55.0%; Pred. No. 2.3; 7; Indels tive 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08978741
Patent No. 610076
GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman; TILE OF INVENTION: O-Fucosyltransferase; NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/09248588; Patent No. 6231864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ), TYPE: PRT
), ORGANISM: Ehrlichia chaffeensis
US-08-953-326-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 FLVNVALVFMVVYISYIYAD 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 FLVTVPLVCTIVYDSCLYMD 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 IKFILNICLLFAAIFLGYSY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT COGGANISM: Hepatitis B virus US-09-248-588-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 55.0%
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
US-09-248-588-11
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US-08-978-741-6
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0S-08-953-326-23

1 Sequence 23, Application US/08953326

2 Patent No. 6.551872

3 GENERAL INFORMATION:

4 APPLICANT: Barbet, Anthony F.

5 APPLICANT: Buridge, Michael J.

5 APPLICANT: Buridge, Michael J.

5 APPLICANT: Buridge, Michael J.

7 APPLICANT: Buringe, Michael J.

7 APPLICANT: Narandiwa, Fred R.

5 APPLICANT: Narandiwa, Fred R.

7 TITLE OF INVENTION: Animals and Humans

7 TITLE OF INVENTION: Animals and Humans

7 TITLE OF INVENTION: NUMBER: US/08/953,326

7 CURRENT APPLICATION NUMBER: US/08/953,326

7 CURRENT PAPLICATION NUMBER: 08/953,326

7 CURRENT PILING DATE: 1997-10-17

8 EARLIER PILING DATE: 1996-10-17

8 EARLIER PILING DATE: 1996-10-17

8 EARLIER PILING DATE: 1996-10-17

8 SOFTWARE: PATENTIN VET: 2.0

8 SOFTWARE: PATENTIN VET: 2.0

8 SOFTWARE: PATENTIN VET: 2.0

8 EARLIER PILING DATE: 1996-10-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.6%; Score 93.5; DB 4; Length 26; 95.5%; Pred. No. 2.6e-08; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 40.0%; Proce 55; DB 4; Length 205;
Best Local Similarity 40.0%; Pred; No. 0.18;
Matches 8; Conservative 7; Mismatches 5; Indels
                                    REFERENCE/DOCKET NUMBER: 310098.403
TELECOMMUNICATION INCORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: UNCORMATION: 1 inear
SECULE TYPE: protein
US-08-954-211-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
US-08-953-326-24
; Sequence 24, Application US/08953326
; Patent No. 6251872
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKFLVNVALVFMVVYISYIYAD 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKFLVNVAL-FMVVISXIXAD 21
                REGISTRATION NUMBER: 31,392
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APPLICANT: Ganta, Roman R.
APPLICANT: McGuire, Travis C.
APPLICANT: Burridge, Michael J.
APPLICANT: Nyika, Aceme
APPLICANT: Nyika, Aceme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKFLVNVALVEMVVXISYIY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 IKFILNVCLLFAAIFLGYSY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 86.6
Best Local Similarity 95.5
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Ehrlichia canis
US-08-953-326-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
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| Sequence 2, Application US/09134513
| Sequence 2, Application US/09134513
| Patent No. 6210964
| Patent No. 6210964
| APPLICANT: Brown, Edward M. APPLICANT: Bai, Mei
| APPLICANT: Bai, Mei
| APPLICANT: Quin, Stephen J. TITLE OF INVENTION: The Avian Extracellular Calcium-Sensing TITLE OF INVENTION: Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1058;
                                Krapcho, Karen J.

Hammerland, Lance G.

WENTION: CHIMERIC RECEPTORS AND METHODS FOR VENTION: IDENTIFYING COMPOUNDS ACTIVE AT VENTION: METBOTROPIC GLUTAMATE RECEPTORS AND VENTION: THE USE OF SUCH COMPOUNDS IN THE VENTION: TREATMENT OF NEUROLOGICAL DISORDERS VENTION: AND DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.7%; Score 45; DB 2;
45.0%; Pred. No. 35;
Live 5; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.

ZIP: 90071-2066
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTERO for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,289A
FILING DATE: July 25, 1996
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/001,526
FILING DATE: July 26, 1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Vinson & Elkins L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 220/004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
                 APPLICANT: Fuller, Forrest H.
APPLICANT: Krapcho, Karen J.
APPLICANT: Krapcho, Karen J.
APPLICANT: Hammerland, Lance G.
TITLE OF INVENTION: IDENTIFYING CO
TITLE OF INVENTION: METABOTROPIC G
TITLE OF INVENTION: METABOTROPIC G
TITLE OF INVENTION: TREATMENT OF N
TITLE OF INVENTION: TREATMENT OF N
TITLE OF INVENTION: TREATMENT OF N
TITLE OF INVENTION: AND DISEASES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
CITY: Los Angeles
COLUMNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   785 KFITFSMLIFFIVWISFIPA 804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1058 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 45.08
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sin
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.4%; Score 49; DB 3; Length 397; 50.0%; Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Plasmid insert encoded protein US-09-333-729A-7
                                     MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genetech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/978,741 CLING DATE: 26-No. 6100076-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: Wang, Yang
APPLICANT: Spellman, Michael W.

APPLICANT: Spellman, Michael W.

TILLE OF INVENTION: O'FUCOSyltransferase;
FILE REFERENCE: P1041P1D1-Substitute
CURRENT APPLICATION WUMBER: US/09/333,729A
CURRENT FILING DATE: 1999-06-15

PRIOR FILING DATE: 1997-11-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-687-289A-5; Sequence 5, Application US/08687289A; Patent No. 5981195
                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/792498
FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                             NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KFLVNVALVFMVVYISYIYA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 KFLVNVALLLLLLLSGAWA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KFLVNVALVFMVVYISYIYA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 397 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Conservative
                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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US-09-333-729A-7
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41.7%; Score 45; DB 1; Length 1078;
45.0%; Pred. No. 36;
Live 5; Mismatches 6; Indels
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Patent No. 576359
GENERAL INFORMATION:
APPLICANT: Bedward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: OALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Stite A 170
STREET: Suite 470
STREET: Suite 470
STREET: Gailfornia
COMMENTION: MOLECULES
STREET: Gailfornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPOTER READABLE FORM:
MEDIUM TYPER: 3.5" Diskette, 1.44 Mb storage
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
               PRILICATION NUMBER: 08/353,/04

RELIGATIONE: December, 1994

RELING DATE: 21 October, 1994

APPLICATION NUMBER: 0.5. 08/392,827

FILING DATE: 23 Aquast, 1994

APPLICATION NUMBER: 0.5. 08/11,248

FILING DATE: 22 October, 1993

APPLICATION NUMBER: 0.5. 08/009,389

FILING DATE: 22 February, 1993

APPLICATION NUMBER: 0.5. 08/017,127

FILING DATE: 23 February, 1993

APPLICATION NUMBER: 0.5. 07/934,161

FILING DATE: 12 February, 1992

APPLICATION NUMBER: 0.5. 07/934,161

FILING DATE: 23 Aquast, 1992

APPLICATION NUMBER: 0.5. 07/934,044

FILING DATE: 23 Aquast, 1991

ATTORNEY-AGENT INFORMATION:

REGISTRATION NUMBER: 38,179

REFERENCE/DOCKET NUMBER: 38,179

REFERENCE/DOCKET NUMBER: 38,179

REFERENCE/COCKET NUMBER: 38,179

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION POR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

SUNDER: Amino acids
PRIOR APPLICATION DATA: described below: APPLICATION NUMBER: 08/353,784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,565
FILING DATE: 7 June, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               805 KFITFSMLIFFIVWISFIPA 824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 45.0%
Local 9; Conservative
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                                                                                                  COUNTRY: U.S.

2IF: 2004-1008
COMPUTER READABLE PORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IRW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMITA Release #1.0, Version #1.30
CUBRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/134,513
FILING DAYE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08485588
Patent No. 5688938
Patent No. 568938
Paten
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CURRENT APPLICATION DATA:
APPLICATION NUBER: 105/08/485,588
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
       1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BRI331/13003
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: SARZO, MICHAEL A.
REGISTRATION NUMBER: 36,912
REFERENCE/DOCKET NUMBER: BR133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)639-6585
TELEPHONE: (202)639-6604
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1059 amino acids
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STRANDEDNESS: no
                                         Washington
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MOLECULE TYPE: pr
HYPOTHETICAL: NO
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US-08-485-588-7
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CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR PAPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: 00/537,784

PILING DATE: 10 December 1994

APPLICATION NUMBER: 00/537,784

APPLICATION NUMBER: 00/538,784

APPLICATION NUMBER: 00/538,784

APPLICATION NUMBER: 00/509,389

FILING DATE: 20 october, 1994

APPLICATION NUMBER: 00/509,389

FILING DATE: 12 Cetcber, 1993

APPLICATION NUMBER: 0.5.00/127

PILING DATE: 12 Pebrary, 1993

APPLICATION NUMBER: 0.5.07/749,451

FILING DATE: 11 Febrary, 1993

APPLICATION NUMBER: 0.5.07/749,451

FILING DATE: 11 Febrary, 1991

APPLICATION NUMBER: 0.5.07/749,451

FILING DATE: 11 Febrary, 1991

APPLICATION NUMBER: 0.5.07/749,451

FILING DATE: 13 August, 1991

APPLICATION NUMBER: 0.5.07/749,451

FILING DATE: 13 PEBRARY 100/6

FELEXOPMENT/AGENT INFORMATION:

TELEPANOR: (213) 489-1600

TELERONEL TON INFORMATION:

TELEPANOR: (213) 489-1600

TELERONEL 1078 manno acids

TYPE: amino acid

TYPE: amino acid

NOS-08-484-565-7
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Gaps

Search completed: January 29, 2002, 10:59:59 Job time: 2145 sec

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RTS* protein. Syn PRMSP1(p19)A prote PRMSP1(p19)A prote PRMSP1(p19)S prote PRMSP1(p19)S prote Merozoite surface Modified merozoite surface Modified merozoite Andified major menbrane a Plasmodium falcipa Human VEGF-x prote Human VEGF-x prote Human UEGF-x prote Human UEGF-x prote Plasmodium cynomol

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Plasmodium knowles N19 polyepitope ca Plasmodium falcipa A peptide which ma Immunogenic branch Plasmodium falcipa Circumsporozolte (P.falciparum deriv

AAR91632 AAR68840 AAR10640 AAB10640 AAB10641 AAB3629 AAX70295 AAX10551 AAX40255 AAX65435 AAX6525 AAX64253 AAX64253 AAX64253 AAX64253 AAX64253

ALIGNMENTS

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AAY70278 standard; Protein; 350 AA
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131
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RESULT
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1 MKFLVNVALVEMVVXISXIX........DFFGISYYEKVLAKYKDDLE 350
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| SIDSB/gcgdata/geneseqfy/geneseqp/AA1901 DAT:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                         protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence;
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                                                                                                                                                                     OM protein
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                                                                                                                                                                                                                                        Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Recombinant vaccin	NS1 81-RLfdelta9.	NS181RLFAuth plasm	NS1 81-RLfAuth. P	NS1_81 (NANP) 4 RL fAu	NS1_81(NVDP)4RLfAu	NS1 81-RLfAuth + (Merozoite surface	Sequence encoded b	CS protein of mala	Sequence encoded b	
	ID	AAY70278	AAR13175	AAR07945	AAR13176	AAR13178	AAR13179	AAR13177	AAB37609	AAP83144	AAP60416	AAP80835	
	DB	21	12	11	12	12	12	12	. 22	σ	^	σ	
	Query Match Length DB ID	350	309	319	319	335	335	327	108	411	412	412	
ø	Query	100.0	13.1	12.8	12.8	12.8	12.8	12.6	11.5	11.2	11.2	11.0	
	Score	1923	252	247	247	247	247	243	222	215.5	215.5	211.5	,
	Result No.	1	7	m	4	2	9	7	80	6	<i>چ</i>	/	

Recombinant vaccine CDC/NIIMALVAC-1.
Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine;
T-cell epitope; tetanus toxoid; antigenic epitope; treatment;
circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2;
liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; MSP-2;
apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175;
EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen;
Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody;
honey bee.
Chimeric - Apis sp.
Chimeric - Clostridium tetani.
Chimeric - Plasmodium falciparum.
Key Location/Qualifiers
Peptide 1.,22
/note= "Derived from Honey bee"
Protein 23350
/label= Mature_CDC/NIIMALVAC-1
/note= "Recombinant multivalent malarial vaccine"
WO200011179-A1.
02-MAR-2000.

19-AUG-1999;

```
The polypeptide is prepd. by genetic engineering of genes encoding the P. falciparum circumsporozoite (CS) protein [Dame et al., Science 225: 593 (1984)], and the influenza virus non-structural protein [NSI), [Baze et al., Nucleic Acids Research, 8: 5845 (1980)]. The DNA encoding the 1st 81 AAS of the N-terminal of NSI (1980)]. The DNA encoding the 1st 81 AAS of the N-terminal of NSI (NSI_81) is linked via a synthetic sequence to DNA encoding Region turn is fused to DNA encoding Region [I.contg. flanking regionless the 18 AA signal region, which in turn is fused to DNA encoding Region II.contg. flanking region sess the first nine N-terminal AAS. This CS fusion is designated REIGeltage. The PTO residue separating the ASP (at the C-terminal of the linker) from Rifeltage is an artifact of a filled in BamHI site. The peptide can be used in a vaccine for protection against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptide comprising immunogenic determinants from P falciparum - for vaccine against malaria infection in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= AAs 297-412 of CS protein
/note= "Region II flanking region minus 9 N-term-
inal AAs"
                                               Immunogenic determinant; circumsporozoite; CS; vaccine; malaria; hybrid; influenza virus; non-structural protein 1; fusion.
                                                                                                                                                                                                                                                                                   "Influenza virus nonstructural protein 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 13.1%; Score 252; DB 12; Length 309; Local Similarity 45.0%; Pred. No. 7.8e-13; les 54; Conservative 1; Mismatches 1; Indels 64
                                                                                                                                                                                                                                                                                                                                                                                                                          /note= 80.7
89.193
/label= AAs 19-123 of CS protein
/note= "Region 1 contg. flanking region less
signal sequence"
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                                                                                                                                                                                                                                      1..81
/label= N-terminal of NS1
                                                                                                                                                                                                                                                                                   /note= "Influenza virus n
82.87
/label= synthetic linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hollingdale MR;
                                                                                                                                                                                                                                                                                                                                                                                         'label= artifact
'note= "see comments"
                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 7; 18pp; English.
                                                                                                                    Plasmodium falciparum.
Tnfluenza virus (A/PR/8/34/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89US-0447746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SMIK ) SMITHKLINE BEECHÂM.
(USSA ) US SEC OF THE ARMY.
(BIOM-) BIOMEDICAL RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90EP-0313257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KHKKLKQPGDGNP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gordon DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1991-179771/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 AA;
NS1_81-RLfdelta9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-DEC-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gross MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
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Region
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 IVQYDNFNANPNANPNANPDGNCEDIPHVNEFSAIDLGNAEKYDKMDEPQHYGKSLTPLE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELYKPNDKSLYQYIKANSKFIGITELSNTFINNAGQHGHMHGNEREDERTLTKEYEDIVL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 KEFTYMINFGRGONYWEHPYQKSDQPKQYEQHLTDYEKIKEGKPLDKFGNIYDYHYEHSS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                      Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKFLVNVALVFMVVYISYIYADHHHHHHHKHKKLKQPGDGNPWSPCSVTCGKPKDELDYEN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 1923; DB 21; Length 350; Best Local Similarity 100.0%; Pred. No. 5.8e-151; Matches 350; Conservative 0; Mismatches 0; Indels .0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSSTKSSSPSNVKSASLATRLMKKFKAEIRDFFGISYYEKVLAKYKDDLE 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NAIM-) NAT INST IMMUNOLOGY.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 43-44; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ė
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                                                                                                                                                                                                              Lal AA, Shi YP, Hasnain SE;
                          99WO-US18869.
                                                                          98US-0097703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                              WPI; 2000-237654/20.
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Sequence

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Gaps

64;

29-AUG-1991

AAR13175;

AAR13175

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(first entry)

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AAR13176 standard; Protein; 319 AA.
                                                                        NS1_81-RLfAuth.
                                                       29-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                     Gross MS,
                                        AAR13176;
                                                                                                                                                                       Peptide
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                AAR13176
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         239 istewspcsvtcgngiqvr1kpgsankpkdeldyendiekkickmekcssvfnvvnssig 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
42 ----WSPCSVTCG------KPKDELDYENDIEKKICKMEKCSSVFNVVNSNSG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----KPKDELDYENDIEKKICKMEKCSS 74
                                                                                                                                                                                                                                                                                                                                                                                                  The product is useful in preparation of vaccines for treatment and prophylaxis of plasmodium sporozite infection. It may be easily produced in large pure quantities(from a transformed E.coli expression system.
                                                                                                                                                                                                                                                                                                                                                  New polypeptide used in malaria vaccine - comprises immunogenic determinants from 1st and 2nd flanking regions of plasmodium surface protein and intermediate repeat domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.8%; Score 247; DB 11; Length 319;
41.5%; Pred. No. 2.Je-12;
ative 1; Mismatchés 1; Indels 74
                                                                                                                                                                                             /label- Fragment of circumsporozite protein 204..319
                                                                                                                                                                                                             /label- Fragment of circumsporozite protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 KHKKLKQPGDGNP------
                                                                                                                                                              1..81
/label= NS181 protein fragment
/note= "from plasmid pMG-1"
                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 11-12; 24pp; English.
                                                                                                                                                      Location/Qualifiers
                                                      AAR07945 standard; protein; 319 AA.
                                                                                                     NS181RLFAuth plasmid product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOLASDIC NEDCONTICE
                                                                                                                                                                                                                                                             90EP-0304720
                                                                                                                                                                                                                                                                           89US-0346863
                                                                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM
                                                                                      22-FEB-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    r matcn
Local Similarity 41.5
les 54; Copservative
                                                                                                                                                                                     ..193
                                                                                                                                     Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                            Gross MS, Young JF;
                                                                                                                                                                                                                                                                                                                           WPI; 1990-350299/47.
N-PSDB; AAQ06580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1111111: 1
299 vfnvvnssig 308
                                                                                                                                                                                                                                                                                                                                                                                                                                           319 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VENVVNSNSG 84
                                                                                                                                                                                                                                                                                                                                                                                                                            expression system.
                                                                                                                      Malaria; vaccine.
                                                                                                                                                                                                                                                            01-MAY-1990;
                                                                                                                                                                                                                                                                           33-MAY-1989;
                                                                                                                                                                                                                                             22-NOV-1990
                                                                                                                                                                                                                            EP398540-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                      AAR07945;
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Domain
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Matches
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the P. falciparum circumsporozoite (CS) protein | Dame et al.,

Science 225: 593 (1984), and the influenza virus non-structural

Science 225: 593 (1984), and the influenza virus non-structural

protein 1 (NSI), | Baez et al., Nucleic Acids Research, 8 : 5845

(1980)]. The DNA encoding the 1st 81 AAs of the N-terminal of NSI

(NSI,81) is linked via a synthetic sequence to DNA encoding Region

I contg. flanking regionless the 18 AA signal region, which in

turn is fused to DNA encoding Region II-contg. flanking region.

C This CS fusion is designated REfAuth. The Pro residue separating

the Asp (at the C-terminal of the linker) from REfAuth is an arti-
fact of a filled in Bamil site; the Gly separating Region I and

C Region II-contg. CS flanking regions is an artifact of a synthetic

FORI/TATHII I linker. The peptide can be used in a vaccine for

protection against malaria.

The complete nucleotide and AA sequences are given in EP-304720,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The polypeptide is prepd. by genetic engineering of genes encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polypeptide comprising immunogenic determinants from P falciparum - for vaccine against malaria infection in humans.
Immunogenic determinant; circumsporozoite; CS; vaccine; malaria;
hybrid; influenza virus; non-structural protein 1; fusion.
                                                                                                                                                                                                                                                                                                 'note= "Influenza virus nonstructural protein 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Region 1 contg. flanking region less signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="see comments"
|185..39
|/185..3 As 288-412 of CS protein
|/note="Region II flanking region"
                                                                                                                                                                                                                                      1..81
/label= N-terminal of NS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89..193
/label- AAs 19-123 of CS
                                                                                                                                                                                                                                                                                                                                       82..87
/label= synthetic linker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "see comments"
                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= artifact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= artifact
                                                                                                                                Influenza virus (A/PR/8/34).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90EP-0313257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89US-0447746
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(USSA ) US SEC OF THE ARMY.
(BIOM-) BIOMEDICAL RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gordon DM,
                                                                                              Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1991-179771/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-DEC-1990;
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29-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                        AAR13179;
      Gross MS,
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                                                                                      42 ------WSPCSVTCG-------WPKDELDYENDIEKKICKMEKCSS
                                                                                                                                                                                                                                                                                                           /note= "Influenza virus nonstructural protein 1" 82..97
/label= immunodominant repeat region
/note= "four tetrapeptide repeat units"
                                                                                                                                                                                                                                            circumsporozoite; CS; vaccine; malaria; non-structural protein 1; fusion.
                                                           74;
                                                                                                                                                                                                                                                                                                                                                              Jubel= artifact
/note= "see comments"
105..209
/label= AAs 19-123 of CS protein
/note= "Region lontg. flanking region less
signal sequence"
                                            Length 319;
                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           /....315
/label= AAS 288-412 of CS protein
/note= "Region II flanking region"
                                             Score 247; DB 12;
Pred. No. 2.1e-12;
1; Mismatches 1;
    filed May 1, 1990.
See also AAR12306-R12311 and AAR13175-R13179.
                                                                                                                                                                                                                                                                                                  1..81
/label= N-terminal of NS1
                                                                                                                                                                                                                                                                                                                                          98..103
/label= synthetic linker
                                                                                                                                                                                                                                                                                                                                                                                                               /label= artifact
/note="see comments"
                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                     AAR13178 standard; Protein; 335 AA.
                                                                             29 KHKKLKQPGDGNP-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK) SMITHKLINE BEECHAM.
(USSA) US SEC OF THE ARMY.
(BIOM.) BIOMEDICAL RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89US-0447746.
                                               12.8%;
41.5%;
                                                                                                                                                                                                                                                                    Plasmodium falciparum.
Influenza virus (A/PR/8/34).
                                                                                                                                                                                                                  29-AUG-1991 (first entry)
                                                                                                                                                                                                                                               Immunogenic determinant;
hybrid; influenza virus;
                                               Query Match
Best Local Similarity 41.5
Matches 54; Conservative
                                                                                                                                                                                                                               NS1_81(NANP)4RLfAuth.
                                                                                                                                            1111111: 1
299 vfnvvnssig 308
                                                                                                                                     75 VFNVVNSNSG 84
                          319 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-DEC-1990;
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                                                                                                                                                                                                     AAR13178;
                          Sequence
                                                                                                                                                                                                                                                                                                                                            Peptide
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Region
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AAR13178
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The polypeptide is prepd. by genetic engineering of genes encoding the P. falciparum circumsporozoite (CS) protein [Dame et al., ct the P. falciparum circumsporozoite (CS) protein [Dame et al., ct science 225 : 593 (1984)], and the influenza virus non-structural protein 1 (NS1), [Baez et al., Nucleic Acids Research, 8 : 5845 (1880)]. The DNA encoding the 1st 81 AAs of the N-terminal of NS1 (NS1_81) is linked to a synthetic sequence encoding four repeat units from the immunodominant region, which in turn is linked via a synthetic sequence to DNA encoding Region I contg. flanking region This is linked to DNA capton Is so the CS flanking region in The Pro residue septore arating the Asp (at the C-terminal of the linker) from the Region creding the Asp (at the C-terminal of the linker) from the Region of I-contg. CS flanking region is an artifact of a filled-in BamHI creding the Gly separating the Region I and II-contg. CS flanking region in a vaccine for protection against malaria. See also AAR12306-R12311 and AAR13175-R13179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 ------WSPCSVTCG------KPKDELDYENDIEKKICKMEKCSS 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Influenza virus nonstructural protein 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunogenic determinant; circumsporozoite; CS; vaccine; malaria; hybrid; influenza virus; non-structural protein 1; fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /______immunodominant repeat region
/note= "four variant tetrapeptide repeat units"
98..103
/label= synthetic linker
                                                                                                    Polypeptide comprising immunogenic determinants from P falciparum for vaccine against malaria infection in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 247; DB 12;
Pred. No. 2.3e-12;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1..81
/label= N-terminal of NS1
Hollingdale MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR13179 standard; Protein; 335 AA.
                                                                                                                                                                                                        Example 4; Page 11; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum.
Influenza virus (A/PR/8/34).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 KHKKLKQPGDGNP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NS1_81(NVDP)4RLfAuth.
   Gordon DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1111111: 1
315 vfnvvnssig 324
                                                         WPI; 1991-179771/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 335 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 VFNVVNSNSG
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2;

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AAR13177 standard; Protein; 327 AA.
                                           AAR13177;
                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                 Region
 AAR13177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The polypeptide is prepd. by genetic engineering of genes encoding the P falciparum circumsporozoite (CS) protein [Dame et al., Science 225: 593 (1984)], and the influenza virus non-structural protein 1 (NSI), [Baez et al., Nucleic Acids Research, 8: 5845 (1980)]. The DNA encoding the 1st 81 AAs of the N-terminal of NSI (NSI_2H) is linked to a synthetic sequence encoding four repeat units (the variant form) from the immunodominant region, which in turn is linked via a synthetic sequence to DNA encoding Region I contg. flanking region II-contg. flanking region II-contg. flanking region II-contg. flanking region in the Region II-contg. CS flanking region is an artifact of a filled-in BamHI site; the Gly separating the Region II-contg. CS flanking region is an artifact of a filled-in BamHI site; the Gly separating the Region II-contg. CS flanking region is an artifact of a synthetic Fokl/TthIII I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255 eqylkkiknsistewspcsvtcgngiqvrikpgsankpkdeldyendiekkickmekcss 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 -------WSPCSVTCG------KPKDELDYENDIEKKICKMEKCSS
                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptide comprising immunogenic determinants from P falciparum for vaccine against malaria infection in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.8%; Score 247; DB 12; Length 335; 41.5%; Pred. No. 2.3e-12; ative 1; Mismatches 1; Indels 74
                    /loc.209
/label- AAs 19-123 of CS protein
/note- "Region 1 contg. flanking region less
signal sequence"
                                                                                                             /note="see comments"
211..335
1abel= AAS 288-412 of CS protein
/note="Region II flanking region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          See also AAR12306-R12311 and AAR13175-R13178. O
                                                                                                                                                                                                                                                                                                                                                             Gross MS, Gordon DM, Hollingdale MR;
/label= artifact
/note= "see comments"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 5; Page 11; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 KHKKLKQPGDGNP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (62)
                                                                                                                                                                                                                                                                                                                    (USSA ) US SEC OF THE ARMY. (BIOM-) BIOMEDICAL RES INST.
                                                                                                                                                                                                                                            90EP-0313257
                                                                                                                                                                                                                                                                        89US-0447746
                                                                                                                                                                                                                                                                                                     SMIK ) SMITHKLINE BEECHAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54; Copservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1991-179771/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1111111: 1
315 vfnvvnssig 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        335 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 VFNVVNSNSG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           against malaria
                                                                                                                                                                                                                                            06-DEC-1990;
                                                                                                                                                                                                                                                                       08-DEC-1989;
                                                                                                                                                                                                               19-JUN-1991
                                                                                                                                                                                   EP432965-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                            Region
                                                                                   Region
                                                                                                                             Region
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RESULT

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The polypeptide is prepd. by genetic engineering of genes encoding the P. falciparum circumsporozoite (CS) protein [Dame et al., Science 225: 593 (1984)], and the influenza virus non-structural protein 1 (NS1), [Baez et al., Nucleic Acids Research, 8: 5845 (1980)]. The DNA encoding the 1st 81 AAs of the N-terminal of NS1 (NS1_81) is linked via a synthetic sequence to DNA encoding Region I contg. flanking region less the 18 AA signal region. This is linked to a synthetic sequence encoding two repeat units from the immunodominant region, which in turn is fused to DNA encoding Region II-contg. flanking region. The Pro residue separating the Asp (at the C-terminal of the linker) from the Region I-contg. CS flanking region is an artifact of a filled-in Bamil site; the Gly separating the repeat units and the Region II-contg. CS flanking region is an artifact of a synthetic FOKI/TthIII I linker. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polypeptide comprising immunogenic determinants from P falciparum - for vaccine against malaria infection in humans.
                                                                                         Immunogenic determinant; circumsporozoite; CS; vaccine; malaria;
hybrid; influenza virus; non-structural protein 1; fusion.
                                                                                                                                                                                                                                "Influenza virus nonstructural protein 1"
                                                                                                                                                                                                                                                                                                                                                         /note= "Region 1 contg. flanking region less
                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "two tetrapeptide repeat units"
                                                                                                                                                                                                                                                                                                                                                                                                     /label- immunodominant repeat region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203..327
/label- AAS 288-412 of CS protein
/note= "Region II flanking region"
                                                                                                                                                                                                                                                                                                                      89..193
/label= AAs 19-123 of CS protein
                                                                                                                                                                                                 1.81
/label= N-terminal of NS1
                                                                                                                                                                                                                                                                                                                                                                      signal sequence"
                                                                                                                                                                                                                                              82..87
/label= synthetic linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hollingdale MR;
                                                                                                                                                                                                                                                                                                         /note= "see comments"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="see comments"
203..327
                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 10; 18pp; English.
                                                                                                                                                                                                                                                                                           /label= artifact
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= artifact
                                                                                                                                   Plasmodium falciparum.
Influenza virus (A/PR/8/34/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89US-0447746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SMIK ) SMITHKLINE BEECHAM.
(USSA ) US SEC OF THE ARMY.
(BIOM-) BIOMEDICAL RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90EP-0313257
                            29-AUG-1991 (first entry)
                                                         NS1_81-RLfAuth + (NANP)2.
                                                                                                                                                                                                                                                                                                                                                                                      . 201
                                                                                                                                                                                                                                 'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gross MS, Gordon DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1991-179771/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-DEC-1989;
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Length 108;

SSXS

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Query Match
Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                          AAP83144;
                                                                                                                                                                                                                                                                                                                                                                   Vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                               28
                                                                                                                                                                                 88
                                                                                                                                                                                                                                     AAP83144
                                                                                                                               qq
                                                                                                                                                                                 g
                                                      δ
                                                                            q
                                                                                                                                                         δ
                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to non-natural variants of a C-terminal fragment of a plasmodium merozoite surface protein-1 (MSP-1). The non-natural variants have reduced affinity for at least 1 antibody capable of blocking a second antibody that inhibits the proteolytic cleavage of plasmodium MSP-1_4_2, and has the same affinity for at least one third antibody that inhibits the proteolytic cleavage of plasmodium MSP-1_1_1. The non-natural variants of the present invention are useful for immunising a mammal against malaria, and can be used to treat malaria. The present sequence is MSP-119 protein.
                                                                                                        5
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ن
                                                                                                                                                                                                 139 eepsdkhiegylkkiknsistewspcsvtcgngigvrikpgsankpkdeldyendiekki 298
                                                                                                                                                           179 khkkikqpgdgnapnanpnanpnanpnknhqgngqghnmpndpnrnvdenanannavknnnn 238
                                                                                                                                  --- 41
                                                                                                                                                                                     99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Uthaipibull
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel variants of the C-terminal fragment of Plasmodium merozoite surface protein-1, useful as vaccines for treating or preventing malaria
    peptide can be used in a vaccine for protection against malaria.
See also AAR12306-R12311 and AAR13175-R13179.
                                                                                                           82;
                                                                                 Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Merozoite surface protein; protazoacide; vaccine; malaria.
                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Syed S,
                                                                                 Score 243; DB 12;
Pred. No. 4.7e-12;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feeney J, Morgan W,
                                                                                                                                                                                         ---WSPCSVTCG----
                                                                                                                                                                                                                                                                                                                                    AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; Fig 15; 126pp; English.
                                                                                                                                                                                                                                                                                                                                  AAB37609 standard; Protein; 108
                                                                                                             ü
                                                                                                                                                                                                                                                                                                                                                                                                                 Merozoite surface protein-119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99GB-0009072.
99US-0311817.
99CA-2271451.
                                                                                   / 12/6%;
39.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-APR-2000; 2000WO-GB01558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MEDI-) MEDICAL RES COUNCIL
                                                                                                                                                                                                                                                          ckmekcssvfnvvnssig 316
                                                                                                                                                                                                                                          84
                                                                                                                                                                                                                                                                                                                                                                                       27-FEB-2001 (first entry)
                                                                                                 Local Similarity 39.1 nes 54; Conservative
                                                                                                                                                                                                                                            67 CKMEKCSSVFNVVNSNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Birdsall B,
                                                                                                                                      KHKKLKQPGDGNP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-015762/02.
N-PSDB; AAC68977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ą.
                                              327 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200063245-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-MAY-1999;
25-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Holder A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                              AAB37609
                                                Sequence
                                                                                      Query Match
                                                                                                                                                                                                                                                                                                            œ
                                                                                                                                         53
                                                                                                                                                                                          42
                                                                                                                                                                                                                                                                      299
                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                       AAB37609
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Sequence of the CS gene (AAN81108) is from lambda-mPfl. A recombinant DNA molecule is claimed, comprising functional DNA coding sequence fused, in phase, to a portion of the Pre-S2 region of a hepatitis B virus (HBV) Pre-S2-S protein coding sequence. The functional DNA coding sequence comprises the Pre-S2 coding sequence, Pre-S1 coding sequence or entire Pre-S1-Pre-S2 coding sequence, the CS protein coding sequence of Plasmodium, or a HIV coding sequence such as an HIV envelope gene sequence, e.g. HIV C7 protein coding region, HIV Peptide 121 coding region, or HIV Dreesman peptide coding region.
                         .,
                                                                                                    --EDSGSNGKKIT 110
                         Gaps
                                                                                                                  23.HHHHHHHKHKKLKQPGDGNPWSPCSVTCGKPKDELDYENDIEKKICKMEKCSSVFNVVNSN 82
                                                                    DNA encoding hepatitis B virus antigens and hybrids contg. them used for expression in yeast to obtain vaccines and bivalent vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123..146.
/note="Repeat region, repeat unit = NANPNVDP"
211..286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Repeat region, repeat unit = NANP"
                           Indels
                                                                                                                                                                                                                                                                                                                         Sequence encoded by the circumsporozoite (CS) gene from
                                                                                                                                                                                                                                                                                                                                                              antigen; immunogen; probe; hybridisation;
Score 222; DB 22;
Pred. No. 5.4e-11;
8; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example; Fig 3Aa-3Af; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ż
                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                               AAP83144 standard; protein; 411 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harford
                                                                                                                                                                                                                                                                                                                                                                                                                                                106..120
/note="Region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87US-0009325.
  11.5%;
35.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88EP-0870008.
                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cabezon T, De Wilde M,
                             Conservative
                                                                                                          83 SGCFRHLDEREECKCLL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SMIK ) SMITH KLINE-RIT
                                                                                                                                                                                                                                                                                                                                                                                 immunoassay; diagnosis.
                                                                         |||||||||
2 hhhhhh-----2
                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1988-229751/33
                                                                                                                                                           111 CECTKPDSKPI 121
                                                                                                                                                                             cectkpdsypl 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAN81108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-1987;
                                                                                                                                                                                                                                                                                                     20-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-AUG-1988
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Circumsporozoite gene; Plasmodium falciparum; lambda mPfl; vaccine; yeast glyceraldehyde-3P-dehydrogenase gene (TDH3) promoter; yeast ornithine carbamoyl transferase gene (ARG3); repeat region.
                                                                                                                                                     Sequence encoded by the circumsporozoite (CS) gene of Plasmodium
                                                                                 AAP80835 standard; protein; 412 AA.
                                                                                                                                                                  falciparum in lambda mPfl
            Plasmodium falciparum
 71 KCSSVFNVVNSNSG
                                                                                                                              18-SEP-1990
                                                                                                                                                                                                                                                                                                                                                           WO8805817-A.
                                                                                                                                                                                                                                                                                                                                                                                   11-SEP-1988,
                                                                                                       AAP80835;
                                                                                                                                                                                                                                                                           Region
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                                                                     AAP80835
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                      Dp
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                                                                                              ıı ||:|
328 khiegylkkikn-sistewspcsvtcgngnqvrikpgsankpkdeldyendiekkickme 386
                                                           Gaps
                                                                                --KPKDELDYENDIEKKICKME 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Plasmodium CS gene was used to isolate peptides capable of inducing an immune response to the parasite. Peptide antigens may be synthesised in pure form and used to generate an immune response in vaccination against malaria. The featured repeat units are claimed and must be present in Ropies of 2-1000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New immunologically active pure synthetic peptide(s) - used for protection against infection by malaria parasite.
                                                          19:
                                   Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sobre 215.5; DB 7; Length 412 pred. No. 1.2e-09; 2; Mismatches 7; Indels 1
                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schneider I;
                                 DB 9;
                                  Score 215.5; DB 9;
Pred. No. 1.2e-09;
2; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   کر"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dame JB, Williams JL,
                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                   /label- Repeat unit
                                                                                                                                                                                                             AAP60416 standard; Protein; 412 AA.
                                                                               29 KH----KKLKQPGDGNPWSPCSVTCG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 2; 49pp; English.
                                                                                                                                                                                                                                                                                   CS protein of malaria parasite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.2%;
62.2%;
                                  11.2%;
62.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       85EP-0107794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84US-0624564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (USDC ) US SEC OF COMMERCE. (USGO ) US GOVERNMENT. (USSA ) US SEC OF THE ARMY.
                                                                                                                                                                                                                                                             (first entry)
                                           Best Local Similarity 62.2
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                           Sporozoite; vaccination.
                                                                                                                                        387 kcssvfnvvnssig 400
                                                                                                                              84
                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1986-008635/02.
                                                                                                                              71 KCSSVFNVVNSNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             412 AA;
411 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McCutchan TF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUN-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUN-1985;
                                                                                                                                                                                                                                                            13-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                               02-JAN-1986
                                                                                                                                                                                                                                                                                                                                                                                                        EP166410-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                    AAP60416;
                                  Query Match
 Sequence
                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                        RESULT 10
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/note="repeat region, repeat unit=NANPNVDP" /note="repeat region, repeat unit=NANP" 212..287 /note="repeat region, repeat unit=NANP"

148..207

Location/Qualifiers 124..147

(first entry)

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Plasmid WR201 was obtained from the Walter Reed Army Institute of
Research, and results from insertion of a 2.3 kb EcoRI fragment from
lambda mpfl encoding the complete CS protein gene P. falciparum into
vector pUCB. A recombinant DNA vector is claimed, which comprises a DNA
sequence contg. the coding sequence of the CS P. falciparum operatively
linked to an expression control sequence. Prefd. expression control
sequences include the yeast glyceraldehydrogenase gene (TDH3)
promoter and the yeast ornithine carbamoyl transferase gene (TDH3)
promoter and the yeast ornithine carbamoyl transferase gene (TDH3)
promoter and the yeast ornithine carbamoyl transferase gene (TDH3)
promoter and the yeast ornithine carbamoyl transferase gene (TDH3)
promoter and the yeast ornithine carbamoyl transferase gene (TDH3)
promoter and the yeast ornithine carbamoyl transferase gene (TDH3)
promoter and the yeast ornithing its first 50bp. Also claimed is a
transformed host cell, a method of culturing the cell to produce CS, the
protein and a vaccine. The vector comprises a 192 bp Sau3A fragment
coding for 16 tetrapeptide repeats of the P. falciparum CS protein
derived from Sau3A digestion of a 1215 bp StuI-RsaI fragment of WR201
containing the P. falciparum CS protein coding sequence minus
approx. its first 50 bp, or two, three, four or more tandem copies of
such 192 bp Sau3A fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Expression of P. falciparum circumsporozoite protein by yeast using recombinant DNA vector having coding sequence linked to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Fig 2a; 44pp; English.
88WO-BE00002
                                                                                                87US-0008791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression control sequence
                                                                                                                                                                                                      (SMIK ) SMITH KLINE RIT SA.
                                                                                                                                                                                                                                                                                                             Gathoye AM;
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1988-235171/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         412 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAN81781
                                                                                                30-JAN-1987;
25-JAN-1988;
                                                                                                                                                                                                                                                                                                       De Wilde M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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3;

19; Gaps

7;

Conservative

53

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q

KH----KKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKME 70

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16-NOV-1991;
27-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-NOV-1992;
                                                                                                                                                                                                                                                                                                                     RTS* protein
                                                                                                                                                                                                                                                                                                  27-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9310152-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAY-1993
                                                                                                                                                                                                                                                                                                                                                       strain 768;
S protein.
                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                 AAR37797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cohen J,
                                                                         response
                                                                                          Sequence
                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                               Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                            RESULT 13
                                                                                                                                                         29
                                                                                                                                       Matches
                                                                                                                                                                                                                                                     AAR37797
                                                                                                                                                                                                                                                                                8×3333333333
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                                                                                                                                                           ò
                           <u>ښ</u>
                                                                                                                                                                                                                                                                                                              'note= "Derived from S. cerevisiae TDH3 gene sequence"
                                                       329 khieqylkkikn-sistewspcsvtcgngiqvrikpgsankpkdeldyendiekkickie 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the RTS hybrid protein which is encoded by the RTS expression cassette. This hybrid consists of a methionine residue derived from S. cerevisiae TDH3 gene sequence, three amino acids, Met-Ala-Pro, derived from a nucleotide sequence created by the cloning procedure used to construct the hybrid gene, a stretch of 189 amino acids representing amino acids 210 to 398 of the
                                                                                                                                                                                                                                                                                                                                                  of
                            Gaps
                                            29 KH-----KKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKME 70
                                                                                                                                                                                                                                                                                                                                                                             (adw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hybrid protein comprising Plasmodium circumsporozoite protein and HBsAg - useful as a vaccine for treating patients susceptible to Plasmodium infections
                                                                                                                                                                                                                                                                                                                                                   csp
                                                                                                                                                                                                                           RTS; expression cassette; hybrid protein; S. cerevisiae; TDH3; cloning; circumsporozoite protien; CSP; Plasmodium falciparum; strain 7G8; hepatitis B virus; HBV; adw serotype; preS2 protein;
                            19;
                                                                                                                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                                                                                                            /note= "Carboxy terminal amino acids from HBV serotype) preS2 protein"
        Length 412;
                                                                                                                                                                                                                                                                                                                                                  /note= "Represents amino acids 210-398 of
         Score 211.5; DB 9; Length Pred. No. 2.6e-09; 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         /note= "S protein of HBV (adw serotype)"
                                                                                                                                                                                                                                                                                                                                 'note= "Cloning artefact"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                            P. falciparum"
                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                  AAR37796 standard; Protein; 424 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 5; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92WO-EP02591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91GB-0024390
92US-0842694
           11.0%;
60.8%;
                                                                                                                                                                                          (first entry)
                    Best Local Similarity 60.8 Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                     194..197
                                                                                                                                                                                                                                                                                                                                                                                                198..424
                                                                                               388 kcssvfnvvnssig 401
                                                                                     71 KCSSVFNVVNSNSG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cohen J, De Wilde M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1993-182494/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ42566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                             WO9310152-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                27-MAY-1993
                                                                                                                                                                                         27-SEP-1993
                                                                                                                                                                                                            RTS protein
                                                                                                                                                                                                                                                           S protein.
                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                        AAR37796;
              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                               Key
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/note= "Derived from S. cerevisiae TDH3 gene sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          circumsporozoite protien (CSP) of Plasmodium falciparum strain 7GB, an amino acid Arg created by the cloning procedure, four amino acids, pro-Val-Thr-Asn, representing the four carboxy terminal residues of hepatitis B virus (HBV), adw serotype, pres2 protein, and a stretch of 226 amino acids specifying the S protein of HBV, adw serotype. This protein, and RTS* (see also AAR37797), may be combined with adjuvant and used in a vaccine for preventing plasmodium infections. The vaccines produce a humoral response and also a cellular immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Represents amino acids 210-398 of the CSP of
                                                                                                                                                                                                                                                                                                                                                                                                                             KH----KKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKME 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Carboxy terminal amino acids from HBV (adw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RTS; expression cassette; hybrid protein; S. cerevisiae; TDH3; cloning; circumsporozoite protien; CSP; Plasmodium falciparum; strain 7G8; hepatitis B virus; HBV; adw serotype; preS2 protein;
                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                      14; Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "S protein of HBV (adw serotype)"
                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                 Score 210.5; DB 14;
Pred. No. 3.3e-09;
1; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               serotype) preS2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Cloning artefact"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P. falciparum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR37797 standard; Protein; 424 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91GB-0024390.
92US-0842694.
                                                                                                                                                                                                                                                                                                                                   10.9%;
ilarity 63.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92WO-EP02591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198..424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194..197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                De Wilde M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-182494/22.
N-PSDB; AAQ42567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81
                                                                                                                                                                                                                                                                                                                                                                   1 Similarity
45; Conserv
                                                                                                                                                                                                                                                                    424 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 KCSSVFNVVNS
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This is the amino acid sequence of a recombinant protein comprising amino acids 1613-1705 of the Plasmodium falciparum merozoite surface protein 1 (MSP1) 19 kD C-terminal fragment (p19), linked to a glycosylphosphatidylinositol membrane anchoring sequence. p19 is the C-terminal fragment of the 42 kD MSP1 from Plasmodium species. The recombinant protein can be used for the production of anti-malarial vaccines, where the p19 fragment provides a high level of protective immunity since it includes epitopes not presented in the p42 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "amino acids derived from P. falciparum MSP1 p19 fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "glycosylphosphatidylinositol anchoring sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant protein containing the merozoite surface protein-1 p19 fragment - useful in anti-malarial vaccines, diagnosis and protein purification
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 18; Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium vivax; merozoite surface protein; MSP1; p19; Plasmodium falciparum; malaria; vaccine; immunity; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ľ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.3%; Score 198.5; DB 18;
llarity 44.2%; Pred. No. 5.3e.09;
Conservative 5; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 ENDIEKKICKMEKCSSVFNVVNSNSGCFRHLDERECKCLL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 ------EDSGSNGKKITCECTKPDSKPI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 nnggcdadakcteedsgsngkkitcectkpdsypl 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mendis K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW22592 standard; Protein; 116 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                               Disclosure; Fig 1B; 85pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Longacre-Andre S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PfMSP1(p19)A protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-FR00291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INSP ) INST PASTEUR.
(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum
                                       WPI; 1997-425033/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                             ¥
                                                           N-PSDB; AAT94550
                                                                                                                                                                                                                                                                                                                                                                                             116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barnwell JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-AUG-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                               Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW22592;
     Roth C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roth C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                         This sequence represents the RTS* hybrid protein which is encoded by the RTS* expression cassette. This hybrid consists of a methionine created derived from S. cerevisiae TDH3 gene sequence, three amino acids. Met-Ala-Pro, derived from a nucleotide sequence created by the cloning procedure used to construct the hybrid gene, a stretch of 189 amino acids representing amino acids 210 to 398 of the circumsporozoite protien (GSP) of Plasmodium falciparum strain NFS4, an amino acids Arg created by the cloning procedure, four amino acids, or amino acids Arg. representing the four carboxy terminal residues of hepatitis B virus (HBV), adw sercype, pres2 protein, and a stretch of 226 amino acids specifying the S protein of HBV, adw sercype. This protein, and RTS (see also AAR37796), may be combined with an adjuvant and used in a vaccine for preventing plasmodium infections. The vaccines produce a humoral response and also a cellular (mmune).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96..116
/note= "glycosylphosphatidylinositol anchoring sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note- "amino acids derived from P. falciparum MSP1 p19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------- KPKDELDYEND 61
Hybrid protein comprising Plasmodium circumsporozoite protein and HBsAg – useful as a vaccine for treating patients susceptible to Plasmodium infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium vivax; merozoite surface protein; MSP1; p19;
Plasmodium falciparum; malaria; vaccine; immunity; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Longacre-Andre S, Mendis K, Nato F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 207.5; D
Pred. No. 5.9e-
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---GNPWSPCSVTCG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW36103 standard; Protein; 116 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fragment"
                                                                             Disclosure; Fig 9; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 tekkickmekcssvfnvvnssig 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PfMSP1(p19)A protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 IEKKICKMEKCSSVFNVVNSNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.8%;
51.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INSP ) INST PASTEUR.
(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-FR00290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96FR-0001822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 51.8
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 KHKKLKQPGD---
                                                                                                                                                                                                                                                                                                                                                                                                                             424 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barnwell JW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW36103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Region
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This is the amino acid sequence of a recombinant protein comprising amino acids 1613-1705 of the Plasmodium falciparum merozoite surface protein 1 (MSP1) 19 kD C-terminal fragment (p19), linked to a glycosylphosphatidylinositol membrane anchoring sequence. p19 is the C-terminal fragment of the 42 kD MSP1 from Plasmodium species. The recombinant protein can be used for the production of anti-malarial vaccines, where the p19 fragment provides a high level of protective immunity since it includes epitopes not presented in the p42 fragment.
                                                                  Recombinant protein containing Plasmodium merozoite surface protein-1 p42 fragment - useful in antimalarial vaccines, also new antibodies for diagnosis and protein purification
                                                                                                                                                             Disclosure; Fig 1B; 85pp; French.
WPI; 1997-425034/39.
P-PSDB; AAW22592.
                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence
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7 Gaps 39; Query Match
10.3%; Score 198.5; DB 18; Length 116;
Best Local Similarity 44.2%; Pred. No. 5.3e-09;
Matches 42; Conservative 5; Mismatches 9; Indels 39; 59 ENDIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLL---100 ------EDSGSNGKKITCECTKPDSKPI 121 54 nnggcdadakcteedsgsngkkitcectkpdsypl 88 q ò

Search completed: January 29, 2002, 10:21:40 Job time: 416 sec

27 98.5 5.1 3418 5 US-09-08 28 98.5 5.1 3418 5 US-09-08 29 98 5.1 174 6 US-09-08 31 97 5.0 195 5 US-09-70 32 95 4.9 207 5 US-09-70 33 94 4.9 342 5 US-09-70 35 94 4.9 390 5 US-09-70 36 94 4.9 390 5 US-09-70 37 94 4.9 390 5 US-09-70 38 93.5 4.9 267 5 US-09-70 41 91 4.7 456 5 US-09-70 42 91 4.7 456 5 US-09-70 43 91 4.7 456 5 US-09-70 44 91 4.7 456 5 US-09-70 45 91 4.7 456 5 US-09-70 46 91 4.7 456 5 US-09-70 47 466 5 US-09-70 48 91 4.7 456 5 US-09-70	90.5 4.7 2167 5 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CORRECANT: HOIGET, Anthony APPLICANT: HOIGET, Anthony APPLICANT: Birdsall, Berry APPLICANT: Eeney, James APPLICANT: Seeney, James THILE OF INVENTION: Malaria Vaccine TILE REFERENCE: 18396/1005 CURRENT APPLICATION NUMBER: US/09/978, CURRENT FILING DATE: 2001-10-16 PRIOR FILING DATE: 2000-04-20 PRIOR FILING DATE: 2000-04-20 PRIOR FILING DATE: 1999-05-13	PRIOR APPLICATION NUMBER: 2,271,451 PRIOR FILING DATE: 1999-05-25 PRIOR FILING DATE: 1999-04-20 NUMBER OF SEQ ID NOS: 3 SOFTWARE: PatentIn version 3.0 SEQ ID NO 1 LENGTH: 96 TYPE: PRT ORRANISM: Plasmodium falciparum US-09-978-756-1	Query Match Best Local Similarity 44.1%; Pred. Ratches 41; Conservative 5; Miss of DIEKKICKMEKCSSVENVVNSNSGCFRHLDB 1 INSCHOCKKOCPONSGCFRHLDB DD 1 NISCHOCKKOCPONSGCFRHLDB DD 54 GGCDADAKCTEEDSGSNGKKITCECTKFDS) RESULT 2 US-09-978-756-2 S-9209-06-2 S-9209-06-2 S-9209-06-2 S-9209-06-2 S-9209-06-3 S-
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. OM protein - protein search, using sw model Run on: January 29, 2002, 10:16:24; Search time 120.95 Seconds (without alignments) 105.903 Million cell updates/sec Title: US-09-763-397A-2 Perfect score: 1923 Sequence: 1 MKFLVNVALVFMVYISYIYDFFGISYYEKVLAKYKDDLE 350 Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5	Searched: 173191 seqs, 36597120 residues Total number of hits satisfying chosen parameters: 173191 Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Applied first A5 purmmasion	Database: Pending TIST 43 SUMMATES Database: Pending Patents AA_New:* 1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:* 2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:* 4: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:* 5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:* 6: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:* 7: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:* 7: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:* 8: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:* 7: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:* 8: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:* 7: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:* 8: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:* 7: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:* 7: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:* 8: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:* 7: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:* 8: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:* 7: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:* 6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:* 7: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:* 6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:* 7: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:* 7: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:* 8: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:* 7: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:* 8: /cgn2_6/ptodata/SUNITIONEW_COMB.pep:* 8: /cgn2_6/ptodata/SUNITIONEW_COMB.pep:* 8: /c	SCORE MATCH LENGTH DB ID SCORE MATCH LENGTH DB ID 196.5 10.2 96 5 US-09-978-756-1 Sequence 1, A 196.5 10.2 376 5 US-09-978-756-2 Sequence 2, A 196.5 10.2 631 5 US-09-117-415B-2 Sequence 2, A 196.5 10.2 631 5 US-09-117-415B-2 Sequence 22, B 196.5 10.2 631 5 US-09-117-415B-2 Sequence 22, B 196.5 10.2 631 5 US-09-117-415B-18 Sequence 18, B	0.2 631 5 US-09-117-415B-16 Sequence 20, 0.2 1602 5 US-09-269-874A-7 Sequence 7, 8 Capuence 16, 0.2 1602 5 US-09-269-874A-7 Sequence 7, 8 Capuence 3, 9 Capuence 133 Capuence 134 Capuence 1

Sequence 11, Appl Sequence 261, Appl Sequence 261, App Sequence 2054, A Sequence 3054, A Sequence 7603, Ap Sequence 7603, Ap Sequence 7603, Ap Sequence 12299, A Sequence 12299, A Sequence 12299, A Sequence 21299, A Sequence 3195, A	· 13-02	9 5; Length 96; 8; Indels 39; Gaps 2;
18 5 US-09-084-471C-11 18 5 US-09-084-471C-13 74 6 US-10-005-368-261 10 5 US-09-708-427-30544 10 5 US-09-708-427-30544 10 5 US-09-613-591D-130 10 5 US-09-613-591D-130 10 5 US-09-708-427-7603 10 5 US-09-708-427-7603 10 5 US-09-708-427-12299 10 10 10 10 10 10 10 10 10 10 10 10 10 1	ALIGNMENTS /09978756 /Y Y The state of t	196.5; DI No. 1.7e- No. 1.7e- Matches EREECKCLL. EREECKCLL. KPI 121 1: 86
341885 117486 119555 19555 2007 2007 3342 3342 3347 4466 5466 5466 5466 5466 5466 5466 54	് ദ്രീപ്പിച്ച 🕏 വല വല വല വല വ	10.2%; Score Larity 44.1%; Pred. Conservative 5; Mis KMEKCSSVENVNSNSGCFHILD ::! VKKQCPONSGCFHILD
3.5 3.5 3.6 3.6 3.6 3.6 3.6 3.6 3.6 3.6	Pplicat MATION: Older, Birdsal Birdsal Birdsal Feeney, Syed, Syed, Syed, Syed, Syed, Syed, Starlow NG DATE: ATION NG	ich al Similarity 44.1%; Pred. 41; Conservative 5; Miss DIEKKICKMEKCSSVFNVNSNSGCFRHLD
22 22 22 22 22 22 22 22 22 22 22 22 22	RESULT 1 195-09-978-756-1 Sequence 1, A GENERAL INFOR APPLICANT: PRIOR FILING	Query Match Best Local Matches 4 Oy 61 DIE 1 1 Db 1 NIS OY 100 Db 54 GGC

Length 594; Indels

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APPLICANT: Davidson, Eugene
Yang, Shutong
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coleman, COLEMAN SUDOL SAPONE, PC
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44.1%; Pred. No. 1.6e-07;
tive 5; Mismatches 8;
                                                                                                                       DB 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WordPad (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,415B
FILLNG DATE: 29-Jul-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                                                                                                                                                                                534 GGCDADAKCTEEDSGSNGKKITCECTKPDSYPL 566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: R12-030 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 679-0090 TELEFAX: (212) 679-9121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of a MSA1 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: US-09-117-415B-22
                 MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-117-415B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Henry D. Coleman STREET: 714 Colorado Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Coleman, Henry D. REGISTRATION NUMBER: 32,559
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22 Application US/09117415B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 613 amino acids
TYPE: amino acid
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                                                                                                                     10.2%;
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                                                                                                                       Query Match 10.29
Best Local Similarity 44.19
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Bridgeport
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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Matches 41; Conserv
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TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition
of a MSAl Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSE: Henry D. Coleman, COLEMAN SUDOL SAPONE, PC STREET: 714 Colorado Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 376;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 196.5; DB 5 Pred. No. 8.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-Jul-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 GGCDADAKCTEEDSGSNGKKITCECTKPDSYPL 348
                                                                                             CURRENT APPLICATION NUMBER: US/09/978,756
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: PCT/GB00/01558
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 1999-04-20
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-25
PRIOR PAPLICATION NUMBER: 2,271,451
PRIOR FILING DATE: 1999-05-25
PRIOR PELING DATE: 1999-05-25
PRIOR PELING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 ------EDSGSNGKKITCECTKPDSKPI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: R12-030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPad (ASCII)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Coleman, Henry D. REGISTRATION NUMBER: 32,559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 679-0090
TELEFAX: (212) 679-9121
RMATITON FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2) Application US/09117415B; Sequence 2) Application US/09117415B; GENERAL INFORMATION:
APPLICANT: Davidson, Eugene
                                                            TITLE OF INVENTION: Malaria Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 594 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Plasmodium falciparum
US-09-978-756-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.28;
44.18;
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Connecticut
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41; Conservative
                                                                              FILE REFERENCE: 18396/1005
  Feeney, James
                                         Syed, Shabih
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
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Best Local Similarity
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Length 613;

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518 NISQHQCVKKQCP-----QNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENN 570
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GENERAL INFORMATION:
APPLICANT: Davidson, Eugene
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition
of a MSAl Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 10.2%; Score 196.5; DB 5
Best Local Similarity 44.1%; Pred. No. 1.6e-07;
Matches 41; Conservative 5; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPAG (ASCII)
CURRENT APPLICATION DATE:
RAPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLL
                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-Jul-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      571 GGCDADAKCTEEDSGSNGKKITCECTKPDSYPL 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 ------EDSGSNGKKITCECTKPDSKPI 121
                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: COleman, Henry D.
REGISTRATION NUMBER: 32,559
REFERENCE/DOCKET NUMBER: R12-030
TELECOMMUNICATION INFORMATION:
TELEPAR: (212) 679-0121
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R12-030
           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad (ASCII)
                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 20: US-09-117-415B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry D. Coleman,
STREET: 714 Colorado Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Coleman, Henry D.
REGISTRATION NUMBER: 32,559
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TELEPHONE: (212) 679-0090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 631 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Bridgeport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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                                                                                        APPLICANT: Davidson, Eugene
Yang, Shutong
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition
Of a MSAl Peptide
CORRESPONDENCES: 24
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                         ADDRESSEE: Henry D. Coleman, COLEMAN SUDOL SAPONE, PC STREET: 714 Colorado Avenue CITY: Bridgeport
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1.6e-07;
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MEDUUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-Jul-1998
CLASSIFICATION: 435
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44.1%; Pred. No. 1.6e
tive 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: COLOman, Henry D.
REGISTRATION NUMBER: 32,559
REFERENCE/DOCKET NUMBER: R12-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 679-0090
TELEFAX: (212) 679-9121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
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CORRESPONDENCE ADDRESS:
ADDRESSE: Henry D. Coleman,
STREET: 714 Colorado Avenue
RESULT 5
US-09-117-475B-18
; Sequence 18, Application US/09117415B
rewRRAL JAPORMATION:
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                           STATE: Connecticut
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Connecticut
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Best Local Similarity 44.15
Matches 41; Conservative
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ZIP: 10017
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36216 Coleman, COLEMAN SUDOL SAPONE, PC SEQUENCE CHARACTERISTICS: LENGTH: 649 amino acids

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TYPE: PRT
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                                                                                                                                     Length 649;
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GENERAL INFORMATION:
APPLICANT: Bujard, Hermann
TITLE OF INVENTION: Recombinant Process for Preparing a
TITLE OF INVENTION: Complete Malaria Antigen, GP190/MSP1
FILE REFERENCE: GRUE-003
CURRENT APPLICATION NUMBER: US/09/269,874A
CURRENT APPLICATION NUMBER: US/097/05441
PRIOR APPLICATION NUMBER: DE 19640817.2
PRIOR FILING DATE: 1997-10-02
PRIOR PILING DATE: 1996-10-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09269874A; GENERAL INFORMATION:
APPLICANT BUJATG, Hermann
TITLE OF INVENTION: Recombinant Process for Preparing a
TITLE OF INVENTION: Complete Malaria Antigen, GP190/MSP1
FILE REFERENCE: GRUE-003
CURRENT APPLICATION NUMBER: US/09/269,874A
CURRENT FILING DATE: 1999-08-02
PRIOR APPLICATION NUMBER: PCT/EP97/05441
PRIOR APPLICATION NUMBER: DE 19640817.2
PRIOR REPLICATION NUMBER: DE 19640817.2
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44.1%; Pred. No. 5e-07;
tive 5; Mismatches 8;
                                                                                                                                   Score 196.5; DB 5;
Pred. No. 1.7e-07;
5; Mismatches 8;
                                                                                                                                                                                                                61 DIEKKICKMEKCSSVFNVNNSNSGCFRHLDEREECKCLL----
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                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 7
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-117-4158-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-09-269-874A-7
                                                                                                                                         10.2%;
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Best Local Similarity 44....
France 41; Conservative
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Best Local Similarity 44.19
Matches 41; Conservative
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US-09-269-874A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bulard, Hermann
TITLE OF INVENTION: Recombinant Process for Preparing a
TITLE OF INVENTION: Complete Malaria Antigen, GP190/MSP1
FILE REFERENCE: GRUE-003
CURRENT APPLICATION NUMBER: US/09/269,874A
CURRENT FILING DATE: 1999-08-02
PRIOR APPLICATION NUMBER: PCT/EP97/05441
PRIOR APPLICATION NUMBER: DE 19640817.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 10.2%; Score 196.5; DB 5; Best Local Similarity 44.1%; Pred. No. 5.2e-07; Warches 41. Conservative 5; Mismatches 8;
                                                                                                                                  DB 5;
                                                                                                                               Score 196.5; DB 5;
Pred. No. 5.1e-07;
5; Mismatches 8;
                                                                                                                                                                                                                             61 DIEKKICKMEKCSSVFNVNSNSGCFRHLDEREECKCLL--
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GENERAL INFORMATION:
APPLICANT: Holder, Anthony
APPLICANT: Birdsall, Berry
APPLICANT: Birdsall, Berry
APPLICANT: Morgan, William
APPLICANT: Syed, Shabih
TILE OF INVENTION: Malaria Vaccine
TILE REFERENCE: 18396/1005
CURRENT APPLICATION NUMBER: US/09/978,756
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: PCT/GB00/01558
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: 09/311,817
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-13
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NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-269-874A-3; Sequence 3, Application US/09269874A; GENERAL INFORMATION:
LENGTH: 1621
TYPE: PRT
ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Plasmodium falciparum
                                                                                                                                       10.28;
44.18;
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                                                                                                                                         Query Match 10.2%
Best Local Similarity 44.1%
Matches 41; Conservative
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US-09-978-756-3
                                                      ; ORGANISM: F10
US-09-269-874A-5
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/note= "fusion protein composed of
                                                                                                                                                                                                                                                                                                                Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/09/402,181A
FILING DATE: 29-Sep-1997
CLASSIFICATION: CUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     melittin signal sequence and full length hTRT protein" sequence become sequence and full length sequence become become become become sequence of 13:
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APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/724,643 ELLING DAPE: 01-0CT-1996 APPLICATION NUMBER: US 08/844,419 FILING DAFE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
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FLING DATE: 14-MG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-MG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/854,050 FILING DATE: 09-MAY-1997
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                                                                                                                         Sequence 613, Application US/09402181A
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 613:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1189 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                            Morin, Gregg B.
Harley, Calvin B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1..1189
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
     577 GVSQDTSTN-
                                                                                                       US-09-402-181A-613
                                                                                                                                                                                                                                                                                                                                                         .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |: || : | : | : | 389 DAKINGNRFT----GTAKSLID-DNTNTAPFVKELFSKKANPN-NPDPNSDTL----- 435
                                                                                                                                                                                                                                                                                                                                                                                                                                 436 -------EGGFYGESGDELAGKFLSNDNATFVVFGGKRDKTTEPVATKTVYF 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 STGFEKPSTSFVGNEEI-GSIIDGKGLNDEVN-NQIEDETVPVSNKEY-----YEY 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 NFGRGQNYWEHPYQKSDQ--PKQYEQHLTDYEKIKEGKPLDKF---GNIYDYHYEHSSPS 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 DSGSNGKKITCECTKPDSKPIVQYDNFNANP-----NANPNANPDGNCEDIPHVNEF 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 -- OYIKANSKFIGITELSNTFINNAGQHGHMHGNEREDER--TLTKEYEDIVLKEFTYMI 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  530 NYGRPNKQFTKKINASVQKNPAYFGQH-------DKFYFNGNYYDLSAKEANKL 576
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                         43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: LACTORERIN RECEPTOR GENES OF MORAXELLA
FILE REFERENCE: 10399 MIS
CURRENT APPLICATION NUMBER: US/09/445,096A
CURRENT PILING DATE: 2000.03-22
PRIOR PILING DATE: 1997-06-03
PRIOR PILING DATE: 1997-06-03
PRIOR FILING DATE: 1998-06-02
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 905;
                                                                                                                                                                                                                                                                                                        DB 5; Length 394;
                                                                                                                                                                                                                                                                                                                                                       11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     50 GKPKDELDYENDIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 STKSSSPSNVKSASLATRLMKKFKAEIRDFFGISYYEKVLAKYKD 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   323 ENPNPTCNENNGGCDADATCTEEDSGSSRKKITCECTKPDSYPL 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 ----TEDSGSNGKKITCECTKPDSKPI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 SAIDLGNAEKYDKMDEPQHYGKSLTPLEELYKPND-----
                                                                                                                                                                                                                                                                                                      Score 187.5; DB : Pred. No. 4.5e-07,
                                                                                                                                                                                                                                                                                                                                                 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1) Score 109.5; ilarity 21.4%; Pred. No. 1.2; Conservative 32; Mismatches
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 9909072.2
PRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
LENGTH: 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 70, Application US/09445096A GENERAL INFORMATION:
                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-09-978-756-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                Query Match 9.8%;
Best Local Similarity 41.3%;
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Loosmore, Sheena M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang, Quijun
Yang, Yan-Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Du, Run-Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 61; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-445-096A-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-445-096A-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 70
LENGTH: 905
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Gaps

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Sequence 30543, Application US/09708427

Sequence 30543, Application US/09708427

Sequence 30543, Application US/09708427

GENERAL INFORMATION:

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID

TITLE OF INVENTION: THEREBY

TITLE OF INVENTION: THEREBY

TITLE OF INVENTION: THEREBY

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11.09

NUMBER OF SEQ ID NOS: 83364

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 CS-----SVFNVVNSNSGCFRHLDEREECKCLLEDSGSNGKKITCECTKPDSKPIVQYD 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 CHGPDHELSLEN-----GHMTERSCYVCRVSIQGMFYK---CRQCSFEAHPLCTYA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 NFNANP------NANPNANPDGNCEDIPHVNEFSAIDLGNAEKYDKMDEPQHY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 PMHASSPDLLVTKQRSLHGHAGQPSPPHQYGQGIPY------GYPHMGQPEPY 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 GKSLTPLEELYKPNDKSLYQYIKANS---KFIGITELSNTFINNAGQHGHMHGNEREDER 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 HHHHKHKKLKQPGDGNPWSPCSVTCGKPK------DELDYENDIEKKICK---MEK 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230 TLTKEYEDIVLKEFTYMINFGRGONYWE---HPYQKSDQPKQYEQHLTDYEKIKEGKP 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 PYTPQ------GDGHQHQQQNHHPYMNSGSPKSESSAVSTTKKKKKP 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 HFTHNHLLTQVNGIG-----TYTCDGCKLYGEGRIYRCSDCDYDLHEYCATCPSILLNS
                                                                                 LOCATION: 1..1189
CTHER INFORMATION: /note= "fusion protein composed of melitin signal sequence and full length hTRT protein"
SEQUENCE DESCRIPTION: SEQ ID NO: 613:
US-09-721-477-613
                                                                                                                                                                                                                                                                                                                                                              Score 108; DB 5; Length 1189;
Pred. No. 2.2;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35, Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.5%; Score 105.5; D. 20.1%; Pred. No. 0.62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 1..286
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Ceres Seq. ID 1829492
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKFLVNVALVFMVVXISYIYAD 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                        5.6%;
                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 5.6
Best Local Similarity 100.
Matches 22; Conservative
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature LOCATION: 1..286
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Best Local Similarity
Matches 60; Conserva
                                MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 30543
LENGTH: 286
                                                          FEATURE
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                                                                                                                                   Gaps
                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF INVENTION: Human relowerage calarytic successions of the property of
                                                              5.6%; Score 108; DB 5; Length 1189;
100.0%; Pred. No. 2.2;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Andrews, William H. INVENTION: Human Telomerase Catalytic Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17618
APPLICATION NUMBER: WO PCT/US97/17618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 613:
                                                                                                                                                                                                                                                                                                                                                                                  5.09-721-477-613
Sequence 613, Application US/09721477
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Nakamura, Toru
Morin, Greeg B.
Harley, Calvin B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                  1 MKFLVNVALVEMVVXISYIYAD 22
                                                                                                                                                                                                 1 MKFLVNVALVFMVVYISYIYAD 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                           Query Match 5.6'
Best Local Similarity 100.'
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF
                                                                                                                                                                                                                                                                                                                                                                 RESULT
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13;

Gaps

91;

62

Search completed: January 29, 2002, 10:58:07 Job time: 2503 sec

us-09-763-397a-2.rapn

Page 7

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GenCore version 4.5
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OM protein - protein search, using sw model

January 29, 2002, 10:15:49 Run on:

; Search time 144.96 Seconds
(without alignments)
183.920 Million cell updates/sec

1923 1 MKFLVNVALVFMVVXISYIY.....DFFGISYYEKVLAKYKDDLE 350 US-09-763-397A-2 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

11666666	213.5 208.5 207.5 200.5 200.5 200.5 196.5 196.5	11.2 11.2 10.8 10.8 10.8 10.2 10.2 10.2	424 4124 4124 388 388 1055 11726 1726 1639	. 04000040004	A54533 A54529 A54529 A39756 A39756 A306M A47848 A45948 A45948 A45948 A45948 A45948	msporcoite msporozoite msporozoite msporozoite msporozoite oite surfac merozoite merozoite merozoite merozoite
	196 196 196 196 196 196 196 196 196 196	, , , , , , , , , , , , , , , , , , ,	110001 10001 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000 10000	- 000000000000	SAZQKI AZ6868 A26898 A32594 A44986 C022QAB C022QAB C022QAA A200AM A4969 A20319 A2068 A32068	major merozoite su major merozoite su major merozoite su probable major sur apical membrane an circumsporozoite portroumsporozoite portroumsporozo

circumsporozoite p	circumsporozoite p	circumsporozoite p	thrombospondin-rel	circumsporozoite p	erythrocyte-bindin	circumsporozoite p	circumsporozoite p	66K merozoite surf	hypothetical prote	protein-tyrosine k	circumsporozoite p	rhoptry-associated	serine/threonine-s	. apical membrane an
A48571 D41156	C41156	A41156	S04531	OZZÓMY	A37793	OZZOMB	OZZÓBK	A39238	E71616	T18287	A54504	S27833	H71621	A44944
0 0	7	~	~		~	-	-	~	7	7	~	7	-	7
386 387	387	395	559	367	1435	332	348	563	1247	1338	429	782	2485	295
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99	9	9	9	9	Φ	_	_	Ĭ	_	w	_			
125 6 125 6	125 6												121	119.5

ALIGNMENTS

Thail

RESULT 1		
Ab4b33		
circumsporozoite protein - malaria parasite (Plasmodium falciparum) (strain T4,	rum) (strain T4,	-
C;Species: Plasmodium falciparum		
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000	09-Jun-2000	
C; Accession: A54533		
R;del Portillo, H.A.; Nussenzweig, R.S.; Enea, V.		
Mol. Biochem. Parasitol. 24, 289-294, 1987		
A; Title: Circumsporozoite gene of a Plasmodium falciparum strain from Thailand.	n from Thailand.	
A; Reference number: A54533; MUID:87315205		
A; Accession: A54533		
A;Status: preliminary		
A; Molecule type: DNA		
A; Residues: 1-424 		
A; Cross-references: GB:M19752; NID:q160216; PIDN:AAA29555.1; PID:q160217	D:q160217	
C; Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology	repeat homology	
F;348-402/Domain: thrombospondin type 1 repeat homology <thr1></thr1>	1	

ä 13; Gaps Length 424; Indels 11.3%; Score 216.5; DB 2; 61.1%; Pred. No. 3.3e-08; ive 3; Mismatches 12; Query Match 11.3 Best Local Similarity 61.1 Matches 44; Conservative

26 HHHKHKKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKMEKC 72 q

84 73 SSVFNVVNSNSG οy

SSVFNVVNSSIG 413 402 Q

RESULT 2
CizQAF
Circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate IMTM22)
C; Species: Plasmodium falciparum
C; Species: Plasmodium falciparum
C; Date: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jun-2000
C; Accession: A03388
R; Dame, J.B.; Williams; J.L.; McCutchan, T.F.; Weber, J.L.; Wirtz, R.A.; Hochmayer, W. Science 225, 593-599, 1984
A;Title: Structure of the gene encoding the immunodominant surface antigen on the spo. A; Reference number: A03388; MUID:84250215
A; Accession: A03388
A; Molecule type: DNA
A; Residues: 1-412 < CDAM>A; Residues: 1-412 < CDAM>A; Residues: 1-412 < CDAM>A; Comment: Residues: 1-6 are the probable signal sequence.
C; Comment: Residues: 1-16 are the probable signal sequence.
C; Comment: Residues: 1-16 are the probable signal sequence.
C; Comment: There are 41 copies of a 4-residue repeating unit in the middle domain of C; Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
F; 336-390/Domain: thrombospondin type 1 repeat homology

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A, Crossiones: 1-405 Court, R.; Matile, H.; Pink, J.R.; Sinigaglia, F. B, Caspers, P.; Gentz, R.; Matile, H.; Pink, J.R.; Sinigaglia, F. B, Caspers, P.; Gentz, R.; Matile, H.; Pink, J.R.; Sinigaglia, F. B, Caspers, P.; Gentz, R.; Matile, H.; Pink, J.B.; 185-190, 1989
Mol. Blochem. Parasitol. 35, 185-190, 1989
A, Feference number: A45527
A, Multiple: Mol. Mats. Mol. B, Multiple: Mild isolates of Plasmodium falciparum show extensive polymorphism in T cell A; Reference number: A60657; Multiple: Mild isolates of Plasmodium falciparum show extensive polymorphism in T cell A; Reference number: A60657; Multiple: Mild isolates of Plasmodium falciparum contintion of the control 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RO-71)
                                                                                                                                                                                                                                                                                                                                                                                               A;Title: DNA sequence of the gene encoding a Plasmodium falciparum malaria candidate A;Reference number: S05428; M0ID:89345189
A;Accession: S05428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C-terminal region of
                                                                                                                                                                                                 malaria parasite (Plasmodium falciparum) (isolate NF54)
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merozoite surface antigen 1 - malaria parasite (Plasmodium falciparum) (strain 1 c) species: Plasmodium falciparum
A; variety: Plasmodium falciparum
A; variety: strain R0-71
C; Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jun-2000
C; Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jun-2000
C; Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jun-2000
A; Polle, R.; Bujard, H.; Cooper, J.A.
Submitted to the EMBL Data Library, July 1994
A; Pescence number: S47282
A; Reference number: S47282
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
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A;Residues: 319-336,334-373 <LOC>
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
F;329-383/Domain: thrombospondin type 1 repeat homology <THR1>
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A;Experimental source: strain RO-71
C;Superfamily: major merozoite surface antigen
C;Keywords: glycoprotein; merozoite; surface antigen
                                                                                                                                                                                                                  circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate C;Species: Plasmodium falciparum C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jun-2000 C;Accession: S05428; A45527; I60657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 1.4e-07;
4; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --GNPWSPCSVTCG---
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1 Similarity 51.8%;
43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 17, 5854, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-405 <CAM>
                                                        SSVFNVVNSSIG 377
84
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Best Local Similarity
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   SSVFNVVNSNSG
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C.Specials: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 20-Aug-1999
C.Accession: A39756 #sequence_revision 14-Feb-1992 #text_change 20-Aug-1999
C.Accession: A39756 #sequence_revision 14-Feb-1992 #text_change 20-Aug-1999
C.Accession: A39756 #G68-6689, 1991
A.Title: Circumsporozoite protein gene from Plasmodium reichenowi, a chimpanzee malaria A.Accession: A39756 #UID:91201303
A.Accession: A39756 #UID:91201303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Lockyer, M.J.; Schwarz, R.T.
Nol. Biochem. Parasitol. 22, 101-108, 1987
A;Title: Strain variation in the circumsporozoite protein gene of Plasmodium falciparum.
A;Reference number: A54529; MUID:87115616
A;Accession: A54529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            circumsporozoite protein - malaria parasite (Plasmodium falciparum) (strain Wellcome) C;Species: Plasmodium falciparum C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000 C;Accession: A54529
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A;Residues: 1-388 <LALD
A;Cross-references: GB:M60972; NID:g160228; PIDN:AAA29561.1; PID:g160229
A;Cross-references: GB:M60972; NID:g160228; PIDN:AAA29561.1; PID:g160229
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
F;312-366/Domain: thrombospondin type 1 repeat homology <THR1>
                                                                         3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GB:M15505; NID:g160214; PIDN:AAA29554.1; PID:g160215 A; Cross-references: GB:M15505; NID:g160214; PIDN:AAA29554.1; PID:g160215 C; Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology C; Keywords: tandem repeat C; Keywords: tandem repeat F; 366-420/Domain: thrombospondin type 1 repeat homology <THR1>
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                                                                            Gaps
                                                                                                                                     --KPKDELDYENDIEKKICKME 70
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          Length 412;
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                                                                            Indels
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             DB 1;
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Pred. No. 5.8e-08;
1; Mismatches 12
          Score 215.5; DB 1
Pred. No. 3.8e-08;
2; Mismatches 7
                                                                                                                                               KH----KKLKQPGDGNPWSPCSVTCG---
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Best Local Similarity 59.7%;
Matches 43; Conservative
                    11.2%;
62.2%;
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                       Query Match 11.29
Best Local Similarity 62.23
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                               KCSSVFNVVNSSIG 401
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Best Local S
Matches 42
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major merozoite surface antigen - malaria parasite (Plasmodium falciparum) (fragments C; Species: Plasmodium falciparum C; Species: Plasmodium falciparum C; Species: Plasmodium falciparum C; Species: 17-Peb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jun-2000 C; Accession: A4545 Species: 17-Peb-1994 #text_change 09-Jun-2000 C; Accession: A4545 Species: Proteolytic processing of the Plasmodium falciparum merozoite surface protein A; Reference number: A45545; MUID: 92131048 A; Accession: A45545 MUID: 92131048 A; Astatus: preliminary A; Astatus: preliminary A; Astatus: Preliminary A; Astatus: A4545; MUID: Backbone (NCBIN:77612, NCBIP:77621) C; Superfamily: major merozoite surface antigen C; Keywords: glycoprotein; merozoite; surface antigen; tandem repeat
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A;Accession: S05603
A;Molecule type: mRNA
A;Residues: 1-1639 < MYLD-
A;Cross-references: EMBL:X15063; NID:g9896; PIDN:CAA33163.1; PID:g9897
B;Myler, P.J.
Nucleic Acids Res. 17, 5401, 1989
A;Title: Nucleotide and deduced amino acid sequence of the gp195 (MSA-1) gene from Pl
A;Reference number: S04850; MUID:89345116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - malaria parasite (Plasmodium falciparum)
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C;Species: Plasmodium falciparum
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jun-2000
C;Accession: S05603; S04850
R;Myler, P.J.
submitted to the EMBL Data Library, April 1989
                                                                                                                                                                                                                                                                                                                                                                            1606 GKFQDML----NISQHQCVKKQCP-----ENSGCFRHLDEREECKCLLNYKQEGDKCV 1654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :| : | ::| 339
287 NISQHQCVKKQCP-----QNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENN 339
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                                                                                                                                                                                                                           Length 1726;
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                                                                                                                                                                                                                                                                                                                                           GKPKDELDYENDIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----EDSGSNGKKITCECTKPDSKPI 121
                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 196.5; DB 2;
Pred. No. 8.5e-07;
5; Mismatches 8;
                                                                                                                                                                                                                        Score 200.5; DB 2
Pred. No. 2.7e-06;
6; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLL
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                    A;Molecule type: DNA
A;Residues: 1-1726 <CHA>
A;Cross-references: GB:M37213
C;Superfamily: major merozoite surface antigen
C;Reywords: surface antigen
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10.2%;
Best Local Similarity 44.1%;
Matches 41; Conservative 5
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ilarity 43.3%;
Conservative
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Best Local Similarity
Matches 45; Conserv
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A; Molecule type: mRNA
preliminary
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A. Residues: 1104-1726 (WEB2>
A. Cross-references: EMBL: X03831
C. Comment: The merozoite stages of different strains have strain-specific surface antige
C. Comment: P. falciparum has three stages: sporozoite, merozoite, and gametocyte. The me
C. Superfamily: major marozoite surface antigen; tandem repeat
F. 1-19/Domain: signal sequence #status predicted <SIG>
F. 10-1726/Product: major merozoite surface antigen #status predicted <MAT>
F. 57-187, 1-36, 100-105, 109-120/Region: 3-residue repeats (S-G-T)
F. 757-765/Region: 3-residue repeats (T-E-E)
F. 133, 272, 501, 567, 638, 827, 839, 924, 944, 990, 1016, 1114, 1221, 1613, 1658/Binding site: carbohy
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C;Species: Plasmodium falciparum
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jun-2000
C;Accession: A45948
R;Chang, S.P.; Kramer, K.J.; Yamaga, K.M.; Kato, A.; Case, S.E.; Siddiqui, W.A.
A;Title: Plasmodium falciparum: gene structure and hydropathy profile of the major meroz
A;Reference number: A45948; MUID:89005525
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Nucleic Acids Res. 14, 3311-3332, 1986
A:Tille: Variation in the gene encoding a major merozoite surface antigen of the human
A;Reference number: A23386; MUID:86205236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A23386
A; Molecule type: DNA
A; Residues: 1-1104 (ARB1>
A; Cross-references: EMBL:X03831
B; Weber, J.L.; Sim, B.K.L.; Lyon, J.A.; Wolff, R.
Nucleic Acids Res. 16, 1206, 1988
A; Title: Merozoite surface protein sequence from the Camp strain of the human malaria | A; Reference number: S06361; MUID:88143999
A; Accession: S06361
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C;Date: 30-Sep-1987 #sequence_revision 31-Mar-1991 #text_change 09-Jun-2000
C;Accession: A23386; S06361
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10.4%; Score 200.5; DB 1; Length 1726;
Best Local Similarity 43.3%; Pred. No. 2.7e-06;
Matches 45; Conservative 6; Mismatches 10; Indels 43;
                                                        651;
                                                        Length
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                                                                                                                                                                                                                                                                                ------EDSGSNGKKITCECTKPDSKPI 121
                                Score 200.5; DB 2;
Pred. No. 8e-07;
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9
                                               10.4%;
ilarity 43.3%;
Conservative
                                            Query Match
Best Local Similarity
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probable major surface antigen (83K, 19K, 42K) precursor - malaria parasite (Plasmodi probable major surface antigen (83K, 19K, 42K) precursor - malaria parasite (Plasmodi probacies: Plasmodium falciparum (5, Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 09-Jun-2000 (5, Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 09-Jun-2000 (5, Accession: A24594 M.J.; Odink, K.G.; Sandhu, J.S.; Riveros-Moreno, V.; Nicholl Nature 317, 270-273, 1985 A; Accession: A24594 M.J.; Béol4355 A; Accession: A24594 A; MulD:86014355 A; Accession: A24594 A; Accession: A245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Tanabe, K.; Mackay, M.; Goman, M.; Scaife, J.G.
J. Mol. Biol. 195, 273-287, 1987
A;Title: Allelic dimorphism in a surface antigen gene of the malaria parasite Plasmod
A;Reference number: A26868; MUID:88011243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Plasmodium falciparum
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jun-2000
C;Accession: A26868
                                                                                                                                                                                                                                                               -----EDSGSN 105
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F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1701/Product: major merozoite surface antigen #status predicted
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Pred. No. 2.3e-05;
7; Mismatches 11;
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                                                                                                                   DB 2;
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Pred. No. 2.8e-05;
4; Mismatches 4;
                                                                                                             Score 187.5; DB 2
Pred. No. 2.3e-05;
7; Mismatches 11
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A;Molecule type: DNA
A;Residues: 1-1701 <TAN>
C;Superfamily: major merozoite surface antigen
C;Superfamily: major merozoite surface antigen C;Keywords: surface antigen
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1 Similarity 41.3%;
43; Conservative
                                                                                                                      9.8%;
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36;
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C; Species: Plasmodium falciparum
C; Species: Plasmodium falciparum
C; Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
C; Accession: A54498
M. G; Coppel, R. L.; McIntyre, P.; Langford, C.J.; Woodrow, G.; Brown, G.V.;
Mol. Biochem. Parasitol. 27, 291-302, 1988
A; Title: Variation in the precursor to the major merozoite surface antigens of Plasmodiu
A; Accession: A54498
A; MulD: 88142999
A; Accession: A54498
A; Accession: A54498
A; MulD: 88142999
A; Accession: A54498
A; MulD: B142999
A; Accession: A54498
A; Residues: 1-1701 < PET>
A; Residues: 1-1701 < PET>
A; Residues: 1-1701 < PET>
A; Cross-references: GB:M19143; NID: 9160412; PIDN: AAA29653.1; PID: 9160413
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A;Title: Polymorphism of the precursor for the major surface antigens of Plasmodium falc A;Reference number: A91030; MUID:86136024
A;Accession: A25120
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F:1614-1631/Domain: membrane anchor #status predicted <MBN>
F:97,259,755,759,835,911,955,1049,1156,1165,1436,1563/Binding site: carbohydrate (Asn)
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C;Species: Plasmodium falciparum
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jun-2000
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                                 A;Cross-references: EMBL:X15063
C;Superfamily: major merozoite surface antigen
C;Superfamily: major merozoite; surface antigen
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1639/Product: major merozoite surface antigen #status predicted <MAT>
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Pred. No. 5.2e-06;
3; Mismatches 3; Indels 3;
                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                             Score 196.5; DB 2;
Pred. No. 4.9e-06;
5; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                   DIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1579 GGCDADAKCTEEDSGSNGKKITCECTKPDSYPL 1611
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Best Local Similarity 50.0
Matches 38; Conservative
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                  A; Residues: 1504-1639 <MYL2>
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Best Local Similarity
Matches 41; Conserv
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C; Accession: A25120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 DEMRHFYKDNKYVKNLD--ELTLCSRHAGNMIPDNDKNSNYKYPAVYDDKDKCHILYIA 253
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9.3%; Score 179; DB 2;
Best Local Similarity 25.0%; Pred. No. 2.7e-05;
Matches 82; Conservative 22; Mismatches 86,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341 --------VFELS------
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106 GKKITCECTKPDSKPI 121
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homo sapien apis mellif homo sapien

apis

P05691 P04922 P02894 O14628 P01501 Q14839 P13817 P09346

plasmodium plasmodium

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HHHKHKKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKMEKC 72
                                                                                                                                                                                                                                                                                                                                                                MOI. Biochem. Parasitol. 24:289-294(1987).
-!- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOWINANT
SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
VERTEBRATE HOST).
                                                                                                                                                                                                                                                                                                                        MEDLINE-87315205; PubMed-3306373; del. Portillo H.A., Nussenzweig R.S., Enea V.; "Circumsporozoite gene of a Plasmodlum falciparum strain from
                                                                                                                                                                                                                         01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CIRCUMSPORZOITE PROTEIN PRECURSOR (CS).
Plasmodium falciparum (isolate t4 / Thalland).
Bukaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TAXID-5846;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CIRCUMSPOROZOITE PROTEIN.
45 X 4 AA TANDEM REPEATS OF
710AB14238786CD9 CRC64;
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Pred. No. 5.2e-08;
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                                                                                                                                                   ALIGNMENTS
           KNOB_PLAFN
CSP_PLAFL
CSP_PLAKU
CSP_PLAKH
Z195_HUMAN
                                                                                             KNOB_PLAFG
RBP2_PLAVB
Y044_UREPA
                                                               MEL_APIME
CHD4_HUMAN
                                                                                     KNOB_PLAFA
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InterPro; IPR003067; Cromsprzoite.
InterPro; IPR000884; TSP1.
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PRINTS; PR01303; CRMSPR20ITE.
SMART; SM00209; TSP1; 1.
Malaria; Sporozoite; Repeat; S.
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Best Local Similarity
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1 MKFLVNVALVFMVVYISYIY......DFFGISYYEKVLAKYKDDLE 350
                                                                         Search time 80.65 Seconds
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P21303
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- 2000 Compugen Ltd.
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CSP_PLASI
TRAP_PLAFA
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AMA1_PLAFC
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MSP1_PLAF3
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CSP_PLACL
CSP_PLACB
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CSP_PLAMA

    protein search, using sw model

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CSP_PLAFA
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          GenCore
Copyright (c) 1993
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Match Length
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                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 KH-----KKLKQPGDGNPWSPCSVTCG-------KPKDELDYENDIEKKICKME 70
                                                                                                                                                                                                                                                                                       -i- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURPACE ANTIGEN OF THE ORGANISM.
                                                                                                                                                                                CIRCUMSPOROZOITE PROTEIN.
41 X 4 AA TANDEM REPEATS OF P-N-A-N.
1EEEED3DE90965F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 412;
                                                                                                                                       Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.2%; Score 215.5; DB 1; Length 41
62.2%; Pred. No. 5.9e-08;
ive 2; Mismatches 7; Indels
                                                                                                         21-JUL-1986 (Rel. 01, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Malaria; Sporozoite; Repeat; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                           PIR: A03388; OZZQAF.
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             412 AA; 44420 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
                                                                                                 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; K02194; AAA29524.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 KCSSVFNVVNSNSG 84
                       402 SSVFNVVNSSIG 413
             73 SSVFNVVNSNSG 84
                                                                                                                                                                                                                                                                                    VERTEBRATE HOST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                          NCBI_TaxID=5833;
                                                                                                21-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
SEQUENCE
                                                                              CSP_PLAFA
P02893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
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CSP_PLAFW
IP CSP_PI
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                                                                     CSP_PLAFA
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PRT;

STANDARD;

CSP_PLAFW

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 HHHKHKKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKMEKC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERTEBRATE HOST).
-1- MISCELLANDOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SUBRACE ANTIGEN OF THE ORGANISM.
-1- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                            Lockyer M.J., Schwarz R.T.; "Strain variation in the circumsporozoite protein gene of Plasmodium
                                                                                                                                                                                                                                                                                                                 falciparum.";
Mol. Biochem. Parasitol. 22:101-108(1987).
-!- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT
-!- FUNCTION: THE CIRCUMSPOROZOITE (THE INFECTIVE STAGE OF THE
SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CIRCUMSPOROZOITE PROTEIN.
47 X 4 AA TANDEM REPEATS OF N-A-N-P.
BD57A9A152B85E03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5854;
                                                                                        Plasmodium falciparum (isolate Wellcome).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.1%; Score 213.5; DB 1; Length 59.7%; Pred. No. 8.8e-08; Live 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1992 (Rel. 23, Last Sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
                   Last sequence update)
Last annotation update)
                                                                     CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pram; Proudou, Cara-c, --
PRINTS, PR01303; CRCMSPRZOITE.
MART; SM00209; TSP1; 1.
Malaria; Sporozoite; Repeat; Signal.
crcnal.
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SEQUENCE FROM N.A.
MEDLINE-91201303; PubMed-2016283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A54529; A54529.
InterPro; IPR003067; Cromsprzoite.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-87115616; PubMed=3543671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequ
20-AUG-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47402 MW;
Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00090; tsp_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                442 AA;
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nes 43; Conserv
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Plasmodium falciparum (isolate ro-33 / Ghana)
     MEDLINE-92155298; PubMed-1346766;
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                                       Hackett C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERTEBRATE HOST).

-!- MISCELLANDOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTICEN OF THE ORGANISM.
-!- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                HHHKHKKLKQPGDGNPWSPCSVTC------GKPKDELDYENDIEKKICKMEKC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "DNA sequence of the gene encoding a Plasmodium falciparum malaria candidate vaccine antigen.";
Nucleic Acids Res. 17:5854-5854(1989).

      Malaria; Sporozoite; Repeat; Signal.
      1

      SIGNAL
      1

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      1

      1
      38

      CHAIN
      17

      1
      267

      6
      X

      4
      2245

      MW;
      C031EEFBE2E35604

      CRC64;

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                                                                                                                                                                                                                                                                                                                                                                                                                   ch 10.8%; Score 208.5; DB 1; Length 388; l Similarity 58.3%; Pred. No. 1.7e-07; 42; Conservative 4; Mismatches 13; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum (isolate NF54).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campbell J.R.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSP_PLAFO STANDARD: PRT; 397 AA. P19597; 025798; 01-FEB-1991 (Rel. 17, Created) Carlon (Rel. 39, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
                                                                                                                                                                                                                                                                  PIR; A39756; A39756.
InterPro: IPR003067; Crcmsprzoite.
InterPro: IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-89345189; Pubmed-2668895;
Campbell J.R.;
                                                                                                                                                                                                                                                                                                 Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                      EMBL; M60972; AAA29561.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSVENVVNSSIG 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 SSVFNVVNSNSG 84
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [3]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=5843;
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                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
SEQUENCE
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                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE=89564998; PubMed=2671723;
Caspers P., Gentz R., Matile H., Pink J.R., Sinigaglia F.;
Caspers P., Gentz R., Matile H., Pink J.R., Sinigaglia F.;
The circumsporozoite protein gene from NF54, a Plasmodium falciparum isolate used in malaria vaccine trials."
Mol. Biochem. Parasitol. 35:185-190(1999)
-!- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE VERTEBRATE HOST).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27; Gaps
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Davis J.R., Cortese J.F., Herrington D.A., Murphy J.R., Clyde D.F., Thomas A.W., Baqar S., Cochran M.A., Thanassi J., Levine M.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MSPI_CLAF3
ID MSPI_PLAF3
STANDARD; PRT; 1682 AA.
AC P19588; 025921;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DF MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CIRCUMSPOROZOITE PROTEIN.
43 X AA TANDEM REPEATS OF N-A-N-P.
A -> ANDHANDHA (IN REF. 4).
9E81146F59EBCEA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 207.5; DB 1; Length 397;
Pred. No. 2e-07;
4; Mismatches 9; Indels 27
                                                                                              "Plasmodium falciparum: in vitro characterization and human infectivity of a cloned line."; Exp. Parasitol. 74:159-168(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Malaria; Sporozoite; Repeat; Signal.
SIGNAL 1 16 PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X15363; CAA33421.1; -.
EMBL; M83886; AAA29521.1; -.
EMBL; M22982; AAA29527.1; -.
PIR; S05428; S05428.
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
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PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
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Best Local Similarity 51.8%;
Matches 43; Conservative
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(POTENTIAL).
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CARBOHYD
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Dp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1562 GKFQDML----NISQHQCVKKQCP-----QNSGCFRHLDEREECKCLLNYKQEGDKCV 1610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                  (POTENTIAL).
PTM: MEROZOTTE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 4 KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SUBFACE ANTIGENS OF MEROZOTTES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                       SEQUENCE OF 1-1061 FROM N.A.
MEDLINE-88166657; PubMed-3327688;
Certa U., Rotmann D., Matile H., Reber-Liske R.;
TA naturally occurring gene encoding the major surface antigen
Precursor p190 of Plasmodium falciparum lacks tripeptide repeats.";
EMBO J. 6:4137-4142(1987).
                                                                                                                                                                             merozoite surface antigen-1.";
Exp. Parasitol. 81:47-54(1995).
-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
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                                                                                                                            SEQUENCE OF 1032-1682 FROM N.A. MEDILINE-95354793, PubMed-7628566; Tolle R., Bujard H., Cooper J.A.; Plassmodium falciparum: variations within the C-terminal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43;
                                                                                                                                                                                                                                                                                                                                                                                                                   PIR: S06286; S06286.
InterPro; IPR000561; EGF-like.
Pfam: PF00008: EGF;
Malaria; Meoros; EGF;
Transmembrane; GPI-anchor.
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MEMBRANE ANCHOR (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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                   NCBI_TaxID=5834;
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ID MSP1_P
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Weber 11., Sim B.K.L., Tyon J.A., Wolff R.;
"Merozoite surface protein sequence from the Camp strain of the human malaria parasite plasmodium falciparum.';
Nucleic Acids Res. 16:1206-1206(1988).
- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
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                                                                   SURFACE ANTIGENS)
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Interpro; IPR000561; EGF-like.
Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
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                                                                                                                                              Plasmodium falciparum (isolate Camp / Malaysia).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBL_TaxID=5835;
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Pred. No. 3.5e-06;
6; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                    Weber J.L., Leininger W.M., Lyon J.A.; "Variation in the gene encoding a major merozoite s the human malaria parasite Plasmodium falciparum.";
Ol-CCT-1996 (Rel. 10, Last sequence update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE (PMMGA) (P195).
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MEDLINE=86205236; Pubmed=3517809;
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SEQUENCE OF 1104-1726 FROM N.A.
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|larity 43.3%;
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13-Aug-1987 (Rel. 05, Created)

STANDARD;

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P04932;
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                                                                                                                                                                                      "Plasmodium falciparum: gene structure and hydropathy profile of the major merozoite surface antigen (gp195) of the Uganda-Palo Alto
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PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 4 KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                     Exp. Parasitol. 67:1-11(1988).
-1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
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Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
Transmembrane; GP-anchor.
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                                                                                                     Plasmodium falciparum (isolate Palo Alto / Uganda).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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Chang S.P., Kramer K.J., Yamaga K.M., Kato A., Case S.E.,
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MEROZOITE SURFACE PROTEIN 1
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Pred. No. 3.5e-06;
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                     STANDARD;
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                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                         NCBI_TaxID=57270;
                                                                                  (PMMSA) (GP195).
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                     MSP1_PLAFP
P50495;
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RESULT

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-!- PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 4
KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF
MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                                                                                                                              REVISIONS, SEQUENCE FROM N.A.
Pan W., Tolle R., Bujard H.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                 13-AUG-1987 (Rel. 05, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
                                                                                                                                                                                                                                                                                                                            "Polymorphism of the precursor for the major surface antigens of Plasmodium falciparum merozoites: studies at the genetic level."; EMBO J. 4:3823-3829(1985).
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Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
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                                                                                                                                                                                                                                                                                 Mackay M., Goman M., Bone N., Hyde J.E., Scaife J., Certa U., Stunnenberg H., Bujard H.;
                                                                                                                                                             Plasmodium falciparum (isolate Kl / Thailand).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Pred. No. 6.1e-06;
5; Mismatches 8;
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TRIPEPTIDE SG(TP)
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N-LINKED (GLCNAC)

N-LINKED (GLCNAC)
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1630 AA
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                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-86136024; Pubmed-3004972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X03371; CAA27070.1; -. PIR; A25120; SAZQK1.
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Best Local Similarity 44.1'
Matches 41; Conservative
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STANDARD;
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MSP1_PLAFW P04933;

RESULT 10 MSP1_PLAFW

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     1526 NISQHQCVKKQCP-----QNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENN 1578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peterson M.G., Coppel R.L., McIntyre P., Langford C.J., Woodrow G., Brown G.V., Anders R.F., Kemp D.J.;
"Variation in the precursor to the major merozoite surface antigens of Plasmodium falciparum.";
Mol. Biochem. Parasitol. 27:291-302(1988).
-:- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YEAM: MERCACUTE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MERCACUTES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                          01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT-1996 (Rel. 14, Last annotation update)
MEROZOTIE SURFACE PROTEIN 1 PRECURSOR (MEROZOTIE SURFACE ANTIGENS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interproj IPR000561; EGF-like.
Pfam: PF00008; EGF: 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein; Transmembrane; GF1-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum (isolate FC27 / Papua New Guinea).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED GLCNAC. .) (POTEN N-LINKED GLCNAC. .) (
                                                                                                                                                                                                                                                          PRT; 1701 AA.
                                                                                             1579 GGCDADAKCTEEDSGSNGKKITCECTKPDSYPL 1611
                                                                 ------EDSGSNGKKITCECTKPDSKPI 121
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SEQUENCE FROM N.A.
MEDLINE-88142999; PubMed-2449612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M19143; AAA29653.1; -.
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P13819;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-66014155; PubMed-2995820;
MHOLINE-66014155; PubMed-2995820;
NHOLder A.A., Lockyer M.J., Odink K.G., Sandhu J.S., Riveros-Moreno V., Nicholls S.C., Hillman Y., Davey L.S., Tizard M.L.V., Schwarz R.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Holder A.A.;
Submitted (MAR-1991) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                                                                                                            13-AUG-1987 (Rel. 05, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "primary structure of the precursor to the three major surface antigens of Plasmodium falciparum merozoites."; Nature 317:270-273(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A24594; A24594.
InterPro; IPR000561; EGF-like.
Pfam; PF00008; EGF; IJ
Malaria; Mercopie; Polyprotein; Repeat; Signal; Glycoprotein;
Transmembrane; GPI-anchor.
                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum (isolate Wellcome).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBI_TaxID=5848;
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MEROZOITE SURFACE PROTEIN 1.
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Pred. No. 6.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC.
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| 1570 GGCDADAKCTEEDSGSNGKKITCECTKPDSYPL 1602
                                                                                                                                                               1639 AA
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N-LINKED
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ilarity 44.1%;
Conservative
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                                                                                                                                                                  STANDARD;
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nes 41; Conserv
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Freeman R.R.;

REVISIONS

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                                           Gaps
Score 187.5; DB 1; Length 1701;
Pred. No. 2.7e-05;
7; Mismatches 11; Indels 43;
                                                                              50 GKPKDELDYENDIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLL
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CARBOHYD

Query Match

Best Loc Matches

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(POTENTIAL)

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AMA-1 OR PF83.
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P22621;
            CARBOHYD
SEQUENCE
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1581 GKFQDML----NISQHQCVKKQCP-----ENSGCFRHLDEREECKCLLNYKQEGDKCV 1629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42
                                                                                                                                                                                                                                                                                           parasite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- PTM: MEROZÓITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 4 KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                               01.AUG-1988 (Rel. 08, Created)
03.MAY-2000 (Rel. 39, Last sequence update)
30.MAY-2000 (Rel. 39, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1 - SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum merozoites: studies at the genetic level.";
EMBO J. 4:3823-3829(1985).
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-115 FROM N.A.
MEDILINE-86136024; PubMed=3004972;
MEDILINE-86136024; PubMed=3004972;
MEDILINE-86136024; PubMed=3004972;
Stunnenberg H., Bujard H.;
Polymorphism of the precursor for the major surface antigens of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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InterPro; IPR000561; BGF-like.
Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
Transmembrane; GPI-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                               MEDLINE-88011243; PubMed-3079521;
Tanabe K., Mackay M., Goman M., Scaife J.G.;
"Allelic dimorphism in a surface antigen gene of the malaria plasmodium falciparum.";
J. Mol. Biol. 195:273-287(1987).
                                                                                                                                                                                                       Guinea).
Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROZOITE SURFACE PROTEIN 1
                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
                                  1630 ENPNPTCNENNGGCDADATCTEEDSGSSRKKITCECTKPDSYPL 1673
                       -----EDSGSNGKKITCECTKPDSKPI 121
                                                                                                                                                                                                     (isolate mad20 / Papua New Apicomplexa; Haemosporida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED GLCNAC...
                                                                                                        PRT; 1701 AA
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REVISIONS TO 1403; 1569 AND 1629.
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PIR; A26868; A26868.
PIR; B25120; B25120.
                                                                                                        STANDARD;
                                                                                                                                                                                                     Plasmodium falciparum
Eukaryota; Alveolata;
NCBI_TaxID=70153;
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL).
                                                                                                                                                                             PMMSA) (P190).
                                                                                                                              01-AUG-1988 (
30-MAY-2000 (
30-MAY-2000 (
                                                                                                        MSP1_PLAFM
P08569;
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MSP1_PLAFM
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                                                                                                                                                                                                                                                               1581 GKFQDML----NISQHQCVKKQCP-----ENSGCFRHLDEREECKCLLNYKQEGDKCV 1629
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APTCAL MEMBRANE ANTIGEN 1.
EXTRCELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-N (IN REF. 1; AAA29476).
H -> N (IN REF. 1; AAA29476).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1991 (Rel. 19, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
My. 3FC2EC59AF96EA98 CRC64;
                                                                                                                                                                   43;
                                                                                                                       Length 1701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum (isolate FC27 / Papua New Guinea).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5837;
                                                                                                                                                                   Indels
                                                                                                                                                                                                                   50 GKPKDELDYENDIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLL-
                                                                                                                                                                                                                                                                                                                                       1630 ENPNPTCNENNGGCDADATCTEEDSGSSRKKITCECTKPDSYPL 1673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antigen; Glycoprotein.
                                                                                                                                                                                                                                                                                                                 ------EDSGSNGKKITCECTKPDSKPI 121
                                                                                                                    Score 187.5; DB 1;
Pred. No. 2.7e-05;
                                                                                                                                                                   11;
                                                                                                                                                                 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     622 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=89384584; Pubmed=2701947;
  1196 1196 N-LJ
1588 1588 N-LJ
1701 AA; 193768 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A32499; A32499; Apmem_Agl.
InterPro.; IPRO03298; Apmem_Agl.
Pfam; PF03430; Adm.1; 1
Malaria; Signal; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1991 (Rel. 19, Created)
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                                                                                                                    Query Match 9.8%;
Best Local Similarity 41.3%;
Matches 43; Conservative
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AMA-1 OR PF83
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P50489;
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                                                           CARBOHYD
CARBOHYD
           DOMAIN
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                                                                                                                                     Query Match
 TRANSMEM
                                  CARBOHYD
                                                 CARBOHYD
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PLAFC
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                                                                                     12;
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                                                                                                                                                                                                                                                          249
                                                                                                                                                                           DEMRHEYKDNKYVKNLD--ELTLCSRHAGNMIPDNDKNSNYKYPAVYDDKDKKCHILYIA 253
                                                                                                                                                             79 VNSNSG---CFRHLDEREECKCLLEDSGSNGKKITCECTKPDSKPIVQYDNF-NANPNAN 134
                                                                                                                                                                                                            -PNAN----PDGNCEDIPHVNEFSAIDLGNAEKYDKMDEPQHYGKSLTPLEELYKPNDKS 189
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                                                                                       Gaps
                                                                                                             DHHHHHHKHKKLKQPGDGNPWSPCSVTCGKPKDELDYENDIEKKIC---KMEKCSSVFNV 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOI. Biochem. Parasitol. 42:285-287(1990).
-!- FUNCTION: INVOLVED IN PARASITE INVASION OF ERYTHROCYTES.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: STRONG TO AMA-1 FROM P.CHABAUDI AND P.FRAGILE, AND PK66 FROM P.KNOWLESI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91101665; PubMed=2270110;
Thomas A.W., Waters A.P., Carr D.;
"Analysis of variation in PF83, an erythrocytic merozoite vaccine
candidate antigen of plasmodium falciparum.";
Mol. Blochem. Parasitol. 42:285-287(1990).
                                                                                                                                                                                                                                                      190 LYQYIKANSKFIGITELSNTFINNAGOHGHMHGNEREDERTLTKEYEDIVLKEFTYMINF
: ||| DAN |
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20-AUG-2001 (Rel. 40, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN).
                                                                                     Indels 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum (isolate 7G8).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
-> M (IN REF. 1; AAA29476).
-> R (IN REF. 1; AAA29476).
7D41335E249FA18F CRC64;
                                                               Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APICAL MEMBRANE ANTIGEN 1. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Malaria; Signal; Transmembrane; Antigen; Glycoprotein.
                                                              9.3%; Score 179; DB 1; L
25.0%; Pred. No. 3.1e-05;
tive 22; Mismatches 86;
                                                                                                                                                                                                                                   307 LONAKFGLWVDGNCEDIPHVNEFSAIDLFECNKL-\----
                                                                                                                                                                                                                                                                                                                                                                                                                                                622 AA.
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InterPro; IPR003298; Apmem_Ag1.
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(Rel. 40, Last anno
  496 I
503 N
72009 MW;
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  496
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622 AA;
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SEQUENCE FROM N.A.
                                                                            Similarity
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P50492;
  CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                  KICKMEKCSSVFNVVNSNSG---CFRHLDEREECKCLLEDSGSNGKKITCECTKPDSKPI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 VQYDNF-NANPNAN-PNAN----PDGNCEDIPHVNEFSAIDLGNAEKYDKMDEPQHYGKS 175
                                                                                                                                                                                                                                                                                                                                                                        190 ISPMTLDHMRDFYKNNEYVKNLDELTLCSRHAGNMNPDNDKNSNYKYPA-VYDY-ND--- 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----KKCHILYIAAQENNGPRYCNKDESKRNSMFCFRPAKDKSFQNYTYL----SKNV 294
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                          16 ISYIYADHHHHHHHKHKKL------KQPGDGNPWSPCSVTCGKPKDELDYENDIEK 64
POTENTIAL.

(YTOPLASMIC (POTENTIAL).

(YTOPLASMIC (SICHAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176. LTPLEELYKPNDKSLYQYIKANSKFIGITELSNTFINNAGQHGHMHGNEREDERTLTKEY
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                                                                                                                                                                                                                                                                                        Indels 153;
                                                                                                                                                                                                                                     Score 171.5; DB 1; Length 622;
Pred. No. 0.0001;
3; Mismatches 84; Indels 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum (isolate Camp / Malaysia).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295 V--DNWEKVCPRKNLENAKFGLWVDGNCEDIPHVNEFSANDLFECNKL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 YEHSSPSSTKSSSPSNVKSASLATRLMK--KFKAEIRDFFGISYYEK 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1C9C8715D8E2915F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-02001 (Rel. 40, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              622 AA
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                                                                                                                                                                                MM;
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                                                                                                                                                                                                                                                                   Best Local Similarity 23.6
Matches 82; Conservative
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us-09-763-397a-2.rsp

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11;
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                                                                                                                                                                                                                                 99 LEDSGSNGKKITCECTKPDSKPIVQYDNF-NANPNAN-PNAN----PDGNCEDIPHVNEF 152
                                                                                                                                                                                                                                            277 RPAKDKSFQNYTYL----SKNVV--DNWEKYCPRKNLENAKFGLMVDGNCEDIPHVNEF 329
                                                                                                                                                                                                                                                                                                        213 NAGQHGHMHGNEREDERTLTKEYEDIVLKEFTYMINFGRGQNYWEHPYQKSDQPKQYEQH 272
                                                                                                                                                                                                                                                                                                                   153 SAIDLGNAEKYDKMDEPQHYGKSLTPLEELYKPNDKSLYQYIKANSKFIGITELSNTFIN 212
                                                                                                                                                         Query Match 8.9%; Score 171.5; DB 1; Length 622; Best Local Similarity 23.9%; Pred. No. 0.0001; Matches 74; Conservative 24; Mismatches 77; Indels 135; Gaps
                                                                                                                                                                                              45 CSVTCGKPKDELDYENDIEKKIC---KMEKCSSVFNVVNSNSG---CFRHLDEREECKCL 98
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Search completed: January 29, 2002, 11:13:36 Job time: 812 sec

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US-08-113-288B-18

Sequence 18, Application US/08313288B

Sequence 18, Application US/08313288B

Sequence 18, Application US/08313288B

Sequence 18, Application US/08313288B

SETITIE OF INVEWTION:

CLONING, EXPRESSION AND USES OF A TITLE OF INVEWTION:

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

SIPR: 1.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
CONFERNT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,288B
FILING DATE: January 5, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White: John P 8,678
REGISTRICATION NUMBER: 40028-A-PCT-US
TELEPRATION NUMBER: 40008
TELEPRATION NUMBER: 218,678
TELEPRATION NUMBER: 228,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 215.5; DB 1;
Pred. No. 3.2e-12;
2; Mismatches 7;
                  US-08-929-329-5

US-08-653-587-16

US-08-639-501-2

US-09-044-918-2

US-09-150-741-2

US-08-150-741-2

US-08-134-669-2

US-08-189-465-4

US-08-189-462-4

US-08-515-51A-2

US-08-515-51A-2

US-08-515-51A-2

US-08-745A-47

US-08-795-445A-47

US-08-794-186-47

US-08-794-186-47

US-08-794-186-47
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62.2%;
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Best Local Similarity 62.2
Matches 46; Conservative
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  LENGTH:
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Sequence 3, Appli
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Sequence 9, Appli
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59.139 Million cell updates/sec
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being printed,
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Sequence 4
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Sequence 4
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-313-288B-18

US-08-760-797A-1

US-08-932-929B-1

US-08-932-929B-3

US-08-932-929B-3

US-08-290-919-3

US-08-455-655-35

US-08-455-685-35

US-08-455-685-35

US-08-455-685-35

US-08-455-685-35

US-08-455-685-35

US-08-456-45

US-08-133-288B-14

US-08-133-288B-14

US-08-133-28B-14

US-08-139-13

US-08-290-919-12

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Maximum Match 100%
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1 MKFLVNVALVFMVVYISYIY....
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                                                                                                                                                                                                                                                                                                                                                                                                                                  seq length: 0 seq length: 2000000000
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Match 1
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Maximum DB :
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Gaps

19;

Length 412; Indels

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29 KH-----KKLKQPGDGNPWSPCSVTCG-------KPKDELDYENDIEKKICKME 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 3, Application US/08760797A; Sequence 3, Application US/08760797A; Patent NO. 5928902, GENERAL INFORMATION:

APPLICANT: De Wilde, Michel APPLICANT: Cohen, Joseph ; TITLE OF INVENTION: Hybrid Protein Between CS TITLE OF INVENTION: from Plasmodium and HBSAG NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.9%; Score 210.5; DB 4; 63.4%; Pred. No. 9.9e-12; tive. 1; Mismatches 6;
TITLE OF INVENTION: from Plasmodium and HBSAG NUMBER OF SEQUENCES: 4
CORRESPONDENCE_ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALUNESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                           E: SmithKline Beecham Corporation 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,797
FILING DATE: 04-DEC-1996
APPLICATION NUMBER: 08/42,612
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Baumelster, Kirk
REGISTRATION NUMBER: 33,833
REGISTRATION NUMBER: 34,835
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/932,929B FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: ...
ZIP: 19406
COMBUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                        MEDIUM TYPE: Diskette COMPUTER: IBM COmpatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acids
TYPE: amino acid
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Best Local Similarity 63.45
Matches 45; Conservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 610-270-5090
                                                                                  STREET: 709 Swedeland
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                              ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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US-08-932-929B-1
                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                              USA
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                                                                  ADDRESSEE:
                                                                                                                                              COUNTRY:
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Pred. No. 9.9e-12;
1; Mismatches 6; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 KH-----KKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKME 70
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Patent No. 6169171
GENERAL INFORMATION:
APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: Hybrid Protein Between CS
                                                                                                                                                                       Sequence 1, Application US/08760797A
Patent No. 5928902
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: Hybrid Protein Between CS
TITLE OF INVENTION: Hybrid Protein and HBsAG
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER FEADABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 04-DEC-1996
                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B45015-1C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION NUMBER: 08/442,612
FILING DATE: 17-MAY-1995
ATTONIEY/ABENT INFORMATION:
NAME: Baumelster, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: 845015-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.9%;
Best Local Similarity 63.4%;
Matches 45; Conservative 1
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                         388 KCSSVFNVVNSSIG 401
                                       71 KCSSVFNVVNSNSG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 KCSSVFNVVNS 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 19406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
US-08-760-797A-1
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3;

Gaps

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29 KHKKLKQPGD-----KPKDELDYEND 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: de Taisne, Charles
APPLICANT: de Taisne, Charles
APPLICANT: Tine, John A.
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue, 25th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,073
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,783
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/852,305
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/672,183
FILING DATE: 20-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAMME: Frommer, William S.
REGISTRATION NUMBER: 25.50
REGISTRATION NUMBER: 25.50
REGISTRATION NUMBER: 25.50
REGISTRATION NUMBER: 25.30
RECISTRATION NUMBER: 25.30
  B45015-1FWC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 IEKKICKMEKCSSVFNVVNSSIG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/08257073 Patent No. 5766597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 IEKKICKMEKCSSVFNVVNSNSG 84
                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                  10.8%;
51.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066 CURTMS
INFORMATION FOR SEQ 1D NO: 9:
  REFERENCE/DOCKET NUMBER:
                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-932-929B-3
                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 51.8
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                         INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-257-073-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 207.5; DB 2; Length 424;
Pred. No. 1.9e-11;
4; Mismatches 9; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 KHKKLKQPGD-----GNPWSPCSVTCG-----
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Patent No. 6169171
GENERAL INFORMATION
GENERAL INFORMATION: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: Hybrid Protein Between CS
TITLE OF INVENTION: from Plasmodium and HBsAG
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                 SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/760,797A FILING DATE: 04-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932,929B
                                                                       FILING DATE: 04-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/442,612
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Baumelster, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: B45015-
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,797
FILING DATE: 04-DEC-1996
APPLICATION NUMBER: 08/442,612
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Baumelster, Kirk
REGISTRATION NUMBER: 33,833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 IEKKICKMEKCSSVFNVVNSSIG 192
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                                                                                                                                                                                                                                                                                                                                                          information for SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 424 amino acids TYPE: amino acid STARNEDBESS: single STARNEDBESS: single US-08-760-797A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 51.8%;
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                  TELEFAX: 610-270-5090
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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; Sequence 35, Application US/08455625
; Patent No. 5932218
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/note= "X =
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                                                                                                                                                                                                                                         NAME/KEY: Modified-site LOCATION: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 703-205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                            25; Conservative
                                                                                                                              53 amino acids
                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
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COTHER INFORMATION:
US-08-290-919-3
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
US-08-455-625-35
                                                                                                                                                                                                                                                                    LOCATION:
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                                                                                                                              LENGTH:
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                                                                                                                                                                                                                                                                      196 DEMRHFYKDNKYVKNLD--ELTLCSRHAGNMIPDNDKNSNYKYPAVYDDKDKKCHILYIA 253
                                                                                                                                                                                                                                                                                                        79 VNSNSG----CFRHLDEREECKCLLEDSGSNGKKÍTCECTKPDSKPIVQYDNF-NANPNAN 134
                                                                                                                                                                                                                                                                                                                               254 AQENNGPRYCNKDESKRNSMECKO- A FRPAKDISFONYTYLSKNVV--DNWEKVCPRKN 306
                                                                                                                                                                                                                                                                                                                                                                                          135 -PNAN----PDGNCEDIPHVNEFSAIDLGNAEKYDKMDEPQHYGKSLTPLEELYKPNDKS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 LYQYIKANSKFIGITELSNTFINNAGQHGHŅHGNEREDERTLTKEYEDIVLKEFTYMINF 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::: | ||
------FKNKNASMIKS--- 377
                                                                                                                                                                                           Indels 133; Gaps
                                                                                                                                                                                                                                 22 DHHHHHHKHKKLKQPGDGNPWSPCSVTCGKPKDELDYENDIEKKIC---KMEKCSSVFNV 78
                                                                                                                                                       Length 628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: HOLDER, ANTHONY A.
APPLICANT: BLACKMAN MICHAEL J.
APPLICANT: CHAPPEL, JONATHAN A.
TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO MALARIA
TITLE OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                   307 LONAKFGLWVDGNCEDIPHVNEFPAIDLFECNKL-------
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,919
FILING DATE: 04-0CT-1994
CLASSIFICATION: 435
                                                                                                                                                     Query Match
9.1%; Score 175.5; DB 1;
Best Local Similarity 25.0%; Pred. No. 3.5e-08;
Matches 82; Conservative 24; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: CUSHMAN DARBY & CUSHMAN, L.L.P. 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9203821.5
FILING DATE: 22-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00367
FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346 -------ASDQPKQYEQHLTDYEKIKEG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 SNVKSASLATRLMKKFKAEIRDFFGISY 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              378 RRIKSAFLPT---GAFKADRYKSHGKGY 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08290919 Patent No. 5720959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: KOKULIS, PAUL N. REGISTRATION NUMBER: 16,773
                                                          peptide
internal
                       single
; TYPE: amino acid
; STRANDEDNESS: singl;
; TOPOLGX: linear
; MOLECULE TYPE: peptid
; FRAGMENT TYPE: intern
US-08-257-073-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1100 NEW CITY: WASHINGTON STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 20005-3918
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Berzofsky, Jay A.
APPLICANT: Alers, Jeffrey D.
APPLICANT: Pendleton, C. D.
APPLICANT: Pendleton, C. D.
APPLICANT: Phiral, Mutsunori
TITLE OF INVENTION: COMPOSITE SYNTHETIC PEPTIDE CONSTRUCT
TITLE OF INVENTION: LIMPHOCYTES AGAINST HIV
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STREET: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 53;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 SNSGCFRHLDEREECKCLLEDSGSNGKKITCECTKPDSKPI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 212242/HCM/MJL/6BC8/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEPEX: (202) 822-0944
TELEEX: 6744627 CUSH
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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61.0%; Pred. No. 1.5e-05;
tive 3; Mismatches 7;
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APPLICATION NUMBER: US 08/060,988
FILING DATE: 14-MAY-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Berzofsky, Jay A.
APPLICANT: Ahlers, Jeffrey D.
APPLICANT: Pendleton, C. David
APPLICANT: Pendleton, C. David
APPLICANT: Shirai, Mutsunori
TITLE OF INVENTION: MULTIDETERMINANT PEPTIDES THAT ELLCIT
TITLE OF INVENTION: HELPER T-LYMPHOCYTE, CYTOTOXIC T LYMPHOCYTE AND
TITLE OF INVENTION: NEUTRALIZING ANTIBODY RESPONSES AGAINST HIV-1
NUMBER OF SEQUENCES:
                                                                                                             /label- peptide
/note- "peptide from P. falciparum CS antigen"
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                           31 KKLKQPGDGNP------WSPCSVTCGKPKDELDYENDIEKKICKMEKCS 73
                                                                                                                                                                                                                                                   Indels 13;
                                                                                                                                                                                                             Length 66;
                                                                                                                                                                                                           Score 128.5; DB 2;
Pred. No. 3.4e-05;
3; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/060,988
FILING DATE: 14-MAY-1993
APPLICATION NUMBER: 07/847,311
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/151,998
FILING DATE: 29-AUG-1991.
APPLICATION NUMBER: 07/149,692
FILING DATE: 26-JAN-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Beattle, Ingrid A.
REGISTRATION NUMBER: P-42,306
REFERENCE/DOCKET NUMBER: 08830/022003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Fish & Richardson P.C. 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 35, Application US/08455685 Patent No. 6214347 GENERAL INFORMATION:
                                                                                                                                                                                                           6.7%;
51.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPUTER
                                                                                                                                                                                     Query Match
Best Local Similarity 51.00,
-hoq 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
                 MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: peptide US-08-455-685-35
                                                                     MAME/KEY: Peptide
COCATION: 1.66
OTHER INFORMATION:
COTHER INFORMATION:
US-08-455-625-35
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
US-08-455-685-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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                                                       FEATURE:
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                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: MULTIDETERMINANT PEPTIDES
TITLE OF INVENTION: THAT ELICIT
TITLE OF INVENTION: HELPER T-LYMPHOCYTE, CYTOTOXIC T LYMPHOCYTE AND
TITLE OF INVENTION: HELPER T-LYMPHOCYTE, CYTOTOXIC T LYMPHOCYTE AND
TITLE OF INVENTION: HELPER T-LYMPHOCYTE, CYTOTOXIC T LYMPHOCYTE AND
TITLE OF INVENTION: HELPER T-LYMPHOCYTE, CYTOTOXIC T LYMPHOCYTE AND
WUMBER OF SEQUENCES: 48
COMMESSED: FISH & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
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                                                                                                                                                                                                        31 KKLKQPGDGNP------WSPCSVTCGKPKDELDYENDIEKKICKMEKCS 73
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        Length 66;
                                                                                     Indels
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COUNTY: BOSTON
STATE: MA

COUNTY: 0210-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: FASTEM: Windows 95
SOFTWARE: FASTEM OF WINDOWS VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/060,988A
FILING DATE: 14-MAY-1992
APPLICATION NUMBER: 07/847,311
FILING DATE: 05-MG-1991
APPLICATION NUMBER: 07/751,998
FILING DATE: 26-JAN-1982
ATTORNEY AGENT TRORMATION:
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Score 128.5; DB 4
Pred. No. 3.4e-05;
3; Mismatches 11
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                                                                                                                                                                                                                                                                                                                                                                                                         US-08-060-988A-35; Sequence 35, Application US/08060988A; Patent No. 6294322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Berzofsky, Jay A.
APPLICANT: Ahlers, Jeffrey D.
APPLICANT: Pendleton, C. David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 08
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Nara, Peter
APPLICANT: Shirai, Mutsunori
    6.7%;
51.8%;
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Query Match 6.7%
Best Local Similarity 51.8%
Matches 29; Conservative
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Best Local Similarity 51.8
Matches 29; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
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60 -NDIEKKICKMEKCSSVFNVVNSNSGCFRHLDEREECKCLLEDSGSNGKKITCECTKPDS 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---KKLKQPGDGNPWSPCSVTCGK----PKDELDYE-- 59
                                                                                                                                                                                                                                                    ----KPKDELDYENDIEKKICKMEKCSSVFNVVNSNSG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.5%; Score 125; DB 1; Length 559;
21.0%; Pred. No. 0.0017;
ive 46; Mismatches 104; Indels 128;
                                                                                                                                                                                               16;
                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jessell, Thomas M. and Avihu Klar
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                          6.5%; Score 125; DB 6; 40.0%; Pred. No. 0.00093;
                                                                                                                                                                                               10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSEE: Cooper & Dunham LLP
F: 1185 Avenue of the Americas
New York
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                           Sequence 14, Application US/08313288B Sequence 10, Application US/08313288B Patent No. 5750502 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
           FILING DATE: 26-OCT-1987
APPLICATION NUMBER: 649,903
FILING DATE: 12-SEP-1984
APPLICATION NUMBER: 115,634
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amino acid
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                                                                                                                                                                                                 Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                       39 GNPWSPCSVTCG----
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Best Local Similarity
Matches 74; Conserva
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Best Local Similarity
Matches 24; Conserv
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STRANDEDNESS:
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MOLECULE TYPE:
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                                                                      SEQ ID NO:9:
LENGTH: 378
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                                                                                                                                                                                                                                                                                                                                                US-08-313-288B-14
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                                                                                                           5171843-9
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                                                                                                   COMPOSITE SYNTHETIC PEPTIDE CONSTRUCT
ELICITING NEUTRALIZING ANTIBODIES AND CYTOTOXIC T
LYMPHOCYTES AGAINST HIV
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/note= "peptide from P. falciparum CS antigen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 KKLKQPGDGNP-------WSPCSVTCGKPKDELDYENDIEKKICKMEKCS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 128.5; DB 5; Length 66; Pred. No. 3.4e-05; 3; Mismatches 11; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; PATENT NO. 5171843
APPLICANT: NUSSENZWEIG, VICTOR
TITLE OF INVENTION: IMMUNOGENIC POLYPEPTIDE AND METHOD FOR ; PURIFYING IT
                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US94/05142
                                                                                         APPLICANT:
TITLE OF INVENTION: COMPOSITE SYNTHETIC PEPTIDE
TITLE OF INVENTION: ELICITING NEUTRALIZING ANTII
TITLE OF INVENTION: LYMPHOCYTES AGAINST HIV
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/060,988
FILING DATE: 14-MAY-1993
ATORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30330
REGISTRATION NUMBER: 1173-434P
TELECHONEY/ACCET NUMBER: 1173-434P
TELECHONE: 703-205-8050
TELEFAX: 703-205-8050
                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 13-MAY-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/175,112
FILING DATE: 30-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 754,645
FILING DATE: 9-JUL-1985
                                                         Sequence 35, Application PC/TUS9405142 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 66 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: /
; OTHER INFORMATION: /
PCT-US94-05142-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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Matches 29; Conserv
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                                               PCT-US94-05142-35
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                            RESULT 11
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Gaps

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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION NOMBER: US/08/568,459A
FILING DATE: 07-DEC-1995
CLASSIFICATION: UNDER: US/08/568,459A
FILING DATE: 07-DEC-1995
CLASSIFICATION: VERATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAME (619) 235-6076
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSGSNGKKITCECTKPDSKPIVQYDNFN----
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                     Sequence 4, Application US/08568459A Patent No. 5849306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 FGRGQNYWEHPYQKSDQPKQYEQH 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1435 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: NO
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Matches 61; Conserve
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                                          119 KPIVQYONFNANPNANP----NANPDG----NCE-----DI----PHVNEFSAIDL--- 157
                                                                                                                                                                                376 VPKNPEDDREENFDIPKKPENKHDNQNNL----PNDKS------DRNIPYSPLPPKV 422
                                                                                                                                                                                                                          211 INN------ACQHGHMHGNEREDERTLTKEYEDIVLKEFTYMINFGRGQNYWEHPYQ 261
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                                                                                                                                   158 -----GNAEKYDKMDEPQHYGKSLTPLEELYKPNDKSLYQYIKANSKFIGITELSNTF
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                                                                                                                                                                                                                                                                                                                   262 KSDQPKQYEQHLTDYEKIKEGKPLDKFGNIYDYHYEHSSPSSTKSSSPSNVK 313
                                                                                                                                                                                                                                                                                                                                               DB 3; Length 478;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAINST MALARIA, METHODS OF PROTEC DELIVERING POLYNUCLEOTIDE VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Hoffman, Stephen L.
APPLICANT: Hedstrom, Richard C.
APPLICANT: Sedegah, Martha
TITLE OF INVENTION: POLYNUCLEOTIDE VACCINE PROTECTIVE
TITLE OF INVENTION: DELIVERING POLYNUCLEOTIDE OF TITLE OF INVENTION: DELIVERING POLYNUCLEOTIDE VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/155,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 124.5; DB 3;
Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Naval Medical Res. & Dev. Cmd
STREET: Bldg. 1, T-12 8901 Wisconsin Ave
CITY: Bethesda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Mismatches
                                                                                                                                                                                                                                                                      423 LDNERKQSDPQSQDNNGNRHVPNSEDRET---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08155888 Patent No. 6066623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Spevack, A. David
REGISTRATION UNDRER: 24,743
REFERENCE/DOCKET UNDRER: N.C.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 295-6759
TELEPAX: (202) 295-1022
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.5%;
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274 TSEIQEQ-CEEERCPPK-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Maryland
COUNTRY: USA
ZIP: 20889-5606
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Best Local Similarity
Matches 25; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-155-888-2
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GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Peterson, David S.
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         979 GNSLNHEEVKEHTSNSDNVQQSGGIVNMNVEKELKDTLENPSSSLDEGKAHEELSEPNLS 1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 ----NCEDI-----PHVNEFSAIDLGNAEK--YDKMDEPQHYGKSLTPLEELYKPNDK 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1435;
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illarity 23.1%; Pred. No. 0.0081;
Conservative 36; Mismatches 113;
                                                                                                                                                                                                                  ... FALCIPARUM ... FALCIPARUM ... FALCIPARUM ... FALCIPARUM ... FALCIPARUM ... FALCIPARUM ... STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach ... STATE: California ... COUNTRY: US
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Search completed: January 29, 2002, 10:24:00 Job time: 506 sec ,

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plasmodium
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XX MEDLINE-815, 947, AND 808;

XX MEDLINE-815, 947, Bubmed-7985759;

XX JONGWILLINE-85077069; Pubmed-7985759;

XA JONGWILLINE S. . Tanabe K., Hughes M.K., Kanbara H., Hughes A.L.;

A JONGWILLINE S. . Tanabe K., Hughes M.K., Kanbara H., Hughes A.L.;

A JONGWILLINE S. . . Tanabe K., Hughes M.K., Kanbara H., Hughes A.L.;

AM. J. Trop. Med. Hyg. 51:659-668(1994).

IL AM. J. Trop. Med. Hyg. 51:659-668(1994).

REMBL; M83151; AAA2956-1;

REMBL; M83171; AAA2956-1;

REMBL; M83171; AAA2956-1;

REMBL; M83171; AAA2956-1;

RICHEPTO; IPR000864; TSP1.

RICHEPTO; IPR003067; CICIMSPIZOITE.

REMBL; SMART; SMO209; TSP1: 1.

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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 11.3%; Score 216.5; DB 5; Best Local Similarity 61.1%; Pred. No. 1.7e-09; Matches 44; Conservative 3; Mismatches 12;
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                                                                                                                                         Search time 285.36 Seconds
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                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                       January 29, 2002, 10:59:24
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Maximum Match 100%
Listing first 45 summaries
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sp_bacteria:*
sp_fung1:*
sp_human:*
sp_namma1:*
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sp_phage:*
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"Clonal variation in the Plasmodium falciparum circumsporozoite
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la Cruz V.F.;
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SEQUENCE
                  protein
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        1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 HHHKHKKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKMEKC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q99256 PRELIMINARY; PRT; 424 AA.
Q99256;
01-NOY-1996 (TrEMBLrel. 01, Created)
01-NOY-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPONOZOITE PROTEIN (CS). PRECURSOR, VARIANT 2 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                          Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Indels
                                                                                                                                                                                                                                                                                                                                                    Jongwutiwes S., Tanabe K., Kanbara H.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; M83169; AAA29547.1; -.
EMBL; M83149; AAA29562.1; -.
                                                                                                                                                                                                                                                                                                               Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00209; TSP1; 1.
SEQUENCE 424 AA; 45592 MW; F20CEB60636DB98E CRC64;
                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 216.5; DB 5;
Pred. No. 7.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                              424 AA
                                                                                   Created)
                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR000884; TSP1.
Interpro; IPR003067; Crcmsprzolte.
Pfam: PF00090; tsp_1: 1.
PRINTS; PR01303; CRCMSPRZOITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=91270295; Pubmed=2052038;
Lockyer M.J.;
                                                                                                                                                                                                 MEDLINE=84250215; PubMed=6204383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 11.3%;
1 Similarity 61.1%;
44; Conservative
                                                                                01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2001 (TrEMBLrel. 17, CIRCUMSPOROZOITE PROTEIN.
                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             402 SSVFNVVNSSIG 413
                                                                                                                                      Plasmodium falciparum
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Best Local Similarity
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                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
             93 SSVFNVVNSSIG
                                                                                                                                                                                                                                                                                                        la Cruz V.F.;
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Q27425
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Dame J.B., Williams J.L., McOutchen T.F., Weber J.L., Wirtz R.A., Dame J.B., Williams J.L., Haynes J.D., Schneider I., Roberts D., Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H., "Structure of the gene encoding the immunodominant surface antigen on the sporozoite of the human malaria parasite Plasmodium falciparum."; Science 225:593-599(1984).
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VERTEBRATE HOST).

VERTEBRATE HOST THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.

EMBL., MS7489, AAA6342.1;

InterPro; IPR000884; TSP1.

InterPro; IPR000884; TSP1.

InterPro; IPR000806, LSP1.

PARMIS, PR001303; CROMSPRZOITE.

SMART; SM00209; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 HHHKHKKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKMEKC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
MOI. Biochem. Parasitol. 45:179-182(1991).

-i- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 216.5; DB 5; Length 424; Pred. No. 7.5e-09; 3; Mismatches 12; Indels 13
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NCBL_TaxID=5833;
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Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; M83155; AAA29568.1; -
EMBL; M83170; AAA29548.1; -
EMBL; M83183; AAA29565.1; -
EMBL; M83158; AAA29571.1; -
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Last annotation update)
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Q27246;
Q1-NOV-1996 (TrEMBLrel. 01, Cr
Q1-NOV-1996 (TrEMBLrel. 01, La
Q1-JUN-2001 (TrEMBLrel. 17, La
CIRCUMSPOROZOITE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.3%;
61.1%;
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Best Local Similarity
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Jaraticker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;
de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;
"Sequence variation in the non-repeat region of the Plasmodium
falciparum glutdander rich protein (GLDPP) from Brazil, Senegalese, and
Burmese field isolates and from laboratory strains.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
BMBL; AJ269941 CAB64167.1;
InterPro; IPR00084; TSP1.
InterPro; IPR000867; Crcmsprzoite.
Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;
"Sequence variation in the non-repeat region of the Plasmodium
falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and
Burmese field isolates and from laboratory strains.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ269978; CAB64197.1;
InterPro; IPR000884; TSP1.
InterPro; IPR000808, Cromsprzoite.
Pfam; PF00090; tsp_l; 1.
PRINTS; PR01303; CRCMSPRZOITE.
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                                                                                                                                                                                                                                         Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 AA; 9102 MW; A3283B70CEE50FDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
                                                                                                                                                                    (TrEMBLrel. 13, Last sequence update) (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.2%; Score 215.5; DB 5
63.8%; Pred. No. 1.3e-09;
iive 1; Mismatches 11
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                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13,
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Best Local Similarity 63.8
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                               PRELIMINARY;
 410 SSVFNVNSSIG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum
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                                                                                                                                                                  01-MAY-2000
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                     STRAIN-B1;
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NON_TER
SEQUENCE
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Q9U0P1;
                                                                                                                                09U004;
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                                                                                                                                                                                                                                                                                13; Gaps
                                                                                                                                                                                                                                                            26 HHHKHKKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKMEKC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 HHHKHKKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKMEKC 72
                                                                                                                                                                                       Length 432;
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NCBL_TaxID=5833;
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                                                                                                                                                                                                                          12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              la Cruz V.F.; Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46385 MW; 2CE8D9A68E11945F CRC64;
                                                                                                                              432 AA; 46414 MW; 8787E6005578873A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 11.3%; Score 216.5; DB 5;
1 Similarity 61.1%; Pred. No. 7.7e-09;
44; Conservative 3; Mismatches 12;
                                                                                                                                                                                    Score 216.5; DB 5;
Pred. No. 7.7e-09;
3; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    432 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Biochem. Parasitol. 0:0-0(0).
EMBL; M83165; AAA2543.1; -.
Interpro: IPR000884; TSP1.
Interpro: IPR003067; Crmsprzoite.
Pfam; PF00090; tsp_1; 1.
                                  InterPro; IPR000884; TSP1.
InterPro; IPR03067; Crcmsprzoite.
PRAM; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-84250215; PubMed-6204383;
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EMBL; M83166; AAA29544.1; -. EMBL; M83168; AAA29546.1; -.
                                                                                                                                                                                    Query Match
Best Local Similarity 61.1%;
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CIRCUMSPOROZOITE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                        SSVFNVVNSSIG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR01303; CRCM:
SMART; SM00209; TSP1;
                                                                                                                                                                                                                                                                                                                                   73 SSVFNVVNSNSG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 SSVFNVVNSNSG 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                               SMART; SM
SEQUENCE
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11.1%;
59.7%;
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Best Local Similarity 59.7'
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum.
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Best Local Similarity
                                                                                                                                 117 1
117 AA;
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[1]
SEQUENCE FROM N.A.
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01-NOV-1996 (
01-JUN-2001 (
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NON_TER
SEQUENCE
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                                                                                    Gaps
                                                                                                      26 HHHKHKKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKMEKC 72
                                                                                                                   Jongwutiwes S., Tanabe K., Hughes M.K., Kanbara H., Hughes A.L.;
"Allellc variation in the circumsporozoite protein of Plasmodium falciparum from Thai field isolates.";
Am. J. Trop. Med. Hyg. 51:659-668(1994).
EMBL; M83154; AAA29567.1; -.
InterPro: IPR0030684; TSP1.
InterPro: IPR0030684; TSP1.
InterPro: IPR003069; Crcmsprzoite.
Pfam; PF00090; tsp_l: 1.
SMRNT; SR01303; CRCMSPRZOITE.
SMRNT; SM0209; TSP1: 1.
                                                                                    13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 213.5; DB 5; Length 115;
Pred. No. 2.9e-09;
4; Mismatches 12; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                            Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                Length 80;
                                                                                    11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER 1 1 SEQUENCE 115 AA; 12925 MW; A24CB33AEBE3F232 CRC64;
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1-NOV-1996 (TrEMBLrel. 15, Last sequence update)
01-UND-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
                                 BFC6C970CEF0FA3E CRC64;
                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
                                                                DB 5;
                                                             Score 215.5; DB 5
Pred. No. 1.3e-09;
1; Mismatches 11
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                                                                                                                                                                                                                                                                                                                                              STRAIN=822A;
MEDLINE=95077069; PubMed=7985759;
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illarity 59.7%;
Conservative 4
                        80
9102 MW;
                                                                Query Match
Best Local Similarity 63.8%;
Matches 44; Conservative
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    SM00209; TSP1; 1.
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Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                  1
80
80 AA;
                                                                                                                                                             72 SSVFNVNS 80
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SEQUENCE
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                NON_TER
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      SMART;
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Q25795
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09U934
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Doolan D.L., Saul A., Good M.F.;
"Geographically restricted heterogeneity of the Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 HHHKHKKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKMEKC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 HIBQYLKKIQNSLSTEWSPCSVTCGNGIQVRIKPGSANKPKDQLDYENDIEKKICKMEKC 94
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                                                 circumsporozoite protein: relevance for vaccine development. Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
EMBL: M7723; AAA29517.2; ...
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR003067; Crcmsprzoite.
Pfam; PF00090; LSP_1. 1.
PARNIS: PR01303; CROMSPRZOITE.
SMART; SM00209; TSP1: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 117;
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NCBL_TaxID=5833;
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 213.5; DB 5;
Pred. No. 2.9e-09;
4; Mismatches 12;
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Jongwutiwes S., Tanabe K., Kanbara H.;
Mol. Biochem. Parasitol. 0:0-0(0).
EMBL: M81172; AAA29550.1;
Interpro; IPR000884; TSP1.
Interpro; IPR03067; CrCmsprzoite.
PRIMTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
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MEDLINE-84250215; PubMed=6204383;
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56 Matches

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RESULT Q25830

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de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;
"Sequence variation in the non-repeat region of the Plasmodium
falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and
Burmese field isolates and from laboratory strains.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
BMBL; AZ69961: CAB64180.1;
InterPro; IPR000884; TSP1.
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MEDLINE-84250215; PubMed-6204383;
Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A.,
Dame J.B., Williams J.L., Haynes J.D., Schneider I., Roberts D.,
Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.;
Structure of the gene encoding the immunodominant surface antigen on
the sporozoite of the human malaria parasite Plasmodium falciparum.";
Science 225:593-599(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 HIEQYLKTIQNSLSTEWSPCSVTCGNGIQVRIKPGSANKPKDELDYENDIEKKICKMEKC 71
     Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                           Length 80;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                     9047 MW; BA769C90DB031C3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 11.1%; Score 212.5; DB 5; Best Local Similarity 62.3%; Pred. No. 2.2e-09; Matches 43; Conservative 2; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jongwutiwes S., Tanabe K., Kanbara
Mol. Biochem. Parasitol. 0:0-0(0).
EMBL; M83160; AAA29573.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR000884; TSP1.
Interpro; IPR0009067; Crmsprzoite.
Pfam. PF00090; tsp_1.
PRINTS; PR01303; CRCMSPRZOITE.
                                                                                                                                                                                                                                                              Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                     80 AA;
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                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 SSVFNVNS
                                                                                                       STRAIN-D4230;
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 HHHKHKKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKMEKC 72
                                  HHHKHKKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKMEKC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
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                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 213.5; DB 5; Lenyum. Pred. No. 1.3e-08;
 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jongwitiwes S., Tanabe K., Kanbara H.;
Mol. Blochem. Parasitol. 0:0-0(0).
EMBL. M83173; AAA29551.;
InterPro. IPR000884; TSP1.
InterPro: IPR001067; Crcmsprzoite.
Pfam; PF001090; tsp.1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SEQUENCE 442 AA; 47414 MW; BFAF9D939D7862FF CRC64;
                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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   Mismatches
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59.7%;
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   Conservative
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                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                       394 SSVFNVVNSSIG 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSVFNVVNSSIG 431
                                                                                                     73 SSVFNVVNSNSG 84
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Best Local Similarity
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SEQUENCE FROM N.A.
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43;
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09U0P7;
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DDT 1D
DDT 1D
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RESULT 12 09U0P7

420

Matches

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Gaps

13;

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STRAIN-K1;
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MEDLINE-84250215; PubMed-6204383;
Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A.,
Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D.,
Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.;
"Structure of the gene encoding the immunodominant surface antigen on
the sporozoite of the human malaria parasite Plasmodium falciparum.";
Science 225:593-599(1984).
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                                                                                                       26 HHHKHKKLKQPGDGNPWSPCSVTCG------KPKDELDYENDIEKKICKMEKC 72
                                                                                                                     Gaps
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                                                             Length 115;
                                                                                                                                                                                                                                                                                                                   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_raxID=5833;
                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
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NON_TER 1 1

SEQUENCE 115 AA; 12974 MW; 6BB538287260DA90 CRC64;
PROSITE; PS50092; TSP1; 1.
SMART; SMO0209; TSP1; 1.
NON_TER 1 1 1
SEQUENCE 115 AA; 13018 MW; C0A23F5805688237 CRC64;
                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
                                                                                     12;
                                                               DB 5;
                                                             Score 212.5; DB 5
Pred. No. 3.4e-09;
4; Mismatches 12
                                                                                                                                                                                                                                115 AA.
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Mol. Biochem. Parasitol. 0:0-0(0).
EMBL; M83162; AAA29575.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000884; TSP1.
InterPro; IPR003067; Crcmsprzoite.
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PROSITE; PS50092; TSP1; 1.
                                                                Query Match
Best Local Similarity 59.7%;
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                             Plasmodium falciparum
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                                                                                                                                                      73 SSVFNVNSNSG 84
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Best Local Sim.
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Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A., Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D., Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H., "Structure of the gene encoding the immunodominant surface antigen on the sporozoite of the human malaria parasite Plasmodium falciparum."; Science 225:593-599(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
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Pred. No. 1.5e-08;
                                                                                                                                                  Plasmodium falciparum (isolate K1 / Thailand).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45318 MW; F7F70F1C4939DEA7 CRC64;
                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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420 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jongwutiwes S., Tanabe K., Kanbara H.;
Mol. Biochem. Parasitol. 0:0-0(0).
EMBL; M83174; AAA29552.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000884; TSP1.
InterPro; IPR003067; Crcmsprzoite.
Pfam; FR00090; tsp_1; 1.
PRINTS; PR01303; CROMSPRZOITE.
PROSITE; PS50092; TSP1; 1.
                                                                                                                                                                                                                                                                                                        MEDLINE=84250215; PubMed=6204383;
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Best Local Similarity 59.79
Matches 43; Conservative
                                                                                                                     CIRCUMSPOROZOITE PROTEIN.
  PRELIMINARY;
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SEQUENCE 420 AA; 45
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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Q991c6 drosophila Q8137 bean yellow Q65892 bean yellow Q65892 bean yellow Q955pt bacillus ha Q999u6 staphylococ Q2629 chironomus Q915y6 neisseria m Q91cs drosophila Q91cy1 oryza sativ Q9p5v3 neurospora Q9240 plasmodium C04281 phaseolus v Q23814 calliphora Q960k1 staphylococ Q91ck7 entamoeba h

Ogwyvy unidentifie Ogulz8 caenorhabdi O32856 marthomonas O95093 borrella bu O91qt6 arabidopsis

Q9sai2 arabidopsis Q24847 entamoeba h Q9s5c4 unidentifie Q9xdz1 unidentifie

Run on:

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SEQUENCE FROM N.A.
MEDLINE=91304524: PubMed=1852178;
Alano P., Premawansa S., Bruce M.C., Carter R.;
A stage specific gene expressed at the onset of gametocytogenesis in Plasmodium falciparum.";
Mol. Biochem. Parasitol. 46:81-88(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2]
SEQUENCE FROM N.A.
MEDLINE=97008413; PubMed=8855557;
Alano P., Silvestrini F., Roca L.;
"Structure and polymorphism of the upstream region of the pfg27/25
gene, transcriptionally regulated in gametocytogenesis of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=FCC1/HN;
L1 X.R., Yu X.B., Luo S.H., Shan Z.X., Fang J.M., Xu J.;
"Sequence of Plasmodium falciparum encoding Pfg27/25.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; X84904; CAA59328.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15784.1; -. 26004 MW; B19C47E9B191F7A5 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         falciparum.";
Mol. Biochem. Parasitol. 79:207-218(1996).
                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                        01, Created)
        Q83137
Q65892
                                                       09JSY6
09VTS4 '
09LWJ1
09P5V3
                                                                                                        096240
096240
023814
018320
09F0K1
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                                                                                                                                                                                                             09WVV9
09U128
032856
09S093
09LQT6
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Q9XDZ1
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                                                                                                                                                                                 024847
                                    22225
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NCE 217 AA; 2600
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01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                     PFG27/25.
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Q27336;
RESULT
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                                                                                                                                                                                                                                                                                                                                     Q27336 plasmodium
P90588 plasmodium
Q927u8 chlamydia p
Q9m058 arabidopsis
097909 tragelaphus
002089 caenorhabdi
Q9c6w4 arabidopsis
085356 butyrivibri
Q18366 caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9hgeO gibberella
Q9t011 arabidopsis
Q9seg3 arabidopsis
Q13273 arabidopsis
Q9tim6 orobanche c
Q9kqf7 vibrio chol
Q32608 edwardsiell
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O9atv7 hordeum vul
                                                                             (without alignments)
8.201 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                  Search time 285.36 Seconds
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                                                                                                                                                                                                    473505
        4.5
Compugen Ltd.
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                                                                                                                                                                               473505 seqs, 146272329 residues
                                                                  January 29, 2002, 11:12:07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
        GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
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P90588
Q927U8
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O97909
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Q9C6W4
Q085356
Q1874X1
Q9ATV7
Q9HGE0
Q9T011
Q9SG3
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Gapop 10.0 , Gapext 0.5
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032608
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sp_unclassified:*
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_phage:*
                                               protein search, using
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seq length: 200000000
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97
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sp_bacteria:*
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10
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sp_rodent:*
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Match Length
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                                                                                                                    Perfect score:
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Maximum DB
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Result

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Query Match
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Lal A.A., Goldman I.F., Collins W.E., Kumar N.;
Lal A.A., Goldman I.F., Collins W.E., Kumar N.;
Lad a.A., Sequence of a 27-kilodalton gamete antigen of Plasmodium reichenowl and comparison with Pfg27 of Plasmodium falciparum.";
Mol. Biochem Parasitol. 59:175-176(1993).
EMBL; L08799; AB842050.1; -..
NON_TER 217
                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=AR39;
MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Umayam L.A., Utterback T.,
Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B.,
                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                       GAMATE ANTIGEN (FRAGMENT).

Blasmodium reichenowi.

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

NCBI_TAXID=5854;
                                                                                                                                                                                                                                                                                                                              Score 96; DB 5; Length 217;
Pred. No. 1.8e-07;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                               217 AA; 25943 MW; 24945C26C2252AC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria: Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBL_TaxID=83558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CT488 HYPOTHETICAL PROTEIN.
CPN0600 OR CPJ0606 OR CP0141.
                                                                                                                      Last sequence update)
Last annotation update)
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                                                                                   217 AA
                                                                                                              Created)
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MEDLINE-99206606; PubMed-10192388;
                                                                                      PRT;
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03,
                                                                                                                        01-MAY-1997 (TrEMBLrel. 03, 01-NOV-1998 (TrEMBLrel. 08,
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Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              10 KPLDKFGNVYDYHYEH 25
                                                                                                                                                                                                                                                                                                                                                                                 1 KPLDKFGNIYDYHYEH 16
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                         10 KPLDKFGNIYDYHYEH 25
                                                                                      PRELIMINARY;
   1 KPLDKFGNIYDYHYEH
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SEQUENCE
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SECTOBNICE FROM N.A. Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M., Spiegel L.A., Huang E.N., Shah R., O'Shaughnessy A., Rodriguez M., Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M., Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N., Mewes H.W., Lemcke K., Mayer K.F.X., submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!-CATALYTIC ACTIVITY: S-ADBNOSYL-L-METHIONINE - BADENOSYL-L-HETHIONINE - BADENOSYL-L-HETHIONINE - ADBNOSYL-L-HOWOCYSTEINE - BNA 5-METHYLOYTOSINE.
-!-SIMILARITY: TO C-5 CYTOSINE-SPECIFIC DNA METHYLASE FAMILY.
Interpro; IPRO01025; BAH: 2.
Interpro; IPRO010523; C3_DNA_meth.
Pfam; PF01445; BAH: 2.
Pfam; PF01445; BAH: 2.
PRINTS; PR00105; C5METHRRASE.
SMART; SM00439; BAH: 2.
Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Elsen J., Fraser C.M.; "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39."; Nucleic Acids Res. 28:1397-1406(2000).
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MODIFICATION METHYLASE (EC 2.1.1.73) (CYTOSINE-SPECIFIC
                                                                                                                                                                                                                                                                                       Complete proteome.
Sentence 246 AA; 27619 MW; F3990B645AA0083B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                               Score 48; DB 2;
Pred. No. 7.6;
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PROSITE; PS00095; C5_MTASE_2; 1.
Methyltransferase; Transferase.
SEQUENCE 1512 AA; 171154 MM;
                                                                                                                                             EMBL; AE001645; AAD18745.1;
EMBL; AP002547; BAA98813.1;
EMBL; AE002175; AAF38023.1;
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57.1%;
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217 RPIDGFGNIRGIHY 230
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Matches 8; Conserv
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Best Local Similarity
Matches 8; Conserv
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Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Length 207;
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Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL: US741; AAA68327.1; -.
SEQUENCE 339 AA; 38264 MW; DAE289FF34B70503 CRC64;
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Last sequence update)
Last annotation update)
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Pred. No. 13;
3; Mismatches
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STRAIN=BRISTOL N2;
MEDLINE=94150718; Pubmed=7906398;
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Waterston R.;
Submitted (APR-1997) to the ENEMBL; AF000264; AAC71122.1; -..
HSSP; P54149; 1FVG.
Interpro; IPR002569; PMSR.
ProDom; P0003489; PMSR; 1.
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50.08;
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
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119 EPLDKFYQAEDYHQKY 134
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Best Local Similarity 50.0
Matches 8; Conservative
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                                                                                   Nature 368:32-38(1994).
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                                                                                                                                        SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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                                                                                                                                                                                                    Latreille P.
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                                                           elegans."
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MIDDLINE-94150718; Pubbled-7906398;
MIDDLINE-94150718; Pubbled-7906398;
MIDDLINE-94150718; Pubbled-7906398;
MIDDLINE-94150718; Pubbled-7906398;
MIDDLINE-94150718; MIDDLINE N., Gopper J., Coulson A., Bonfield J., Burton J., Conneil M., Copper T., Cooper J., Coulson A., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Johnston E., Jones M., Kershaw J., Hawkins T., Hillier L., John M., Latreille P., Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M., Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M., Smaldon N., Smaldon N., Smaldon N., Smaldon N., Smaldon N., Vaughan K., Waterston R., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schatzl H.M., Wopfner F., Weidenhofer G., Gilch S.;
"Analysis of 27 mammalian and 9 avian PrPs reveals high conservation of non-structural regions of the prion protein.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
HSSP; P04165, IEIG.
InterPro; IPR002935; Kininogen.
InterPro; IPR000817; Prion.
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO DROSOPHILIA ECDYSONE-INDUCED PROTEIN 28/29 KDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24651 MW; 99FD0BAF0B6A0077 CRC64;
                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
9
                                                                                   227 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 47; DB
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam: PF00377; prion: 1.
PRINTS; PR00334; KININOGEN.
PRINTS; PR00334; RIOON.
SMART; SM00157; PRP: 1.
PROSITE; PS00291; PRCON_1; 1.
PROSITE; PS00706; PRION_2; 1.
                                                                                                                                                                                                                                                                                                                                                                       Bovidae; Bovinae; Tragelaphus
                                                                                                                                                                                                                                                                                 Tragelaphus angasii (nyala).
                                                                                                                                  01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 48.5%;
Similarity 57.1%;
8; Conservative
                                                                                                                                                                                                                           PRION PROTEIN (FRAGMENT).
                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|| ||| |: ||
123 RPLTHFGNDYEDHY 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KPLDKFGNIYDYHY 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227 2
227 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=66437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-PBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
NON_TER
SEQUENCE
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                                                                             606160
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Gaps

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RESULT
085356
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RA Theologis A., EGKET J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA White O., Alonso J., Chao H., Chen H., Cheuk R.F., Chin C.W..
RA Ching M.K., Conn L., Conway A.R., Creasy T.H., Dewar K.,
RA Ching M.K., Conn L., Conway A.R., Creasy T.H., Dewar K.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jonkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Luros J.S., Maiti R., Marialali A.,
RA Militscher J., Miranda M., Nuyeen M., Nierman W.C., Osborne B.I.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA WHO, Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome I of the plant Arabidopsis
                                                             ö
                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 408 816-820(2000).

-i- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING BETA-D-GALACTOSE RESIDUES IN BETA-D-GALACTOSIDES.

GALACTOSE RESIDUES IN BETA-D-GALACTOSIDES.

-i- SIMILARITY: TO FAMIL 35 OF GLYCOSYL HYDROLASES.

EMBL, ACOT4360; AAG60136.1; -.

Interpro; IPR001944; Glyco_hydro_35.

Pfam; PF01304; Gla_Lectin; 1.

Pfam; PF01304; Glyco_hydro_35; 1.

PR01304; Glyco_hydro_35; 1.
                                                                 Gaps
                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 779;
                              Score 45; DB 5; Length 339;
Pred. No. 32;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ase; Hypothetical protein.
86342 MW; 888813DF318890B0 CRC64;
                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) BETA-GALACTOSIDASE (EC 3.2.1.23) (LACTASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
80;
                                                                                                                                                                                                      779 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD005612; Gal_lectin; 1.
PROSITE; PS01182; GLYCOSYL_HYDROL_F35; 1.
PROSITE; PS50228; SUEL_LECTIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45;
Pred. No. 8
                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CV. COLUMBIA;
MEDLINE-21016719; PubMed-11130712;
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                                     46.48;
                                                                                                                                                                                                                                     (TrEMBLrel. 17, (TrEMBLrel. 17, (TrEMBLrel. 17,
                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycosidase; Hydrolase;
                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                   |:| ||:::||
188 PIDPFGSLFDY 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 8; Conserv
                                     Query Match
Best Local Similarity
                                                                                                2 PLDKFGNIYDY 12
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SEQUENCE F
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MEDLINE-94150718; pubMed=7906398;
Milson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Lafrenlle P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Lightning J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Slaston J.,
Thierry Mieg J., Thomas K., Yaudin M., Vaughan K., Waterston R.,
Matson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Kalmokoff M.L., Lu D., Whitford M.F., Teather R.M.;

"Evidence for two new lantibiotics (butyrivibriocin OR79A and OR79B),
"Evidence for two new nanerobe Butyrivibrio fibrisolvens.
Isolated from the rumen annerobe Butyrivibrio fibrisolvens.
Identification of the structural gene encoding butyrivibriocin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Merazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Butyrivibrio.
NCBI_TaxID=831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF062647; AAC19356.1; -. Hypothetical protein. NON_TER 793 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4F8A4ADE8FD43D90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8EE72F58A098D997 CRC64;
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05, Last sequence update)
17, Last annotation update)
                                                                                                    Last sequence update)
Last annotation update)
793 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44.5;
Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   336 AA
                                                                                          01-NOV-1998 (TERBELFEL. 08, Last sequence 01-NOV-1998 (TERBELFEL. 08, Last annotat. HYPOTHETICAL 92.6 KDA PROTEIN (FRAGMENT) Butyrivibrio fibrisolvens.
                                                                    Created)
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      793 AA; 92557 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; 268:32-38(1994).

EMBL; 268493; CAA92795.1; -
InterPro; IPRO03893; DUF215.

Pfam; PF02688; DUF215; 1.

PFAM; PF02688; DAF215; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.9%;
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08,
08,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998 (TrEMBLrel. 01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel.
       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 KFGNIY-DYHYEH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
2, Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 KFGKIYIDYLYDH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C33A12.11 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
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                                                                        01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        elegans."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           018366
                                    085356;
       085356
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Gaps

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Indels

5;

2; Mismatches

Conservative

|||:||:||: PLDEFGNLNQPKYGH 326 PLDKFGNIYDYHYEH 16

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Proctor R.H., Seo J.-A., Plattner R.D.;

"Characterization of four clustered and coregulated genes associated
"Characterization of four clustered and coregulated genes
"Third fumonisin biosynthesis in Fusarium verticillioides.";

"Usubmitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.";

"Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.";

"SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

"Remain ARI55773, AAG27132.1;

"Remain Remain Remain Remains and Paravan Like."

"InterPro: IPR001128; CYL_P450.

"Remain PR00173; Oxidored_FAD.

"Remain PR00175; oxidored_FAD.

"Remain PR00175; oxidored_FAD.

"Remain PR00175; oxidored_FAD.

"Remain PR00175; oxidored_FAD.
"Remain PR00175; oxidored_FAD."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Gibberella.
NCBI_TaxID=117187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1115;
 Length 656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5C6D2B947AE86C25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MODIFICATION METHYLASE (EC 2.1.1.73) (CYTOSINE-SPECIFIC
                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                        3;
 DB 10;
96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 3; 1
Pred. No. 1.7e+02;
6; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
                                                                                                                                                                                                            PRT; 1115 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1404 AA
                                      3; Mismatches
     Score 44;
                       Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heme; Monooxygenase; Oxidoreductase.
SEQUENCE 1115 AA; 123276 MW; 5C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
45.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 37.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
                     Best_Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KPLDKFGNIYDYHYEH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                            Gibberella moniliformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T6G15.160 OR AT4G13610.
                                                                                                   ||||| ::||:|
414 KPLDHPADLYDFH 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 ||::|: :::
26 KPLPLLGNLFDFDFDN
                                                                           1 KPLDKFGNIYDYH 13
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=M-3125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METHYLTRANSFERASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3702;
   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS;
                                                                                                                                                                                                                               Q9HGEO;
                                                                                                                                                                                                            Q9HGE0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9T011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
                                                                                                                                                                       RESULT
Q9HGE0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9T011
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                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hordeum vulgare (Barley).

Eukaryota: Viridiplantae: Streptophyta: Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae; Pooldeae;
NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arvidsson A.-K., Wraith A., Jonsson-Rylander A.-C., Larhammar D.;
"Cloning of a neuropeptide Y/Peptide YY receptor from the Atlantic
cod: the Yb receptor.";
Regul. Pept. 0:0-0(1998).
EMBL. APG73925; AADD2833.1; -.
InterPro; IPR000275; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR000237; GPCRRHODDSN.
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadoidei; Gadidae;
                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 13; Length 374; Pred. No. 52;
                     Length 336;
                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ARABINOXYLAN ARABINOFURANOHYDROLASE ISOENZYME AXAH-II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42260 MW; D2A9C9516C4998E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           656 AA; 71999 MW; 4D04531E6948415A CRC64;
                                                                                                                                                                                                                                                                                  01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) NEUROPEPTIDE Y/PEPTIDE YY RECEPTOR YB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
Receptor; Neuropeptide.
SEQUENCE 374 AA; 42260 WW; D2A9C9516C4998E2 CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lee R.C., Burton R.A., Hrmova M., Fincher G.B.;
"Barley arabinoxylan arabinofuranohydrolases.";
Blochen. J. 0:0-0(2001).
EMBL: AF320325; AAK21880.1;
Hydrolase.
SEQUENCE 656 AA: 71000 ...
                   Score 44; DB 5;
Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    656 AA.
                                                                                                                                                                                                                             374 AA
                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
               45.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.4%;
                                                                                                                                                                                                                                                                 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10,
                                                                                                                                                                                                                                                                                                                                                          Gadus morhua (Atlantic cod)
             Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 45.4
Best Local Similarity 42.9
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                            PRELIMINARY;
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278 PLNIFNTVFDWHHE 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 PLDKFGNIYDYHYE 15
                                                                                                                ||::| |||:
189 FGSVXIXHYQ 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
                                                                                           6 FGNIYDYHYE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-8049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09ATV7;
                                                                                                                                                                                                                                                 O9YHX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
Q9ATV7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9ATV7
                                                                                                                                                                                                                            09YHX1
                                                                                                                                                                                       RESULT 11
                                                                                                                                                                                                            09YHX1
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SEQUENCE FROM N.A.

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0;
                                                                                                                                                                      EU SEQUENCE FROM "A."

EU Arabidopsis sequencing project;

BU Arabidopsis sequencing project;

SUBMILTER (MARR-2000) to the EMBL/GenBank/DDBJ databases.

C. 1- CATALYTIC STORINELL-L-HONGCYSTELLE + DNA 5-METHYLOXINE + DNA CYTOSINE - STADENOSYL-L-HONGCYSTELLE + DNA 5-METHYLOXINE.

C. 1- SIMILARITY: TO C.5 CYTOSINE-SPECIFIC DNA METHYLASE FAMILY.

BERL; AL049565; CAB41119.1; ...

REMBL; AL16137; CAB78403.1; ...

RICEPTO: IPR001025; BAH.

RITHER PRO1525; C5_DNA_meth.

REMBL; AL16137; CAB78403.1; ...

RITHER PRO1426; BAH: 2.

REMBL; SN0001525; C5_DNA_meth.

REMBL; SN000439; G5_MRSEL; 1.

REMBL; PRO0175; CSMTASEL; 1.

REMBL; PRO0175; SOU099; C5_MRASEL; 1.

REMBL; PROSITE; PS00099; C5_MRASEL; 1.

REMBL; SN00094; C5_MRASEL; 1.

REMBL; PROSITE; PS00094; C5_MRASEL; 1.

REMBL; SN00094; C5_MRASEL; 1.

REMBL; SNOWENCE 1404 AA; 160211 MW; 2FC7B7AA8ESDCAA8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).

Arabidopsis thaliantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN-CV. COLUMBIA;

STRAIN-CV. COLUMBIA;

MEDLINE-20044094; PubMed-10579493;

MEDLINE-20044094; PubMed-10579493;

MAILTIPLE DNA METHYLTRAINSFERSE Genes in Arabidopsis thaliana.";

Plant Mol. Biol. 41:269-278(1999)

Plant Mol. Biol. 41:269-278(1999)

-1 - CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DNA CYTOSINE = S-ADENOSYL-L-HOMOCYSTEINE + DNA 5-METHYLCYTOSINE.

-1 - SIMLARITY: TO C-5 CYTOSINE-SPECIFIC DNA METHYLASE FAMILY.

ENBL; AF130283; AAF14882.1; -.

HSSP; P20599:1007.
Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W., Mayer K.F.X., Schueller C.; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 10; Length 1404;
Pred. No. 2.2e+02;
3; Mismatches 5; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MODIFICATION METHYLASE (EC 2.1.1.73) (CYTOSINE-SPECIFIC
                                                                                                 EU Arabidopsis sequencing project;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1517 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; EAGOSS; LOCA
InterPro; IPR001025; BAH.
InterPro; IPR001025; C5_DNA_meth.
InterPro; IPR001048; EF hand.
InterPro; IPR001048; EF hand.
Pfam; PF00145; DAM_methylase; 3.
PRINTS; PR00105; CSMETTRFRASE.
SWART; SW00109; CSMETTRFRASE.
PROSITE; PS000094; C5_MTASE_1; 1.
PROSITE; PS00095; C5_MTASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 46.7%;
Matches 7; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || |: :||| :|
102 KPSKKYKKLYDYFFE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KPLDKFGNIYDYHYE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METHYLTRANSFERASE).
                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09SEG3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9SEG3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O9SEG3
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DR PROSITE; PS00018; EF_HAND; UNKNOMN_1.

KW Methyltransferase, Transferase.

SQ SEQUENCE 1517 AA; 171324 MW; AF0B810C3AFDB54A CRC64;

Query Match

Best Local Similarity 45.4%; Score 44; DB 10; Length 1517;

Best Local Similarity 46.7%; Pred. No. 2.4e+02;

Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 KPLDKFGNIYDYHYE 15

| | | | | | | | | | | |

Db 159 KPSKKYKLIYDYFFE 173
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Search completed: January 29, 2002, 11:12:09 Job time: 765 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 29, 2002, 10:26:33; Search time 144.96 Seconds (without alignments) 8.408 Million cell updates/sec

US-09-763-397A-3 97 Perfect score:

1 KPLDKFGNIYDYHYEH 16 Sequence:

Scoring table:

219241 seqs, 76174552 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database :

pir1:* pir2:* pir3:* pir4:* .. .

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	gametocytogenesis	conserved hypothet	. CT488 hypothetical	hypothetical prote		hypothetical prote	pyruvate synthase	transaldolase (EC		catalase (EC 1.11.	hypothetical prote		L96 protein - Tipu	pha	DNA (cytosine-5-)-	DNA (cytosine-5-)-	DNA (cytosine-5-)-	triacylglycerol li	topoisomerase I -	conserved hypothet	hemolysin A - Edwa	hypothetical prote	O)	hypothetical prote			probable membrane	gibberellin 20-oxi	arylphorin precurs
		OT CT	S27829	H72057	C86566	G85090	T34041	T16273	C72427	G65021	A85889	S23422	T19665	CBBY2	JH0225	A38457	T06663	G71402	S59604	A48952	A70358	C82126	T43072	G84155	G81778	T15302	T49616	G71607	S56811	T11848	JQ1044
		Length DB			246 2			339 2							867 2		1404 2	•	•					169 2				1182 2	m	L	687 2
dР		Match L	100.0	49.5	49.5	49.5	47.4	46.4	46.4	45.9	45.9	45.9	45.4	45.4	45.4	45.4	45.4	45.4	45.4	44.3	44.3	44.3	44.3	43.3	43.3	•	43.3	43.3		42.8	42.8
		score	46	48	48	48	46	45	45	44.5	44.5	44.5	44	44	44	44	44	44	44	43	43	43	43	42	42	42	42	42	42	41.5	41.5
	Result	9	1	7	e	₹	2	9	7	89	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

replication factor	hypothetical prote	lysine-rich surfac	cytochrome P450 3	DNA-binding protei	probable GT-like t	probable 3-hydroxy	dynein heavy chain	hypothetical prote	hypothetical prote	deoxynucleotide mo	bioC protein homol	probable trascript	site-specific DNA-	3-isopropylmalate	hypothetical prote
B37281	D96840	S58472	A40843	S39484	F96797	F71660	T30299	T38490	T07456	KIBPD4	B64456	T41149	S15908	C70322	T27670
7	7	П	7	7	7	7	7	7	ď	7	٦	7	7	~	7
273	274	294	503	575	603	720	1114	798	87	241	251	332	358	364	398
42.3	42.3	42.3	42.3	42.3	42.3	42.3	42.3	41.8	41.2	41.2	41.2	41.2	41.2	41.2	41.2
41	41	41	41	41	41	41	41	40.5	40	40	40	40	40	40	40
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ALIGNMENTS

4	
17	329

gametocytogenesis onset-specific protein - malaria parasite (Plasmodium falciparum)

C;Species: Plasmodium falciparum C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jun-2000

C. Accession: \$27829
R. Alano, P.; Premawansa, S.; Bruce, M.; Carter, R.
submitted to the EMBL. Data Library, April 1991
A. Description: A stage specific gene expressed at the onset of gametocytogenesis in P
A. Reference number: \$27829
A. Accession: \$27829
A. Molecule type: mRNA
A. Residues: 1-217 ALA>
A. Residues: 1-217 ALA>
A. Residues: GB: X84904; EMBL: M38286; NID: g1340125; PID: e139902; PID: g1340126

Length 217;

ö Gaps ö Indels 100.0%; Score 97; DB 2; I llarity 100.0%; Pred. No. 4.6e-08; Conservative 0; Mismatches 0; Ouery Match Best Local Similarity Matches 16; Conserv

1 KPLDKFGNIYDYHYEH 16 òγ qq

10 KPLDKFGNIYDYHYEH 25

RESULT

Conserved hypothetical protein CP0141 [imported] - Chlamydophila pneumoniae (strains conserved hypothetical protein C; Species: Ctlamydophila pneumoniae, Ctlamydia pneumoniae (strains C; Species: Ctlamydophila pneumoniae, Ctlamydia pneumoniae (c; Accession: H7205; Csl609 #sequence_revision 23-Apr-1999 #text_change 11-May-2000 C; Accession: H7205; Csl609 #sequence_revision 23-Apr-1999 #text_change 11-May-2000 R; Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, Nature Genet. 21, 385-389, 1999 #7:Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis. A; Reference number: A72000; MUID:99206606

A:Status: preliminary
A;Molecule types: DNA
A;Cross.references: GB:AE001645; GB:AE001363; NID:g4376896; PIDN:AAD18745.1; PID:g437
A;Experimental source: strain CWL029
A;Experimental source: strain CWL029
A;Experimental source: Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39
A;Reference number: A81500; MUID:20150255

A;Status: preliminary A;Moleoule type: DNA Residues: 1-746 <REMA A;Cross-references: GB:AE002175; GB:AE002161; NID:g7189069; PIDN:AAF38023.1; PID:g718

```
C72427

Pyruvate synthase (EC 1.2.7.1) alpha chain - Thermotoga maritima (strain MSB8)

Pyruvate synthase (EC 1.2.7.1) alpha chain - Thermotoga alpha subunit

N;Alternate names: pyruvate--ferredoxin 2-oxidoreductase alpha subunit

C;Species: Thermotoga maritima

C;Species: Thermotoga maritima

C;Dates: 11-Jun-1999 #sequence_revision 18-Jun-1999 #text_change 21-Jul-2000

C;Accession: C72427; A54346

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL:U28741; NID:9861290; PID:9861293; PIDN:AAA68327.1; CESP:F35D A; Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Rosidues: 1-207 cLAT>
A;Cross-references: EMBL:AF000264; PIDN:AAC71122.1; GSPDB:GN00020; CESP:F43E2.5
A;Experimental source: strain Bristol N2; clone F43E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hyporhetical protein F35D2.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep_1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
                                        hypothetical protein F43E2.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 207;
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A;Gene: CESP:F35D2_1
A;Introns: 76/1; 102/1; 136/3; 174/1; 240/2; 268/1; 298/1
A;Introns: 76/1; 02/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 03/1; 
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R;Connell, M.
submitted to the EMBL Data Library, June 1995
A;Description: The sequence of C. elegans cosmid F35D2.
A;Reference number: Z18488
A;Accession: T16573
A;Accession: T16573
A;Atcession: T16573
A;A
                                                                                                                                           Cibate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #tex
CiAccession: T34041
Rilatreille, P. Submitted to the EMBL Data Library, April 1997
Alpescription: The sequence of C. elegans cosmid F43E2.
Algebrace number: 221467
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54.5%; Pred. No. 13;
cive 4; Mismatches
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Pred. No. 5.3;
3; Mismatches
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50.0%;
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119 EPLDKFYQAEDYHQKY 134
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.0
Matches 8; Conservative
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188 PIDPFGSLFDY 198
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A; Residues: 1-339 <CON>
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A; Introns: 83/3
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R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of Chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A65001; MUID:20083488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CT488 hypothetical protein [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Sacession: C86566
C;Accession: C86566
C;Accession: C86566
A;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349
A;Accession: C86566
A;Accession: C86566
                                                 C.Genetics:
Afgene: CPN0600; CP0141
C.Superfamily: unassigned probable phosphoesterases; phosphoesterase core homology
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                                                                                                                                                                                                                                             Length 246;
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Pred. No. 25;
2; Mismatches
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Pred. No. 3.1;
2; Mismatches
                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                  Score 48; DB 2;
Pred. No. 3.1;
2; Mismatches
A; Experimental source: strain AR39, HL cells
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53.3%;
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KPASKYKKIYDYFFE 173
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Best Local Similarity 57.1*
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217 RPIDGFGNIRGIHY 230
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217 RPIDGFGNIRGIHY 230
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Matches 8; Conserva
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A; Residues: 1-246 <STO>
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A; Molecule type: DNA
A; Residues: 1-1512 <ST
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A; Map position: 4
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A.Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.

A.Reference number: A85480; MUD:21074935; PMID:11206551

A.Accession: A85889
A.Status: preliminary
A.Molecule type: DNA
A.Rolecule type: DNA
A.Kross references: GB:AE005174; NID:q12516839; PIDN:AAG57573.1; GSPDB:GN00145; UWGP:
A.Experimental source: strain 0157:H7, substrain EDL933
C.Genetics:
A.Gene: tala
C.Superfamily: human transaldolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cypecies: Pichia angusta
Cybecies: Pichia angusta
Cybecies: Pichia angusta
Cybecies: Pichia angusta
Cybecies: Pichia angusta
Cybecession: 232422
Rybidion, T.; Roggenkamp, R.
FEBS Lett. 303, 113-116, 1992
A/Title: Targeting signal of the peroxisomal catalase in the methylotrophic yeast Han A/Title: Targeting signal of the peroxisomal catalase in the methylotrophic yeast Han A/Accession: 523422
A/Molecule type: DNA
A/Residues: 1-507 CAID>
A/Rosion: S23422
A/Rosidues: 1-507 CAID>
A/Cross-references: EMBL:X56501; NID:g2775; PIDN:CAA39856.1; PID:g2776
Cyseparfamily: catalase
Cyseparfamily: catalase
Cyseparfamily: catalase
Cyseparfamily: Cyseparfamily: As a service of Residues and A/Accession: Cyseparfamily:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apporthetical protein C33A12.11 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C;Accession: T19665
R;Wilkinson, J
submitted to the EMBL Data Library, January 1996
A;Reference number: Z19159
A;Reference number: Z19159
A;Recession: T19665
A;Reference T19665
A;Reference T19665
A;Residues: Preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1.336 <WILL>
A;Residues: L336 <WILL>
A;Cross-references: EMBL:Z68493; PIDN:CAA92795.1; GSPDB:GN00022; CESP:C33A12.11
A;Experimental source: clone C33A12
C;Genetics:
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A;Introns: 149/3; 202/3; 270/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C33A12.9b
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Pred. No. 26;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.9%; Score 44.5; 33.3%; Pred. No. 15
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|larity 47.1%;
|Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 33.3
Matches 9; Conservative
          Nature 409, 529-533, 2001
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Matches 8; Conserv
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                                                                A; Wolecule type: DNA
A; Residues: "MR',1-392 <NEL>
A; Residues: "MR',1-392 <NEL>
A; Experimental Source: Strain MSB
A; Note: an incorrect initiation codon was used
R; Blamey, J.M.; Adams, M.W.
Biochemistry 33, 1000-1007, 1994
A; Title: Characterization of an ancestral type of pyruvate ferredoxin oxidoreductase fro
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C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C; Accession: A85889
R; Perna, N.T.: Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhev
Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: TW0017
C;Superfamily: pyruvate synthase alpha chain; 2-oxoacid ferredoxin oxidoreductase homold
C;Keywords: coenzyme A; oxidoreductase
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C;Species: Escherichia coil
C;Species: Escherichia coil
C;Species: Escherichia coil
C;Species: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 12-Nov-1999
C;Accession: G55021
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y.
A:Rose, D.J.; Mau, B.; Shao, Y.
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Actura: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                A) Reference number: A54346; MUD:94137707
A) Accession: A63446
A) Status: preliminary
A) MOlecule type: nrotein
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16;
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A; Reference number: A72200; MUID:99287316
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Similarity 33.3%;
9; Conservative ·4
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53.38;
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A;Molecule type: protein
A;Residues: 1-43 <BLA>
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Best Local Similarity
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Best Local Similarity
Matches 9; Conserv
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C; Genetics:
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A; Reference number: JH0225; MUID:91078646
A; Accession: JH0225; MUID:91078646
A; Accession: JH0225
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-867 < HOM>
A; Cross-reference
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C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 29-Sep-1999
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 29-Sep-1999
C;Accession: A38457; 316429
J. Cell Biol. 113, 405-416, 1991
A;Title: Laminin receptors in the retina: sequence analysis of the chick integrin alp A;Reference number: A38457; MUID:91185416
A;Accession: A38457
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-1072 < DECS
A; Cross-references: GB: X56559; NID: 963541; PIDN: CAA39909.1; PID: 963542
C; Superfamily: integrin alpha-2b chain
C; Keywords: cell adhesion; cytoskeleton; phosphoprotein; transmembrane protein
F;81-591/Product: L-lactate dehydrogenase (cytochrome) #status predicted <MAT>F;88-159/Domain: cytochrome b5 core homology <CB5>F;200-504/Domain: (S)-2-hydroxy-acid oxidase homology <2HY>F;213,146/Enioding site: heme iron (His) (axial ligands) #status experimental F;429,459,493,513/Bhiding site: FMN (Lys, Asp, Arg, Arg) #status experimental F;453/Active site: His #status experimental
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196 protein - Tipula iridescent virus

196 protein - Tipula iridescent virus

C; Species: Tipula iridescent virus

C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C; Accession: JH0225

R;Home, W.A., Tajbakhsh, S.; Seligy, V.L.

R;Home, W.A., 1990

A;Title: Molecular cloning and characterization of a late Tipula iridescent
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Pred. No. 72;
1; Mismatches
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red. No. 36;
Mismatches
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56;
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Pred. No.
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Best Local Similarity 58.3,
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Best Local Similarity 64.3°
                                                                                                                                                                                                                                                                                              Conservative
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198 PLDNIINLYDFEY 210
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Best Local Similarity
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A,Residues: 395-465, Q',467-513, E',515-591 <LED>
A,Residues: 395-465, Q',467-513, E',515-591 <LED>
B,Gulard, B, Lederer, B, Boldmine 58, 305-316, 1976
A,Title: Complete amino acid sequence of the heme-binding core in bakers' yeast cytochrows. A,Reference number: A90671; MUID:76206228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Superfamily: lactate dehydrogenase (cytochrome); (S)-2-hydroxy-acid oxidase homology; C:Keywords: chromoprotein; electron transfer; flavoprotein; FMN; heme; homotetramer; ird F;1-80/Domain: transit peptide (mitochondrion) #status predicted <TNP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 80,82-164,'E',166-394 <GHR>
R;Guiard, B.; Lederer, F.; Jacq, C.
Rature 255, 422-423, 1975
A;Title: More similarity between bakers' yeast L-(+)-lactate dehydrogenase and liver mid
A;Reference number: A93173; MUID:75156546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:246729; NID:9577134; PIDN:CAA86721.1; PID:9577142; GSPDB:GN0001 R;Ghrir, R.; Becam, A.M.; Lederer, F.
Eur. J. Biochem. 139, 59-74, 1984
A;Title: Primary structure of flavocytochrome b2 from baker's yeast.
A;Reference number: A91136; MUID:84132029
A;Accession: A91136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBO J. 4, 3265-3272, 1985
A;Title: Structure, expression and regulation of a nuclear gene encoding a mitochondrial
A;Reference number: A24583; MUID:86135959
A;Accession: A24583
                                                                                                                                                                                                                                                                                                                                                            .
Tactate dehydrogenase (cytochrome) (EC 1.1.2.3) precursor - yeast (Saccharomyces cerev
Alternate names: cytochrome b2; flavocytochrome B2; protein YM9958.08c; protein YML054
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A;Residues: 'N', 82-94 <GUI2>
R;Lederer, F.; Cortial, S.; Becam, A.M.; Haumont, P.Y.; Perez, L.
Bur. J. Biochem. 152, 419-428, 1985
A;Title: Complete amino acid sequence of flavocytochrome b2 from baker's yeast.
A;Reference number: A91154; MUID:86030284
A;Accession: A23095
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A;Reference number: A44532; MUID:90230315
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C;Species: Saccharomyces cerevisiae
C;Date: 24-Apr.1984 #sequence_revision 31.Mar-1993 #text_change 21-Jul-2000
C;Date: A-Apr.1984; squence_revision 31.Mar-1993 #text_change 21-Jul-2000
C;Accession: A24583; sq9806; A91136; A93173; A23095; A90671; A00175
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A,Residues: 1-591 <GUI1>
A,Cross-references: EMBL:X03215; NID:93632; PIDN:CAA26959.1; PID:93633
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A; Residuce: 88-121, fo', 123-164, 'E', 166-183 <GUI3>
R; Xia, Z.; Mathews, F.S.
J. Mol. Biol. 212, 837-863, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Devlin, K.; Churcher, C. Submitted to the EMBL Data Library, November 1994 A; Reference number: $49800 A; Accession: $49806
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A;Gene. SGD:CYB2; MIPS:YML054c
A;Cross-references: SGD:S0004518; MIPS:YML054c
A;Map position: 13L
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                                                  Score 44;
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                       Query Match
Best Local Similarity
Local 6; Conserve
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A; Residues: 1-591 <DEV>
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DNA (cytosine-5-)-methyltransferase (EC 2.1.1.37) T6G15.160 - Arabidopsis thaliana N.Alternate names: protein T6G15.160
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 23-Apr.1999 #sequence_revision 23-Apr.1999 #text_change 05-May-2000
C; Accession: T06663
R; Bevan, M.: Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X submitted to the Protein Sequence Database, April 1999
A; Reference number: 215791
A; Residues: 1-1404 <BEV>
A; Residues: 1-1404 <BEV>
A; Residues: 1-1404 <BEV>
A; Residues: Left: Columbia; BAC clone T6G15
A; Cosertimental source: cultivar Columbia; BAC clone T6G15
A; Genetics:
A; Genetics:
A; Genetics: A; Geneticon: 4
A; Introns: 57/1: 348/3; 371/2; 872/3; 927/3; 989/1; 1026/2; 1086/3; 1152/3; 1245/3; 1288
C; Keywords: methyltransferase; S-adenosylmethionine
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Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; T-cell epitope; tetanus toxoid; antigenic epitope; treatment; circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum Pfg27 antigenic epitope, P591.
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Soybean POP2/CAF1
Soybean POP2/CAF1
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3.813 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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WPI; 2000-237654/20

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The present sequence is the antigenic epitope P591, derived from gamete specific antigen, Pfg27 of the sexual stage of Plasmodium falcjarum. It is used in the construction of recombinant protein comprises, melittin signal peptide, (His)6 tag, Trecll epitope from tetranus toxoid and 21 antigenic epitopes from Trecll epitopes from Trecll epitopes from tetranus toxoid and 21 antigenic epitopes from Trecll epitope from tetranus toxoid and 21 antigenic epitopes from Trecll epitope from tetranus toxoid and 21 antigenic epitopes from Trecll epitopes epitopes were obtained at different stages of the life cycle of P. falciparum. CDC/NITMALVAC-1 vaccine has antiparasitic actions. Anti-CDC/NITMALVAC-1 vaccine has antiparasitic infections. Anti-CDC/NITMALVAC-1 and prevention of malarial infections antiparasitic antiparamin in biological samples.
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  Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle -
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/label= Mature_CDC/NIIMALVAC-1
/note= "Recombinant multivalent malarial vaccine"
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ive 0; Mismatches 0;
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Chimeric - Clostridium tetani.
Chimeric - Plasmodium falciparum.
                                                                                             Claim 2; Page 17; 52pp; English
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Length 16; Indels

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The present sequence is that of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melitin signal peptide, (His)6 tag. T-cell epitope from tetanus toxoid and 21 antigenic epitopes from circumsporozoite protein (CBS), sporozoite surface protein-2 (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein (MSP-1), MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175), rhoptry associated protein-1 (AAA-1), and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of plasmodium faltiparaum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monoclonal antibodies useful in vaccines against malaria transmission - recognise continuous epitope in the sexual stages of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Continuous epitope of Plasmodium falciparum in the gametocyte stage.
                                                                                                                             Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 97; DB 21;
100.0%; Pred. No. 4.5e-08;
iive 0; Mismatches 0;
      (NAIM-) NAT INST IMMUNOLOGY.
(USSH ) US DEPT HEALTH & HUMAN SERVICES

 P. falciparum in biological samples.

                                                                                                                                                                                               Claim 3; Page 43-44; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA.
                                                                                                                                                                plasmodium falciparum life cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR96217 standard; peptide; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91US-0779494;
93US-0120225.
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                                                       Lal AA, Shi YP, Hasnain SE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transmission; sexual stage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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283 kpldkfgniydyhyeh 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-179336/18.
                                                                                    WPI; 2000-237654/20.
N-PSDB; AAZ51336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                              350 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-OCT-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-SEP-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR96217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kumar N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                  AAR96217 is a continuous epitope derived from Plasmodium falciparum in the sexual stage of development. The epitope was identified using monoclonal antibodies (MADS) 686, 1662, 19F1 and 11612 (ATCC HBILIS5, HBILIS6, HBILIS7, And HBILIS4, respectively). The epitope is shared by 3 reduced male and female gamete surface antigens of mol. wt. 260, 59, and 53 kD, from which the above hybridomas can be produced. The epitope is conserved among parasites from diverse geographical locations and may be expressed in bacteria. The epitope is useful in subunit vaccines to block the transmission of malaria.
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S. epidermidis open reading frame protein sequence SEQ ID NO:892.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis SR1 strain; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                           63.9%; Score 62; DB 17; Length 20; 100.0%; Pred. No. 0.0011; live 0; Mismatches 0; Indels
                                    Claim 1; Column 15-16; 17pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG81899 standard; Protein; 202 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccination; endocarditis.
                                                                                                                                                                                                                                                                                                                           Query Match 63.9
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLAX ) GLAXO GROUP LTD
Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-316495/33.
                                                                                                                                                                                                                                                                                                                                                                                                                              1 KPLDKFGNIYD 11
                                                                                                                                                                                                                                                                   20 AA;
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                                                                                                                                                                                                                                                                       Sequence
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AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the used in vaccination The nucleic acids (I) may be used to produce to vaccinate suppertides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH5391 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to AAH55091 to the present invention of the present invention.

N. B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification,
                 AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4465 to 4464.
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S. epidermidis open reading frame protein sequence SEQ ID NO:1110.
polynucleotide sequences from the present invention. AAH55091 to
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                                                                                                                                                                                                                                            Score 52; DB 22; Length 202;
Pred. No. 0.64;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 18; Page 322; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG82008 standard; Protein; 312 AA.
                                                                                                                                                                                                                                              53.6%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-NOV-2000; 2000WO-US30782.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                              Query Match 53.6
Best Local Similarity 60.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                             1 KPLDKFGNIYDYHYE 15
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41 qpidkfgeiydlnpe 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-316495/33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200134809-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-SEP-2001
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                                                                                                                                                                                    Sequence
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89 AA

SSSXS

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standard; Protein;
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                                                                                                                                                                                                                                    02-DEC-1998;
                                                                            12-OCT-2000
                                                                                                                                                                                               08-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY71534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                     AAY71539
                                                         AAY71539
                                                                                                                                                         Glycine
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                            AAY71539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4455 to 4464.
                                                                                                                                                                                                                                                          y disease; pneumonia; bronchitis; heart disease; sarcoidosis; purulent otitis media; erythema nodosum; pharyngitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                        Gaps
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Pred. No. 3.9;
2; Mismatches 4; Indels
                                                                      Length 312;
                                                                                         Indels
                                                                                                                                                                                                                                          Amino acid sequence of a Chlamydia pneumoniae protein.
                                                                                         3;
                                                                      DB 22;
                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 1074; Disclosure; 1912pp; English
                                                                      Score 52;
Pred. No.
                                                                                                                                                                                 AAY35228 standard; Protein; 262 AA.
                                                                                                                                                                                                                                                                                   vaccine; neutralising epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.5%;
                                                                                                                                                                                                                                                                                                                                                                98WO-IB01890
                                                                                                                                                                                                                                                                                                                                                                                   98US-0107078
97FR-0014673
                                                                       53.6%;
60.0%;
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8; Conservative
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                                                                                                               1 KPLDKFGNIYDYHYE 15
                                                                                                                                55
                                                                                                                                                                                                                                                              Respiratory disease;
sinusitis; purulent o
                                                                                                                          :|:|||| ||| :|
41 qpidkfgeiydlnpe
                                                                                                                                                                                                                                                                                                      Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-357842/30
                                                                AA;
                                           312 AA;
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21-NOV-1997;
                                                                                                                                                                                                                                                                                                                           W09927105-A2
                                                                                                                                                                                                                                                                                                                                                                 20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                              03-JUN-1999.
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Best Local
                                                                                                                                                                                                     AAY35228
                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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AAY35228
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                                                                                               Soybean, POP2 transcription factor; CAF1 transcription factor; ADH2 gene; glucose-repressible alcohol dehydrogenase gene; cell metabolism; transgenic plant; herbicide; expressed sequence tag; EST.
                                         Soybean POP2/CAF1 transcription factor encoded by expressed sequence tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acids encoding transcription factor in plants and seeds, useful for producing transgenic plants, antibodies and selecting a polynucleotide that affects transcription factor polypeptide expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Soybean POP2/CAF1 transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DUPO ) DU PONT DE NEMOURS & CO E I. (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helentjaris TG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY71534 standard; Protein; 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0110585.
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(first entry)
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Matches 7; Conservative
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46 rpvgnfknindynyg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful as herbicides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-412328/35.
N-PSDB; AAD01331.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Allen SM, Weng Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89 AA;
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AAW09620-W09625 are modified lipase sequences derived from Pseudomonas
                                                                                                                                                   New polypeptide with lipase activity – used for prodn. of fatty acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glumae lipase modified to have reverse stereoselectivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas; Chromobacterium; modification; variant; optical isomer; steroeselectivity; drug preparation; 1,4-dihydropyridine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lipase of modified stereo:selectivity - useful for prepn. of optically active isomer 1,4-di:hydro:pyridine cpd., as intermediate
                                                                                                                                                                                                                                The polypeptide has good stability and high lipase activity. I for prodon. of fatty acids from triglycerides, as a reagent for quantitative analysis of troglycerides, and as a catalyst for transesterifying fats and oils.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= substitution
/note= "wild-type Phe replaced with Leu,
important substitution for producing
a lipase of reverse stereoselectivity"
                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 319; 32;
                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                  Score 43; DB
Pred. No. 32;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW09624 standard; Protein; 319 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 9; 10pp; Japanese.
                                                                                                                                                                                                  Claim 1; page 12; 16pp; German.
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                                                                                                                                                                                                                                                                                                                                                                    44.3%;
88JP-0058376.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96JP-0028640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                               from triglyceride(s), etc.
                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 44.3
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AMAN ) AMANO PHARM KK.
                                 (TOXN ) TOYO JOZO CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-500357/50.
                                                                                               1989-293865/41
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                                                                                                                                                                                                                                                                                                                                                                                                                                      4 DKFGNIYDYHY 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||| |: || |
21 dkfanvodywy 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas glumae.
                                                                                                                                                                                                                                                                                                                     AA;
                                                                Ohta H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Misc-difference
                                                                                                                 N-PSDB; AAN9133]
                                                                                                                                                                                                                                                                                                                     319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP08256767-A.
14-MAR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            substitution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAY-1997
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                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW09624;
                                                                Sagai H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10
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             Soybean; POP2 transcription factor; CAF1 transcription factor; ADH2 gene; glucose-repressible alcohol dehydrogenase gene; cell metabolism; transgenic plant; herbicide.
                                                                                                                                                                                                                                                                                                                                                                                New nucleic acids encoding transcription factor in plants and seeds, useful for producing transgenic plants, antibodies and selecting a polynucleotide that affects transcription factor polypeptide expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a CAF1 (also known as POP2) transcription factor from srl.pk0126.b4 clone isolated from soybean root cDNA library srl. CAF1 protein has been shown to bind to another transcription factor CCR4 and regulate the expression of glucose-repressible alcohol dehydrogenase (ADH2) gene. The present sequence is useful for producing transgenic plants with altered levels of POP2/CAF1 transcription factor to control expression of various genes or transgenes. The CAF1 protein may also be used to design or identify inhibitors of cell metabolism that may be useful as herbicides.
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Pred. No. 21;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chromobacterium viscosum var paralipoliticum.
                                                                                                                                                                                                                                                   Ξ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Page 38-39; 46pp; English.
                                                                                                                                                                                                                                                                                                  Allen SM, Weng Z, Helentjaris TG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptide with lipase activity.
                                                                                                                                                                                                                                                 S CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.48;
                                                                                                                                                                                                                                               (DUPO ) DU PONT DE NEMOURS & (PION-) PIONEER HI-BRED INT
                                                                                                                                                                                 99WO-US28322
                                                                                                                                                                                                                98US-0110585
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85 rpvgnfknindynyg 99
                                                                                                                                                                                                                                                                                                                                 WPI; 2000-412328/35
N-PSDB; AAD01326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309 AA;
                                                                                                             WO200032782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAR-1989;
                                                                                                                                                                                 01-DEC-1999;
                                                                                                                                                                                                                02-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-FEB-1990
                                                                               Glycine max.
                                                                                                                                              08-JUN-2000
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Lipase.

AAP91951 RESULT

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Gaps

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species cepacia and glumae and from Chromobacterium viscosum (AAW09625 only). The lipase variants were created in an attempt to find important substitution sites that affect the stereoselectivity of the lipase enzyme. Important substitutions found for Pseudomonas species were Phe221Leu, Val266Leu and Leu2871le. Lipase variants of reverse stereoselectivity are used to produce optically active
                                                                                                                                                                                                                                                                                                                                                                                                                                    pseudomonas glumae lipase modified to have reverse stereoselectivity.
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas; Chromobacterium; modification; variant; optical isomer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lipase of modified stereo:selectivity - useful for prepn. of optically active isomer 1,4-di:hydro:pyridine cpd., as intermediate for prepn. of drugs
                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= substitution
/note= "wild-type Phe replaced with Leu,
important substitution for producing
a lipase of reverse stereoselectivity
                                                                                                                                                                                DB 17; Length 319;
32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            steroeselectivity; drug preparation; 1,4-dihydropyridine;
                                                                                                                                                                                                               Indels
                                                                                                                                                                                                             3;
                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                 Score 43;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Page 9-10; 10pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
221
                                                                                                                                                                                                                                                                                                                                               AAW09625 standard; Protein; 319 AA.
                                                                                                                                                                                 44.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96JP-0028640
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                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                Conservative
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|dkfanvvdywy 31
                                                                                                                                                                                                                                            4 DKFGNIYDYHY 14
                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas glumae
                                                                                                                                        319 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   drug preparation.
                                                                                                            drug preparation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMAN) AMANO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                substitution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-OCT-1996.
                                                                                                                                                                                                                                                                                                                                                                                                        02-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                            AAW09625
                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                     11
                                                                                                                                                                                                                                                                        21
                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                     RESULT 1
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       8888888888
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AA;

319

Sequence

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/label= substitution
/note= "Leu to Phe, in wild-type sequence a Leu residue
is present at position 292 of mature P. glumae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AARR88009-R88018 are protein variants of Pseudomonas glumae lipase. The
                                                                                                                                                                                                   Mutant; lipase; enzymatic detergent; substitution; variant; improved; hydrophobicity.
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ased surface hydrophobicity - useful in enzymatic detergent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "possible site for His to Arg substitution"
                                                                                                                                                                                                                                                                                                                                                       to Tyr substitution"
                                                                                                                                                                                                                                                                                                                                                                           "possible site for Leu to Arg substitution"
                                                                                                                                                                                                                                                                                                                                                                                               "possible site for Thr to Val substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                    to Arg substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                         for Leu to Arg substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             to Phe substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for Thr to Leu substitution"
                                                                                                                                                                                                                                                                                                                                 "possible site for Phe to Arg substitution"
                     .;
0
Length 319;
                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suerbaum HMU;
                      3;
                                                                                                                                                                                 Mature Pseudomonas glumae lipase L292F variant.
 DB 17;
                                                                                                                                                                                                                                                                                                                                                      for Thr
                                                                                                                                                                                                                                                                                                                                                                                                                    for Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                               for Val
          Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas lipase variant with increased
  Score 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "possible site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               has improved in-the-wash performance,
                                                                                                                                                                                                                                                                                                                                                        "possible site
                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "possible site
                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "possible site
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                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                     AAR88018 standard; protein; 319 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peters
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                                                                                                                                                                                                                                                                                                                 lipase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94EP-0201761.
 44.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Frenken LGJ,
                                                                                                                                                                (first entry)
                        Conservative
                                                                                                                                                                                                                                                                                                                                     'note=
                                                                                                                                                                                                                                                                                                                                                        'note=
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                                                                                                                                                                                                                                                                                                                                                                                                   /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-058418/06.
                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 233
                                                                                                                                                                                                                                                             Key
Misc-difference 292
                                                                                                                                                                                                                                                                                                                                              Misc-difference 129
                                                        ||| |: || |
21 dkfanvvdywy 31
                                           4 DKFGNIYDYHY 14
                                                                                                                                                                                                                                        Pseudomonas glumae.
                                                                                                                                                                                                                                                                                                                          23
   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUN-1994;
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Verrips CT;
                                                                                                                                                               02-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-DEC-1995
                                                                                                                                           AAR88018;
                                                                                                  12
                        Matches
                                                                                                            AAR88018
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De Vlieg J,
Verrips CT;
                                                                                                                                                                                                                                                                                                                                                                                              02-AUG-1996
                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                         /label= substitution
/note= "Thr to Tyr, in wild-type sequence a Thr residue
is present at position 129 of mature P. glumae
lipase"
                                                                                                                                                                                                                                                                                                                          Mutant; lipase; enzymatic detergent; substitution; variant; improved; hydrophobicity.
sequences are based upon the wild-type P. glumae sequence disclosed in EP407225-A (UNILEYER PLC). The lipase variants may contain one or more of the amino acid substitutions indicated in the features table. Using these variants it was shown that lipases can be modified in a such a way that interaction with the substrate can be improved without forming large hydrophobic areas on the modified lipase surface which allow aggregation of lipase molecules; the lipase variants show improved in-the-wash lipolytic activity and may
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "possible site for Leu to Arg substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "possible site for Thr to Val substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "possible site for Thr to Arg substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to Arg substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "possible site for Val to Phe substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to Leu substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "possible site for His to Arg substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "possible site for Leu to Phe substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                              "possible site for Phe to Arg substitution"
                                                                                                                                                    ö
                                                                                                                                17; Length 319;
                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                       Mature Pseudomonas glumae lipase T129Y variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "possible site for Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note- "possible site for Thr
                                                                                                                               Score 43; DB ]
Pred. No. 32;
1; Mismatches
                                                                                                                              DB
32;
                                                                                be used in enzymatic detergent compsns.
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
129
                                                                                                                                                                                                                                           AAR88010 standard; protein; 319 AA.
                                                                                                                               44.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94EP-0201761
                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                         Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UNIL ) UNILEVER NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 239
                                                                                                                                                                        4 DKFGNIYDYHY 14
                                                                                                                                                                                          21 dkfanvvdywy 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 134
                                                                                                                                                                                                                                                                                                                                                                                                                                    23
                                                                                                                                                                                                                                                                                                                                                       Pseudomonas glumae
                                                                                                  319 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
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                                                                                                   Sequence
                                                                                                                                Query Match
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/note* "Leu to Arg, in wild-type sequence a Leu residue is present at position 134 of mature P. glumae
                                                                                                                                                                                                                                     AAR88009-R88018 are protein variants of Pseudomonas glumae lipase. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mutant; lipase; enzymatic detergent; substitution; variant; improved;
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                                                                                                                                                                                                                                                         sequences are based upon the wild-type P. glumae sequence disclosed in EP407255-A (UNILEYER PLC). The lipase variants may contain one or more of the amino acid substitutions indicated in the features table. Using these variants it was shown that lipases can be modified in a such a way that interaction with the substrate can be improved without forming large hydrophobic areas on the modified lipase surface which allow aggregation of lipase molecules. the lipase variants show improved in the wash lipolytic activity and may be used in enzymatic detergent compsns.
                                                                                                                Pseudomonas lipase variant with increased surface hydrophobicity has improved in-the-wash performance, useful in enzymatic detergent
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Suerbaum HMU;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ed. No. 32;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43;
Pred. No.
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Frenken LGJ, Peters H,
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292
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Misc-difference 233
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Misc-difference 239
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Misc-difference 282
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21 dkfanvvdywy 31
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Best Local Similarity
Matches 7; Conserv
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Search completed: January 29, 2002, 10:21:41 Job time: 417 sec
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Matches 7; Conservative
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Misc-difference 234
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21 dkfanvvdywy
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                                                                                                                                                                                                                                                                                                                                        Pseudomonas lipase variant with increased surface hydrophobicity has improved in the wash performance, useful in enzymatic detergent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to Arg substitution"
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/note= "possible site for Thr to Arg substitution"
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Pred. No.
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/label= substitution
"mhr to Val,
                                                                                                                                                                                                                                       Peters H,
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63.68;
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                                                                                                                                                                         (UNIL.) UNILEVER NV. (UNIL.) UNILEVER PLC.
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dkfanvvdywy 31
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Best Local Similarity
Matches 7; Conserv
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Misc-difference
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Verrips CT;
                                                28-DEC-1995
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Indels

1; Mismatches

Score 43; DB 17; Length 319; Pred. No. 32;

44.3%;

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AARR8009-R88018 are protein variants of Pseudomonas glumae lipase. The sequences are based upon the wild-type P. glumae sequence disclosed in Ep407225-A (UNILEVER PLC). The lipses variants may contrain one or more of the amino acid substitutions indicated in the features table. Using these variants it was shown that lipases can be modified in a such a way that interaction with the substrate can be improved without forming large hydrophobic areas on the modified lipase surface which allow aggregation of lipase molecules. The lipase variants show improved in the wash lipolytic activity and may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas lipase variant with increased surface hydrophobicity has improved in-the-wash performance, useful in enzymatic detergent
                                                                                                                                                                                                                                /note= "possible site for Leu to Phe substitution"
note= "possible site for Leu to Arg substitution"
                                                 to Phe substitution"
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                                                                                                                                                                           His to Arg substitution"
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                                                           'note= "possible site
                                                                                                                   "possible site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12; Page -; 33pp; English.
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Verrips CT;
                                                                                                                         /note=
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Patent No. 5502168
GENERAL INPORMATION:
GENERAL INPORMATION:
TITLE OF INVENTION: NOVEL CONTINUOUS AND CROSS-REACTING
TITLE OF INVENTION: EPITOPE FOR HUMAN MALARIA VACCINE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: CUSHMAN, DARBY & CUSHMAN
STREET: 1615 L. Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 20; 0.00048;
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ZIP: 20036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/120,225
FILING DATE:
CLASSIFICATION: OF PROBLEM OF PR
                                             US-08-544-332-42

US-08-961-083-72

US-08-005-138E-8

US-08-026-138E-8

US-08-21-193A-56

US-08-241-193A-56

US-08-940-086A-56

US-08-940-086A-56

US-08-244-701B-1

US-08-244-701B-8

US-08-244-701B-8

US-08-248-701B-8

US-08-248-701B-8

US-08-248-701B-8

US-08-248-701B-8

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US-08-268-4

US-08-509-261A-4

US-08-692-892-4

US-08-713-939A-4
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ive 0; Mismatches
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TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 63.9
Best Local Similarity 100.
Matches 11; Conservative
                                                  TOPOLOGY: linear
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RESULT 2
US-08-034-650-10
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                                                                                                                                                                                      Search time 133.18 Seconds
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Sequence 3,
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Sequence
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                                                     Compugen Ltd.
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                         GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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97
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Match Length
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Maximum DB s
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Sequence 3, Application US/08819288
Sequence 3, Application US/08819288
Patent No. 595562
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph
APPLICANT: Alonso, Jose
TITLE OF INVENTION: PLANT GENES FOR SENSITIVITY TO ETHYLENE
TITLE OF INVENTION: AND PATHOGENS
OCRESPONDENCES: ADDRESS:
ADDRESSES: Woodcock Washburn Kurtz Mackiewicz & No. 5955652ris
STREET: One Liberty Place - 46th Floor
                          COMPUTER KEALMELE FURM:
MEDIUM TYPE: Floppy disk
COMPOURE: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,015
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/727,235
FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kokulis, Paul N
REGISFRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: PRK/5970/91731
TELECHMONICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUPTER: USA
ZIP: 19103
ZIP: 19103
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Beardell, Lori Y REGISTRATION NUMBER: 34,293
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TELECOMMUNICATION INFORMATION
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SED ID NO: 10:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 215-568-3439 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 44.3
Best Local Similarity 63.6
Matches 7; Conservative
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CLASSIFICATION: 435
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy COMPUTER: IBM PC COMP
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60 DKFANVVDYWY 70
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US-08-819-288-3
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Sequence 10. Application US/08449015

Datent No. 5804409

GENERAL INFORMATION:
APPLICANT: BOS, Jannetje W.
APPLICANT: VERRIPS, Leon G.
APPLICANT: VISSER, Cornells T.
APPLICANT: VISSER, Christiaan
TITLE OF INVENTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE
TITLE OF INVENTION: LIPASE IN HOMOLOGOUS OR HETEROLOGOUS HOSTS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                       APPLICANT: BOS, Jannetje W.
APPLICANT: FERKEN, Leon G.
APPLICANT: VERRIES, Cornelis T.
APPLICANT: VISSER, Christiaan
TITLE OF INVENTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE
TITLE OF INVENTION: LIPASE IN HOMOLOGOUS OR HETEROLOGOUS HOSTS
NUMBER OF SEQUENCES: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/034,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 43; DB 1;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Kokulis, Paul N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: PNK/5970/91731
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELET : 6714627 CUSH
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                       ADDRESSEE: CUSHMAN, DARBY & CUSHMAN STREET: 1615 L. Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/727,235
FILING DATE: 03-UUL-1991
ATTORNEY/AGENT INFORMATION:
Sequence 10, Application US/08034650 Patent No. 5641671 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
2.1P: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
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Best Local Similarity 63.6
Matches 7; Conservative
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CITY: Washington
STATE: D.C.
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US-08-449-015-10
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                                                                                                                                                                                                                                                                                                                                   STATE:
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Gaps

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Length 358; 3; Indels

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APPLICANT: KOBAYASHI, KATSUNORI
APPLICANT: KOBAYASHI, KATSUNORI
APPLICANT: YAMANAKA, SHIGERU
APPLICANT: YAMANAKA, SHIGERU
APPLICANT: SUZUKI, SHUNICHI
APPLICANT: SUZUKI, SHUNICHI
APPLICANT: TANITA, YUKO
APPLICANT: YOKOZEKI, KENZO
APPLICANT: YOKOZEKI, KENZO
APPLICANT: YOKOZEKI, KENZO
APPLICANT: YOKOZEKI, KENZO
APPLICANT: HASHIGICHI, KENICHI
TITLE OF INVENTION: BACILLUS-DERIVED TRANSGLUTAMINASE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
                  TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene TITLE OF INVENTION: and Pathogens NUMBER OF SEQUENCES: 82
CORRESPONDENCE ADDRESS: 82
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & Norris STREET: One Liberty Place, 46th floor CITY: Philadelphia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1321;
         Trustees of The University of Pennsylvania
VENTION: Plant Genes for Sensitivity to Ethylene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                              COUNTRY: USA

2 I 9103

COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07744A
FILING DATE: 15-JUNE-1995
CLASSIFICATION NUMBER: 08/261,822
FILING DATE: June 17, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 3:
CONTENT OF THE SECTION O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39.5; DB 5;
Pred. No. 2.4e+02;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08596864 Patent No. 5731183 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1321 amino acids
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Best Local Similarity 58.3*
Matches 7; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       678 LDEFWGHLYDFH 689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ANTI-SENSE:
PCT-US95-07744A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-596-864-3
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                                                                                                                                                                                                                                                                                                       1;
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Sequence 3. Application US/08261822A
Patent No. 565053
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R. et al.
TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene
TITLE OF INVENTION: and Pathogens
NUMBER OF SEQUENCES: 82
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5650553ris
STREET: One Liberty Place, 46th floor
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                            Length 1294;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTE: USAN
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,822A
FILING DATE: 17-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 3:
INFORMATION FOR SEQ ID NO: 3:
SUBGENEE (215) 568-3439
INFORMATION FOR SEQ ID NO: 3:
SUBGENEE (ARRACTERISTICS:
                                                                                                                                                                                                                                            Score 39.5; DB 2;
Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39.5; DB 1;
Pred. No. 2.4e+02;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                    4; Mismatches
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58.3%;
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1321 amino acids
TYPE: amino acid
STRANDEDNESS: single
SEQUENCE CHARACTERISTICS:
LENGTH: 1294 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 58.3.
                                                                                                                    ; MOLECULE TYPE: protein US-08-819-288-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                             ||:| |::||:|
678 LDEFWGHLYDFH 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LDKF-GNIYDYH 13
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                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
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PCT-US95-07744A-3
                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY:
STATE:
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Gaps
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APPLICANT: NAKAYAMA, No. 5656471iyuki
APPLICANT: NAKAYAMA, No. 5656471iyuki
APPLICANT: NAKAYAMA, No. 5656471iyuki
APPLICANT: NAKAYAMA, No. 5656471iyuki
ATTILE OF INVENTION: STABILITY AND GENE OF THE SAME
NUMBEN OF SEQUENCES: 6
NUMBER OF SEQUENCES: 6
NUMBER OF SEQUENCES: 6
NUMBER OF SEQUENCES: 6
ADDRESSEE: 745 South 23rd Street
CITY: ALIngton
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
9
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ZIP: 22202
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,876
TILING DATE: 01-APP-1996
TILING DATE: 01-APP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39; DB 2
Pred. No. 44;
2; Mismatches
                                                                                          APPLICATION NUMBER: JS 00/500.000
FILING DATE: 09-FEB-1996
FILING DATE: 09-FEB-1995
FILING DATE: 09-FEB-1995
FILING DATE: 04-FEB-1995
FILING DATE: 04-SEP-1995
FILING DATE: 29-AN-1996
APPLICATION NUMBER: JP 013072/1996
FILING DATE: 29-AN-1996
ATOMNET OBLOW, NORWAN F.
REGISTRATION NUMBER: 24'618
REGISTRATION NUMBER: 24'618
REGISTRATION NUMBER: 10-786-0
TELECOMMUNICATION NUMBER: 10-786-0
TELECOMMUNICATION NUMBER: 10-786-0
TELECOMMUNICATION NUMBER: 10-786-0
TELECOMMUNICATION NUMBER: 10-786-0
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/596,864
APPLICATION NUMBER: US 08/596,864
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-95947
FILING DATE: 30-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08625876 Patent No. 5656471 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 242 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 40.2%;
Best Local Similarity 44.4%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||| :||:|||
| 135 DKFNASFDRIILYDWHYE 152
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                                                                                                                                                                                                                                                                                                                                                                                       JEECUME: 703-412
TELEPHONE: 703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 30-MAR-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein US-08-989-667-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
US-08-625-876-2
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APPLICANT: YAMANAKA, SHIGERU
APPLICANT: YAMANAKA, SHIGERU
APPLICANT: YANYA, KIYOSHI
APPLICANT: SUZUKI, SHUNICHI
APPLICANT: STAVITA, YUGURU
APPLICANT: FTAVITA, YUGURU
APPLICANT: YOKOZEKI, KENZO
APPLICANT: HASHIGUCHI, KENICHI
TITLE OF INVENTION: BACILLUS-DERIVED TRANSGLUTAMINASE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLEAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,667
                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATE: US/08/596,864
FILING DATE: 09-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39; DB Pred. No. 44; 2; Mismatches
                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBA:
APPLICATION NUMBER: 1995
FILING DATE: 09-FEB-1995
PRIOR APPLICATION NUMBER: 17 226316/1995
FILING DATE: 04-SEP-1995
PRIOR APPLICATION NUMBER: JP 013072/1996
FILING DATE: 29-JAN-1996
ATTORNEY AGENT INFORMATION:
NAME: OBLON, NORMAN F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-786-0
                                        3: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-989-667-3
; Sequence 3, Application US/08989667
; Patent No. 5948662
                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 242 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-596-864-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Gaps
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                                                                                                                                                                                                                                                                      Sequence 6, Application US/08625876
Patent No. 5656471
GENERAL INFORMATION:
APPLICANT: MINAGAWA, Hirotaka
APPLICANT: NAKANAMA, NO. 56564711yuki
APPLICANT: NAKANAMA, NO. 56564711yuki
APPLICANT: NAKANOTO, Shinya
TITLE OF INVENTION: LACTATE OXIDASE WITH AN IMPROVED THERMAL
TITLE OF INVENTION: STABILITY AND GENE OF THE SAME
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                       Score 39; DB 1; Length 374;
Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.2%; Score 39; DB 1; Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 71;
0; Mismatches
                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/625,876
FILING DATE: 01-APR-1996
CLASSIPTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-95947
FILING DATE: 30-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-146186
FILING DATE: 13-UNN-1995
APPLICATION NUMBER: JP 7-146186
FILING DATE: 13-UNN-1995
APPLICATION NUMBER: JP 7-1612
REGISTRATION NUMBER: 32,925
REGISTRATION NUMBER: 32,925
REGISTRATION NUMBER: 32,925
REGISTRATION NUMBER: PF-1612
TELECOMMUNICATION NUMBER: PF-1612
TELECOMMUNICATION NUMBER: PF-1612
TELECOMMUNICATION NUMBER: PF-1612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-07-863-169A-5
; Sequence 5, Application US/07863169A
; Patent No. 5420245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street
                       40.2%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
                       Query Match 40.2
Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 40.2
Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-625-876-6
                                                                                                                                               361 KGLDLFDNPYGYEY 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 KGLDLFDNPYGYEY 374
                                                                                                                  1 KPLDKFGNIYDYHY 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KPLDKFGNIYDYHY 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 745 Sout
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                RESULT 11
US-08-625-876-6
                                                                                                                                                           Dp
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APPLICANT: NAKAYAMA, NO. 56564711yuki
APPLICANT: NAKAYAMA, NO. 56564711yuki
APPLICANT: NAKAMOTO, Shinya
TITLE OF INVENTION: LACTATE OXIDASE WITH AN IMPROVED THERMAL
TITLE OF INVENTION: STABILITY AND GENE OF THE SAME
CORRESPONDENCE ADDRESS:
ADDRESSEE: YOUNG & THOMPSON
                                                                                                                                                                                                                                                                                                                                                Score 39; DB 1; Length 374;
Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DUS/MS-DUS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,876
FILING DATE: 01-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 197-95947
FILING DATE: 30-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 37-146186
FILING DATE: 13-JUN-1995
ATTOREX/AGENT INFORMATION:
NAME: PATCH, Andrew J
REGISTRATION NUMBER: 32,925
REGISTRATION NUMBER: 32,925
REGISTRATION NUMBER: 32,925
TELEFRAX: (703) 521-2297
TELEFAX: (703) 685-0573
TELEERAX: (703) 685-0573
TELEERAX: (703) 685-0573
TELEEX: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                REFERENCE/DOCKET NUMBER: PF-1612
TELECOMOUNICATION INFORMATION:
TELEFERAX: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08625876
Patent No. 5656471
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: YOUNG & THOMPSON 745 South 23rd Street
REGISTRATION NUMBER: 32,925
                                                                                                                                                                                                                                                                                                                                              40.28;
57.18;
                                                                                                                                                                                     : 374 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-625-876-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 | | | | | | | 361 KGLDLFDNPYGYEY 374
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KPLDKFGNIYDYHY 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 745 South CITY: Arlington STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                           TYPE: ami
TOPOLOGY:
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ADDRESSEE: ARNOLD WHITE & DURKEE STREET: P.O. BOX 4433
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/424,268
FILING DATE: 4/24/95
CLASSIFICATION: 435
                                                                                              STATE: New Jersey COUNTRY: United States of America ZIP: 07065-0907
                                                                                                                                                                                                                                                                                                                                                                                                18858PC
                                                                                                                                                                                                               OPERATING SYSTEM: System 7.5.3 SOFTWARE: Microsoft Word 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Muthard, David A
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 18856
TELECOMMUNICATION INFORMATION:
TELEFAN: (908) 594-3903
TELEFAN: (908) 544-4703
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.2%;
                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Power Mac
OPERATING SYSTEM: SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 379 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.77
Trans 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO FRAGMENT TYPE: N-termin US-08-424-268-8
                      CORRESPONDENCE ADDRESS:
                                                           P.O.Box 2000
                                         ADDRESSEE: Merck &
    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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94 DKFRDVYDY 102
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US-08-429-964-5
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GENERAL INFORMATION:
APPLICANT: Brown, Michael S.
APPLICANT: Goldstein, Joseph L.
APPLICANT: Goldstein, Joseph L.
APPLICANT: Reiss, Yuval
TITLE OF INVENTION: Tretrapeptide-Based Inhibitors of Farnesyl
TITLE OF INVENTION: Transferase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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Sequence 8, Application US/08424268

Sequence 8, Application US/08424268

Patent No. 5821118

Patent No. 5821108

APPLICANT: Omer, Charles A

APPLICANT: Omer, Charles A

APPLICANT: Gibbs, Jackson B

APPLICANT: Gibbs, Jackson B

APPLICANT: Kohl, Nancy E

TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein

TITLE OF INVENTION: Transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION DATA

PRIOR APPLICATION DATA

APPLICATION NUMBER: US 07/822,011

FILING DATE: 19-7AN-1992

CLASSIFICATION: 530

APPLICATION NUMBER: US 07/937,893

FILING DATE: 18-APR-1991

CLASSIFICATION: 530

APPLICATION NUMBER: US 615,715

FILING DATE: 20-NOV-1990

CLASSIFICATION: 530

APPLICATION NUMBER: US 510,706

FILING DATE: 18-APR-1990

CLASSIFICATION: 530

ATTORNEY AGENT INFORMATION:

NAME: PARKEY, DAVIG L.

REFERENCE/DOCKET NUMBER: UTSD: 297/PAR

TELECOMMUNICATION: 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 72; ; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39;
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/863,169A
FILING DATE: 03-APR-1992
CLASSIFICATION: 530
                                                                                                                                                                                                                                            United States of America
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(713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 5 SEQUENCE CHARACTERISTICS: 12 DEGTH: 379 amir.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     379 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 40.2
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
US-07-863-169A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||| ::|||
| 94 DKFRDVYDY 102
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                                                                                                                                                                                                                                                                  ZIP: 77210
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                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1.3
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Gaps
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Sequence 5, Application US/08429964
Patent No. 5962243
GENERAL INFORMATION:
APPLICANT: BROWN, MICHAEL S.
APPLICANT: REISS, YUVAL
APPLICANT: REISS, YUVAL
APPLICANT: APPLICANT: APPLICANT: JAMES, GUY L.
TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL
TITLE OF INVENTION: TRANSFERASE INHIBITORS
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSED.
                                                   ;
0
Length 379;
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: ILAND
COUNTRY: UNITED STATES OF AMERICA
ZIP: 77210
COUNTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,964
FILING DATE: 27-APR-1995
CLASSIFICATION: 435
Score 39; DB 2;
Pred. No. 72;
2; Mismatches
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Search completed: January 29, 2002, 10:24:01 Job time: 507 sec
                                     APPLICATION NUMBER:
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94 DKFRDVYDY 102
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ZIP: 77210
ZOMPUTER READABLE FORM:
MEDIUTUTYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1 (CONVECTED to ASCII-DOS)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/935,087
FILING DATE: 19920824
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
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APPLICANT: GOLDSTEIN, JOSEPH L.
APPLICANT: GOLDSTEIN, JOSEPH L.
APPLICANT: REISS, YUVAL
TITLE OF INVENTION: THE IDENTIFICATION,
TITLE OF INVENTION: CHARACTERIZATION,
TITLE OF INVENTION: CHARACTERIZATION,
TITLE OF INVENTION: AND INHIBITION OF FARNESYL
TITLE OF INVENTION: PROTEIN TRANSFERASE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/021,625
FILING DATE: 16-FEB-1993
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/822,011
FILING DATE: ABANDONED
CLASSIFICATION: 435
APPLICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32.165
REFERENCE/DOCKET NUMBER: 37.165
REFERENCE/DOCKET N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB 2;
Pred. No. 72;
2; Mismatches
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CITY: HOUSTON
STATE: TEXAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/07935087
Patent No. 6083917
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single;
TOPOLOGY: linear
US-08-429-964-5
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94 DKFRDVYDY 102
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US-07-935-087-5
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Gaps
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Pred. No. 72;
2; Mismatches 1; Indels
                                                                                     UTSD: 269/PAR
US/07/822,011
                                                                                                                                           INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 379 amino acid residues TYPE: amino acid celique
                                               NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFRENCE/POCKET UNMBER: UTSD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-320-7200
TELEFAX: 512-474-7577
              FILING DATE: 01/16/92
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
                                                                                                                                                                                                                                                                                                                               Query Match 40.2
Best Local Similarity 66.7
Matches 6; Conservative
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US-07-935-087-5
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GenCore version 4.5
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OM protein – protein search, using sw model

Run on:

January 29, 2002, 11:13:36; Search time 80.65 Seconds (without alignments) 7.274 Million cell updates/sec

US-09-763-397A-3

1 KPLDKFGNIYDYHYEH 16 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ion	005651 thermotoga	P78258 escherichia	P30263 pichia angu				arabido		O66893 aquifex aeo	P41999 caenorhabdi		P28514 calliphora		Q64148 mesocricetu	P04531 bacteriopha	Q58648 methanococc	P15446 haemophilus		P22541 butyrivibri	P39008 saccharomyc	P25381 saccharomyc	Q64417 cavia porce	Q64406 cavia porce	Q64409 cavia porce	schizo	Q10313 schizosacch		034623 bacillus su		084538 chlamydia t		_	P48190 zea mays (m
SUMMARIES	ID	PORA_THEMA	TALA_ECOLI	CATA_PICAN	CYB2_YEAST	VL96_IRV1	ITA6_CHICK	MTDM_ARATH	LIP_PSEGL	TOP1_AQUAE	NH10_CAEEL	YJD9_YEAST	ARY2_CALVI	RFA2_YEAST	CP3A_MESAU	KDNM_BPT4	YC52_METJA	MTH2_HAEPA	LEU3_AQUAE	GUNA_BUTFI	POP2_YEAST	YCT5_YEAST	CP3E_CAVPO	CP3F_CAVPO	CP3H_CAVPO	NCPR_SCHPO	YD5A_SCHPO	RPOB_NPVAC	DP3A_BACSU	TGL_BACSU	LPXC_CHLTR	PFTA_HUMAN	YWJE_BACSU	MATK_MAI2E
	DB	-			-				Н	-	Н	-	-	-	7	-	7	-				-								-	-		-	-
d	Query Match Length	392	316	507	591	867	1072	1534	358	540	395	1683	759	273	203	241	251	358	364	429	433	491	503	203	203	678	787	876	1115	245	286	379	398	544
	Query Match	46.4		45.9	45.4	45.4	45.4	45.4	٠	44.3	٠	•	•	42.3	42.3	•	41.2	•	41.2		41.2		•		•	•	•	•	٠	。	40.2	。	。	
	Score	45	4	44.5	44	44	44	44	43	43	42	42	41.5	41	41	40	40	40	40	40	40	40	40	40	40	40	40	40	40	39	39	39	39	39
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Ψ.	P42840 Saccharomyc P43573 Saccharomyc	O51124 borrelia bu	P25178 helicobacte	Q9zmz3 helicobacte	O51044 borrelia bu	Ψ	Q01958 entamoeba h	P79217 oryctolagus	_	Q62762 rattus norv
TR2M_ERWHE	YFC3_YEAST	Y097_BORBU	LSPA_HELPY	LSPA_HELPJ	Y011_BORBU	ACP2_ENTHI	CPP2_ENTHI	NY6R_RABIT	NY4R_HUMAN	KC12_RAT
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562	962	128	157	163	279	310	315	371	375	414
40.2	40.2	39.2	39.2	39.5	39.5	39.5	39.5	39.5	39.5	39.2
39	3 G	38	æ :	38	38	38	38	38	38	38
34	36	37	38	36	40	41	42	43	44	45

ALIGNMENTS

ALIGNMENTS	RA_		NCB1_10XID=2330; [1]	SEQUENCE FROM N.A., AND SEQUENCE OF STRAIN-MSB8 / DSM 3109;	"Molecular and phylogenetic characterization of ketolenyalerate ferredoxin oxidoreductases from	and pyruvate ferredoxin oxidoreductase from Ther	SEQUENCE FROM					[3]		Blamey J.M., Adams M.W.W.A.; "Characterization of an ancestral type of	oxidoreductase from the hyperthermophilic						or send
RA - L								National K.E., Clayton R.A., Gill Haft D.H., Hickey E.K., Peters McDonald L., Utterback T.R., McDonald L., Utterback T.R., McDonald L., Utterback T.R., McDonald L., Utterback T.R., McDonald L., Smith H.O., Ven Salzberg S.L., Smith H.O., Ven Evidence for lateral gene tra genome sequence of Thermotoga Interest 39:323-329(1999). [3] SEQUENCE OF 1-43, AND CHARACTE STRAINWABS P. DSM 3109; MEDLINE-94137707; Pubmde-83054 Blamey J.M., Adams M.W.A.; Characterization of an ancest oxidoreductase from the hypert maritima; Blochemistry 33:1000-1007(1994-1-CATALYTIC ACTIVITY: PYRUVA ACTIVITY: PYRUVA ACTIVITY: PYRUVA CATALYTIC ACTIVITY: PYRUVA CATALYTIC ACTIVITY: PYRUVA CONE GAMMA CHAIN. This SWISS-PROT entry is copyr between the European Bioinformatics In use by non-profit institution modified and this statement is entities requires a license also												or send	

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SEQUENCE FROM N.A.
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- K12 genome corresponding to 50.0-68.8 min on the linkage map and
analysis of its sequence features.";
DNA Res. 4:91-113(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K., Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N., Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto U., Oshima T., Oshima T., Sanito N., Sampei G., Satoh Y., Sivasundaram S., Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C., Yamagata S., Horiuchi T.;
                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=KIZ / MG1655;
BEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Riley M., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.,
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-O157.H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed=11206551;
MEDLINE-21074935; PubMed=11206551;
Rose D.J., Mayhew G.F., Evens P.S., Gregor J., Kirkpatrick H.A., Posfal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apdaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacterlaceae;
Escherichia.
                                                                                                                                                                     4;
                                                                                                                                          46.4%; Score 45; DB 1; Length 392; 53.3%; Pred. No. 8.2; tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lida A., Teshiba S., Mizobuchi K.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                     SEQUENCE 392 AA; 44111 MW; ACEF0E34C9EC1818 CRC64;
                                                                                                                                                                                                                                                                                      TALA_ECOLI STANDARD; PRT; 316 AA. P78258; P80218; 26. Created) 01-UUL-1993 (Rel. 35, Last sequence update) 20-NUC-2001 (Rel. 40, Last annotation update) TALA OR E2464 OR 23720 OR ECS3326.
                                                                                             POLY - ALA
                 EMBL; X85171; CAA59457.1; ALT_INIT.
EMBL; AE001690; AAD35111.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=K12;
MEDLINE=97349980; PubMed=9205837;
                                                                                 Oxidoreductase; Complete proteome.
DOMAIN 72 79 POLY-
                                                       Interpro; IPR002880; POR_N. Pfam; PF01855; POR_N; 1.
                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli, and Escherichia coli 0157:H7.
                                                                                                                                                                       Conservative
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214 PLD----LYDYYFEH 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-K12 / W3110;
Iida A., Teshiba S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                             Best Local Similarity
                                              FIGE; TM0017;
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TALA_ECOLI
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                                                                                                                                                                             Hayashi T., Makino K., Ohnishi W., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino K., Ohnishi W., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --- FUNCTION: TRANSALDOLAGE IS IMPORTANT FOR THE BALANCE OF METABOLITES IN THE PENTOSE-PHOSPHATE PATHWAY.
--- CATALYTIC ACTIVITY: SEDOHEPTULOSE 7 PHOSPHATE + D-GLYCERALDEHYDE
--- S-PHOSPHATE - D-ERYTHROSE 4 PHOSPHATE + D-FRUCTOSE 6-PHOSPHATE.
--- PATHWAY: NONOXYDATIVE PART OF THE PENTOSE-PHOSPHATE PATHWAY.
--- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
--- SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
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Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01058; TRANSALDOLASE 2; 1.
PROSITE; PS01054; TRANSALDOLASE 1; 1.
Transferase; Pentose shunt; Multigene family; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
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Best Local Similarity 33.3%; Pred. No. 7.8;
Matches 9; Conservative 4; Mismatches 3; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
990B00ED7937CF19 CRC64;
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01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PXP9 OR PXP-9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRESENCE OF TWO TRANSALDOLASES IN E.COLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, D13159; BAA21821.1; -.
EMBL, AE000333; AAC75517.1; -.
EMBL, D90875; BAA16339.1; -.
EMBL, AE004475; AAG57573.1; -.
EMBL, AE004475; BAS6749.1; -.
EMSP, P30148; 1UCW.
ECOGENE; EG11797; talA.
InterPro, IPRO01585; Transaldolase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sprenger G.A.;
Unpublished observations (JUN-1993).
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                                                                                                                                       STRAIN-0157:H7 / RIMD 0509952;
MEDLINE-21156231; PubMed-11258796;
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                                                                                                                   SEQUENCE FROM N.A.
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GROUPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                         yeast Hansenula polymorpha.";
FEBS Lett. 303.113-116(1992).
-!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND
- SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                MEDLINE-92299073; PubMed-1607006;
Didion T., Roggenkamp R.O.;
"Targeting signal of the peroxisomal catalase in the methylotrophic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
PROXIMAL HEME LIGAND (BY SIMILARITY).
MICROBODY TARGETING SIGNAL (POTENTIAL)
3536ED0A49539CC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JUL-1986 (Rel. 01, Created)
01-APR-1988 (Rel. 07, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CYTOCHROME B2 PRECURSOR (EC 1.1.2.3) (L-LACTATE DEHYDROGENASE
CYTOCHROME) (L-LACTATE FERRICYTOCHROME C OXIDOREDUCTASE) (L-LCR).
CYB2 OR YML054C OR YM9958.08C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structure, expression and regulation of a nuclear gene encoding a mitochondrial protein: the yeast L(+)-lactate cytochrome confloreductase (cytochrome b2)."; EMBO J. 4:3265-3272(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes; Saccharomycetales, Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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PROSITE; PS00437; CAPALASE_1; 1.
PROSITE; PS00438; CAPALASE_2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
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47.1%; Pred. No. 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X56501; CAA39856.1; -. PIR; S23422; S23422. HSSP; P00432; 7CAT. InterPro; IPRO02226; Catalase. Pfam; PF00199; catalase; 1. PRINTS; PR00067; CATALASE. Probom; P0000510; Catalase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57849 MW;
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415 KPDEKYTGEVVPYHWEH 431
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138
348
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138 1
348 3
505 5
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Matches 8; Conserv
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P00175;
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BINDING
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                                                                                                                                                                                                                                                            Ghrir R., Becam A.-M., Lederer F.; "Primary structure of flavocytochrome b2 from baker's yeast. Purification by reverse-phase high-pressure liquid chromatography and sequencing of fragment alpha cyanogen bromide peptides."; Eur. J. Blochem. 139:59-74(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=75156546; PubMed=165435; Guiard B., Lederer F., Jacq C.; "More similarity between bakers'yeast L-(+)-lactate dehydrogenase and liver microsomal sytochrome B5.";
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-:- INDUCTION: BY L-LACTATE. INDUCED DURING RESPIRATORY ADAPTATION.
-:- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Mol. Biol. 212:837-863(1990).
-!- CATALYTIC ACTIVITY: L-LACTATE + 2 FERRICYTOCHROME C = PYRUVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P.PUTIDA S-MANDELATE DEHYDROGENASE, AND TO M.SMEGMATIS LACTATE 2-MONOOXYGENASE.
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MEDLINRE-20203031315; PubMed-2329585;
Xia Z.-X., Mathews F.S.;
"Molecular structure of flavocytochrome b2 at 2.4-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       core in bakers'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 395-591.

MEDLINE-8630284. PubMed=3902473;
Lederer F., Cortial S., Becam A.M., Haumont P.-Y., Perez L.;
"Complete amino acid sequence of flavocytochrome b2 from baker's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WWW="http://www.worthington-biochem.com/manual/L/YLDH.html".
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SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
Devlin K., Churcher C., Barrell B.G., Rajandream M.A.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 88-183.
MEDLINE-76206228; PubMed-776230;
Guard B., Lederer F.;
Gomplete amino acid sequence of the heme-binding yeast cytochrome b2 (L-(+)-lactate dehydrogenase).
Biochimie 58:305-316(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -! - DATABASE: NAME-Worthington enzyme manual;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eur. J. Biochem. 152:419-428(1985).
                                                                                                                                                                                                                     MEDLINE-84132029; PubMed-6365548;
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PIR; A23095, A23095.
PDB; IFCB; 15-JUL-92.
PDB; ILCO; 15-SEP-95.
PDB; ILCO; 15-SEP-95.
SCD; SCD04518; CYR2.
InterPro; IPR001199; Cyt_B5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 FERROCYTOCHROME C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the State of the State of the Service of the Mammalian viruses.

-i- Function: May be involved in tiv genomic dna packaging in A manner relation to the Gag Polyproteins of the Mammalian viruses.

-i- Similarity: Contains 1 of U DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDIANGE 1701750; MEDIANE-91708646; PubMed=1701750; MEDIANE-91708646; PubMed=1701750; MEDIANE M.A., Tajbakhsh S., Seligy V.L.; Monecular cloning and characterization of a late Tipula iridescent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tipula iridescent virus (TIV) (Insect iridescent virus type 1).
Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.
                                                                                                                                                                                                                                                                            Length 591;
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                                                                                                                                                                                                                                             DBADA0751B3C5B83 CRC64;
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Last annotation update)
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Pred. No.
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PIR; JH0225; JH0225.
InterPro; IPR003323; OTU.
Pfam; PF02338; OTU, 1.
Pfam; PR02338; OTV, 1.
PoMAIN 606 745
SEQUENCE 867 AA; 96011 MW; F19DBDE
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01-AUG-1991 (Rel. 19, Last sequ
20-AUG-2001 (Rel. 40, Last anno
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Best Local Similarity 53.8
Matches 7; Conservative
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ID VL96_IRV1
AC P22856;
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HEME LIGAND (BY SIMILARITY).
REMOVES THE SUBSTRATE ALPHA-PROTON AS THE FIRST STEP IN CATALYSIS.
SUBSTRATE BINDING.
Q -> E (IN REF. 3 AND 6).
E -> Q (IN REF. 4).
R -> E (IN REF. 4).
 IN InterPro; IPR003009; FMN_enzyme.

IN InterPro; IPR000262; FMN_hydroxy_acid_dh.

IN Pfam; PF001070; FMN_dh; 1.

IN PROSITE; PS00191; CYTOCHROME_B5_1; 1.

IN PROSITE; PS00555; CYTOCHROME_B5_2; 1.

IN PROSITE; PS00557; FMN_HYDROXY_ACID_DH; 1.

IN PROSITE; PS00557; FMN_HYDROXY_HYDROXY_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_HYDROX_H
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-!- SIMILARITY: CONTAINS 2 BAH DOMAINS
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INTEGRIN ALPHA-6.
INTEGRIN ALPHA-6 HEAVY CHAIN (POTENTIAL).
ENTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X56559; CAA39909.1; -.
PIR; A38457; A38457.
HSSP: P11215; 1A8X.
InterPro: IPR000413; Integrin_alpha.
Pfam; PF001839; FG-GRP: 5.
Pfam; PF00185; INTEGRINA.
SMART; SM00191; Int_alpha; 5.
FROSITE: PS00242; INTEGRINA LPRA; 1.
Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane; Signal; Extracellular matrix; Cytoskeleton; Phosphorylation; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. THE ALPHA SUBUNIT IS COMPOSED OF AN HEAVY AND A LIGHT CHAIN LINKED BY A DISULFIDE BOND. ALPHA-6 ASSOCIATES WITH EITHER BETA-1 OR BETA-4.
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- DEVELOPMENTAL STAGE: ALPHA-6 LEVELS DECREASE WITH AGE.
-1- THM: PHOSPHORYLATED IN VIVO.
-1- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
-1- SIMILARITY: CONTAINS 7 FG-GAP REPEATS.
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           Score 44; DB 1; Length 867; Pred. No. 27;
                                      5; Indels
                                                                                                                                                                                                  Last sequence update)
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                                      Mismatches
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                                     0;
                                                                                                                                                                                   01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last seq
20-AUG-2001 (Rel. 40, Last anno
           Query Match
Best Local Similarity 64.3%;
Matches 9; Conservative (
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FG-GAP 1. FG-GAP 2. FG-GAP 3. FG-GAP 4. FG-GAP 4. FG-GAP 5. FG-GAP 5. FG-GAP 7. FG-GAP 7. POPENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. FS IMILARITY. BY SIMILARITY. BY SIMIL	Score 44; DB 1; Length 1072; Pred. No. 34; 1; Mismatches 4; Indels 0; Gaps PRT; 1534 AA.	Oll-FEB-1994 (Rel. 28, Created) Ol-FEB-1994 (Rel. 28, Created) Ol-FEB-1994 (Rel. 28, Last sequence update) Ol-MC-2001 (Rel. 40, Last annotation update) DNA (CYTOSINE-5)-METHYLTRANSFERASE ATHI (EC 2.1.1.37) (DNA METHYLTRANSFERASE ATHI) (M.ATHI). ATHIM. Arabidopsis thaliana (Mouse-ear cress). Eukaryopta; Varidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. (1) SEQUENCE FROM N.A.	STRAIN=CV COLUMBIA; MEDILINE=91281384; PubMed=8389441; REDILINE=91281384; PubMed=8389441; Finnegan E.J., Dennis E.S.; "Isolation and identification by sequence homology of a putative cytosine methylyltransferase from Arabidopsis thaliana."; Nucleic Acids Res. 21:238-2388(1993) -! FUNCTION: METHYLATES CG RESIDUES. -! CATALYTIC SATIVITY: S-ADENOSYL-L-HTHYLCYTOSINE. -! CATALYTIC ACTIVITY: S-ADENOSYL-L-HTHYLCYTOSINE. -! SIMILARITY: LOW TO OPHER EUKARYOTIC DNA METASE. -! SIMILARITY: SOME TO BACTERIAL RESTRICTION SYSTEMS METHYLTRANSFERASES. -! SIMILARITY: CONPAINS 2 BAH DOMAINS.
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REPEAT RE	Query Match Best Local Similarity Matches 7: Conserva QY 2 PLDKFGNIYDYH 13 1 1 1 1 Db 394 PYDGFGKVYIYH 40 MTDM_ARRATH STAND AT PARBELL AND ATBM_ARRATH STAND	01-FEB-1994 (Rel. 01-FEB-1994 (Rel. 20-AuG-2001 (Rel. DNA (CYTOSINE-5)-METHYLTRANSFERASE, ATHIM, Arabidopsis thalia Eukaryota, Viridip Spermatophyta; Mageurosids II; Brass (NEL_TAXID=3702; [1] SEQUENCE FROM N.A.	STRAIN=CV. CO MEDLINE-93281 Finnegan E.J. "Isolation an cytosine meth Nucleic Acids -!- FUNCTION: -!- CATALYTIC -!- SIMILARIT -!- SIMILARIT -!- SIMILARIT -!- SIMILARIT -!- SIMILARIT -!- SIMILARIT
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                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=94(009622; PubMed=8405390;
Noble M.E.M., Cleasby A., Johnson L.N., Egmond M.R., Frenken L.G.J.;
"The crystal structure of triacylglycerol lipase from Pseudomonas
glumae reveals a partially redundant catalytic aspartate.";
FEBS Lett. 331:123-128(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES-C.viscosum;
MEDLINE-95306500; PubMed=7786905;
Taipa M.A., Liebeton K., Costa J.V., Cabral J.M.S., Jaeger K.-E.;
"Lipase from Chromobacterium viscosum: biochemical characterization indicating homology to the lipase from Pseudomonas glumae.";
Biochim. Biophys. Acta 1256:396-402(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Verrips C.T.; "Cloning of the Pseudomonas glumae lipase gene and determination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Frenken L.G.J., Egmond M.R., Batenburg A.M., Bos J.W., Visser C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                             x RIDGENES; 2003) m.A.L.II.

x InterPro; IPR001525; C5_DNA_meth.

x InterPro; IPR001525; C5_DNA_meth.

x Pfam; PP00145; DNA_methylase; 3.

x PRINTS; PR00105; C5METTRFRASE.

x SMART; SM000439; BAH; 2.

x PROSITE; PS000095; C5_MTASE_1; 1.

x PROSITE; PS00095; C5_MTASE_2; 1.

x Transferase; Methyltransferase; DNA-binding.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., SEQUENCE OF 40-61, AND MUTAGENESIS. SPECIES-P.glumae; STRAIN-PG1 / CBS 322.89; MEDLINE-93119130; PubMed-1476423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0cT-1994 (Rel. 30, Created)
01-0cT-1994 (Rel. 30, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
LIPASE PRECURSOR (EC 3.1.1.3) (TRIACYLGIXCEROL LIPASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas glumae, and Chromobacterium viscosum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the active site residues.";
Appl. Environ. Microbiol. 58:3787-3791(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 40-54, AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [4]
x-ray crystallography (1.6 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.48;
                                                                                                                                                                                                           EMBL; L10692; AAA32829.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 KPAASYRKVYDYFYE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KPLDKFGNIYDYHYE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=337, 42739;
                                                                                                                                                                                                                                   REBASE; 2839; M.AthI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIP_PSEGL
Q05489;
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30-MAY-2000 (Rel. 39, Last sequence update)
20-MGC-2001 (Rel. 40, Last annotation update)
DNA TOPOISOMERASE I (EC 5.99.1.2) (OMEGA-PROTEIN) (RELAXING ENZYME)
SPECIES-C.viscosum; STRAIN=ATCC 6918;
MEDLINE=96275656; PubMed-8683577;
Lang D., Hofmann B., Haalck L., Hecht H.-J., Spener F., Schmid R.D.,
                                                                               -i- SUBUNIT: MONOMER.
-i- SUBCELLULAR LOCATION: SECRETED.
-i- SIMILARITY: STRONG TO OTHER PSEUDOMONAS LIPASES.
-i- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC, HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H->A: NO LOSS OF ACTIVITY.
S->A: COMPLETE LOSS OF ACTIVITY.
D->E: NO LOSS OF ACTIVITY.
D->A: NO LOSS OF ACTIVITY.
D->B: NO LOSS OF ACTIVITY.
D->A: COMPLETE LOSS OF ACTIVITY.
D->A: COMPLETE LOSS OF ACTIVITY.
D->B: NO LOSS OF ACTIVITY.
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H->A: COMPLETE LOSS OF ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam, PF00561; abhydrolase; 1.
PROSITE; PS00120; LIPASE_SER; 1.
Hydrolase; Lipid degradation; Signal; Calcium; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43; DB 1; Length 358;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FE7B5D7A22EC6B4B CRC64;
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SYSTEM.
SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X70354; CAA49812.1; -.
EMBL; A16323; CAA01279.1; -.
EMBL; A32021; CAA02073.1; -.
PIR; A48952; A48952.
PIR; 37291; S37291.
PDB; ITAH; 31-MAY-94.
InterPro; IPR000073; Abhydrolase.
InterPro; IPR00073; Abhydrolase.
InterPro; IPR000739; Est_lip_thioest_actsite.
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1; Mismatches
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CHARGE RELAY S
CHARGE RELAY S
CHARGE RELAY S
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                                                                                                                                                                                                A FATTY ACID ANION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358
3324
3324
3324
3324
1160
1160
2280
3302
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 358 AA;
                                                                      Schomburg D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOP1_AQUAE
066893;
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                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                         -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pohl T.M., Aljinovic G.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
-: SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 191.5 KDA PROTEIN IN NSP1-TADZ INTERGENIC REGION.
XJL039C OR J1216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB 1; Length 395;
Pred. No. 24;
                                                                                       Fulton L., Waterston R.;
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ORPHAN NUCLEAR RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44899 MW; AFDB075D989EEBEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEAR RECEPTOR-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1683 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WormPep; B0280.8; CE00815.
InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001628; zf-C4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C4-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C4-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.3%;
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U10438; AAA19086.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 58.3°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83
38
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188 RFANQSDYHYWH 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16
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18
54
395 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                               SEQUENCE FROM N.A.
                                                                 STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 KFGNIYDYHYEH
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4932;
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P47054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
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                                                                                                                                                                                                                                                                                                             NATURE 392.358(1998).

-I FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.

-I CATALYTIC ACTIVITY: ATP-INDEPENDENT BREAKAGE OF SINGLE-STRANDED DNA, FOLLOWED BY PASSAGE AND REJOINING.

-I SUBUNIT: MONOMER (BY SIMILARITY).

-I SUBUNIT: MONOMER (BY SIMILARITY).

-I SUBUNIT: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS AT ONE END OF THE ENZYME-SEVERED DNA STRAND.

-I SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                MEDLINE-98196666; PubMed-9537320;
Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex aeolicus";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSTICE: PS00396; TOPOISOMERASE_I_PROK; 1.
ISOMERASE: TOPOLSOMERASE; DNA-binding; Complete proteome.
ACT_SITE 281 281 DNA CLEAVAGE (BY SIMILARITY).
SEQUENCE 540 AA; 63427 MW; 89C0604DFF5B042E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB 1; Length 540;
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
NUCLEAR HORMONE RECEPTOR FAMILY MEMBER NHR-10.
NHR-10 OR B0280.8
Caenorhabditis elegans.
                                                                 Bacteria; Aquificales; Aquificaceae; Aquifex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           395 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro: IPR003601; DNAtcpI_ATP_bind.
InterPro: IPR003601; DNAtcpI_DNA_bind.
InterPro: IPR0003802; DNAtcpI_DNA_bind.
InterPro: IPR000380; Toprim.
(UNTWISTING ENZYME) (SWIVELASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01131; Topoisom_bac; 1. Pfam; PF01751; Toprim; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0417; PRTPISMRASEI.
SMART; SM00437; TOPIAC; 1.
SMART; SM00436; TOPIBC; 1.
SMART; SM00493; TOPRIM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000700; AAC06848.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ::| |||| ||:
197 KGSEEFWAIYDYRYEN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KPLDKFGNIYDYHYEH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity
                                                                                                                               SEQUENCE FROM N.A.
                                                                                       NCBI_TaxID-63363;
                                          Aquifex aeolicus.
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P41999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NH10_CAEEL
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InterPro; IPR000896; Hemocyanin.
        Pfam; PF00372; hemocyanin;
                                                                                                                           Query Match 42.8
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         Brill S.J., Stillman B.
                                                                                                                                                                                    :|||::||:| |
748 EKFGH-FDYNYHH 759
                                                                                                                                                                      16
                                                                                                                                                                      4 DKFGNIYDYHYEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               essential
                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cooper
                                                                                                                                                                                                                               RESULT 13
RFA2_YEAST
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                                                                              CHAIN
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                                                                                                                                                                                                                                                       ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete CDNA and gene sequence of the developmentally regulated arylphorin of Calliphora vicina and its homology to insect hemolymph proteins and arthropod hemocyanins.", Biochem Blophys. Res. Commun. 177:963-972(1991).

- FUNCTION: ARYLPHORIN IS A LARVAL STORAGE PROTEIN (LSP) WHICH MAY SERVE AS A STORAGE PROTEIN USED PRIMARILY AS A SOURCE OF AROMATIC AMINO ACIDS FOR PROTEIN SYNTHESIS DURING METAMORPHOSIS. IT IS A CONSTITUENT OF THE SCLEROTIZING SYSTEM OF THE CUTICLE, AND SERVES AS A CARRERE FOR ECDYSTEROID HORMONE.
                                                                                                                                                                                                                                                                                                                                                                                                                  ARYLPHORIN SUBBURT C223 PRECURSOR.
Calliphora vicina (Blue blowfly) (Calliphora erythrocephala).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Calliphora
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -: SUBCELLULAR LOCATION: EXTRACELLULAR.
-:- TISSUE SPECIFICITY: FAT BODY.
-:- SIMILARITY: TO OTHER ARYLPHORINS AND TO ARTHROPOD HEMOCYANINS.
                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                  Length 1683;
                                                                                                                                                                                                                         Score 42; DB 1; Length loc
Pred. No. 1.16+02;
O: Indels
                                                                                                                                                                                                FD2D61FDEA5451C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 24, Last sequence update) (Rel. 35, Last annotation update)
                                                                                POTENTIAL.
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BMBL; X59390; CAA42033.1; -.
PIR; JQ1044; JQ1044.
HSSP; P04253; 1LL1.
                           Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Fat body;
MEDLINE=91282793; PubMed=1711849;
                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 24, Created)
                                                                                                                                                                                                                                    43.3%;
61.5%;
                                                                                                                                                                                                  1683 AA; 191534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: HETEROHEXAMER.
  ; Z49314; CAA89330.1;
S0003576; YJL039C.
                                                                                                                                                                                                                                    Query Match 43.3
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Naumann U., Scheller K.;
                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                     1228 LNKYCSGNIYDFH 1240
                                                                                                                                         1042
1315
1363
1526
1615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-1992 (
01-DEC-1992 (
01-NOV-1997 (
                           Aypothetical
                                                                                                                                                                                                                                                                                                                                                             ARY2_CALVI
P28514;
                                                                                                                                TRANSMEM
TRANSMEM
                                                                                                                                                       PRANSMEM
                                                                                                                                                                                                     SEQUENCE
                                       RANSMEM
                                                  FRANSMEM
                                                             FRANSMEM
                                                                         FRANSMEM
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DEACUENT E ROUT WITH.

MAILTER C.T.C., UTDBAUBS J.H.M., Planta R.J.;

Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.

Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.

-! FUNCTION: BRINDS TO SINGLE-STRANDED SEQUENCES PARTICIPATING IN DNA

REPLICATION IN ADDITION TO THOSE MEDIATING TRANSCRIPTIONAL

REPRESSION (URS1) AND ACTIVATION (CAR1). STIMULATES THE ACTIVITY

OF A COGNARTE STRAND EXCHANGE PROPEIN (SEP1). IT COOPERATES WITH

T-AG AND DNA TOPOISOMERASE I TO UNWIND TEMPLATE DNA CONTAINING THE

SIMIAN VIRUS 40 ORIGIN OF DNA REPLICATION.

-! SUBUNIT: HETEROPITATE ROF 69, 36, AND 13 KDA CHAINS. THE

DNA-BINDING ACTIVITY MAY RESIDE EXCLUSIVELY ON THE 69 KDA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MATAIN=2288C / FY1676;
MEDLINE=9606632; PubMed=7502583;
Maftahl M., Nicaud J.-M., Levesque H., Gaillardin C.;
"Sequencing analysis of a 24.7 kb fragment of yeast chromosome XIV identifies six known genes, a new member of the hexose transporter family and ten new open reading frames.";
yeast 11:1077-1085(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Replication factor-A from Saccharomyces cerevisiae is encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 100-118; 150-172 AND 184-196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REAZ_YEAST STANDARD; PRT; 273 AA.
P26754; p38905;
01-AUG-1992 (Rel. 23, Last sequence update)
01-NV-1997 (Rel. 35, Last annotation update)
01-NV-1997 (Rel. 35, Last annotation update)
REPLICATION FACTOR-A PROTEIN 2 (RF-A) (DNA BINDING PROTEIN BUF1)
RFA2 OR BUF1 OR YNL312W OR N0368.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetels;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBL_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Saccharomyces cerevisiae BUF protein binds to sequences participating in DNA replication in addition to those mediating transcriptional repression (URS1) and activation."; Mol. Cell. Biol. 13:5749-5761(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Luche R.M., Smart W.C., Marion T., Tillman M., Sumrada R.A.,
                                                                                                                                                                                                                                                                                                                      DB 1; Length 759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genes coordinately expressed at S phase.";
                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                 Signal; Storage protein; Glycoprotein; Multigene family SIGNAL
                                                                                                                                                                           ARYLPHORIN SUBUNIT C223.
BE66CC7A2D71352D CRC64;
                                                                                                                                                                                                                                                                                                                         Score 41.5; DE
Pred. No. 59;
4; Mismatches
PRINTS; PR00187; HARMOCYANIN.
PROSITE; PS00209; HEMOCYANIN_1; FALSE_NEG.
PROSITE; PS00210; HEMOCYANIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 5-16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93361008; PubMed=8355713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=W303-1A;
MEDLINE=91357474; PubMed=1885001;
                                                                                                                                                                                                                 759 AA; 92525 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genes Dev. 5:1589-1600(1991).
                                                                                                                                                                                                                                                                                                                                 42.8%;
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TISSUES BY VARIOUS FOREIGN COMPOUNDS, INCLUDING DRUGS, PESTICIDES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.3%; Score 41;
61.5%; Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M73992; -; NOT_ANNOTATED_CDS.
EMBL; S79317; AAB35091.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 148-241 FROM N.A. MEDLINE-82150240; Pubmed-7063418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bacteriophage T4 tRNA region.";
J. Mol. Biol. 185:545-563(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57693 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KPLDKFGNIYDYH 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid sequence.
                                               CARCINOGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          503 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 8; Conserv
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NCBI_TaxID=10665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriophage T4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDNM_BPT4
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        SO THE REPORT OF THE PROPERTY 
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                                                                                                                                                                                    between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CYTOCHROME P450 3A10 (EC 1.14.14.1) (CYPIIA10) (6 BETA-HYDROXYLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Subramanian A., Teixeira J., Wang J., Gil G.;
"A STAT factor mediates the sexually dimorphic regulation of hepatic cytochrome P450 340/Jihocholic acid 6 beta-hydroxylase gene expression by growth hormone.";
Mol. Cell. Blol. 15:4672-4682(1995).
-i- FUNCTION: CATALYZES THE 6 BETA-HYDROXYLATION OF LITHOCHOLIC ACID AND STEROID HORMONES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH + OXIDIZED FLAVOPROTEIN + H(2)0.
-1- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
-1- DEVELOPMENTAL STAGE: EXPRESSED ONLY IN MALE HANSTERS.
-1- INDUCTION: P450 CAN BE INDUCED TO HIGH LEVELS IN LIVER AND OTHER
-! - PTM: PHOSPHORYLATED IN A CELL-CYCLE-DEPENDENT MANNER (FROM THE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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"Cloning, expression and regulation of lithocholic acid 6beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.3%; Score 41; DB 1; Length 273; 40.0%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLY/SER-RICH.
; F6087501E4E28CC1 CRC64;
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                                      PHASE UNTIL MITOSIS).
-!- SIMILARITY: TO OTHER SPECIES RFA2/RPA2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 266:21030-21036(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z46259; -; NOT_ANNOTATED_CDS.
EMBL; Z71588; CAA96241.1; -.
PIR; B37281; B37281.
PIR; S17021; S17021.
TRANSFAC; T01249; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGD; S0005256; RFA2.
InterPro; IPR002309; tRNA-synt_2.
Pfam; PF01336; tRNA_anti; 1.
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SEQUENCE 273 AA; 29936 MW;
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155 KPIDSFNEVLTHHLE 169
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Matches 6; Conserv
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NCBI_TaxID=10036;
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Q64148;
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                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001128; Cyt_P450.
Pfam; PF00067; p450; 1
PRINTS; PR001359; BP450.
PRINTS; PR00463; EP450.
PRINTS; PR00464; EP4501.
PRINTS; PR00464; EP4501.
PROSITE; PS00086; CYTOCHROME_P450; 1.
Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme; Microsome; Endoplasmic reticulum.
BINDING 442 HEME (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Nucleotide sequence of the bacteriophage T4 gene 57 and a deduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 1; Length 503;
Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
DEOXYNUCLEOTIDE MONOPHOSPHATE KINASE (EC 2.7.4.13) (DNK).
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D4D24FEE87FD7F51 CRC64;
-1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
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MEDLINE=89296504; PubMed=2740234;
Koch T., Lamm N., Rueger W.;
"Sequencing, cloning and overexpression between map positions 74.325 and 77.184.
Nucleic Acids Res. 17:4392-4392(1989).
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                                                                                                                                         "Crystal structure of bacteriophage T4 deoxynucleotide kinase with its substrates dGMP and ATP."; EMBO J. 13.3487-3497(1996).

-!- FUNCTION: ACTS ON DGMP, DTMP AND 5-HYDROXYMETHYL-DCMP WHILE EXCLUDING DCMP AND DAMP.

-!- CATALTIC ACTIVITY: ATP + DEOXYNUCLEOSIDE PHOSPHATE = ADP + DEOXYNUCLEOSIDE DIPHOSPHATE.

-!- CATALTIC ACTIVITY: ATP + DEOXYNUCLEOSIDE PHOSPHATE = ADP + DEOXYNUCLEOSIDE DIPHOSPHATE.
MEDLINE=96312945; PubMed-8670851;
Teplyakov A., Sebastiao P., Obmolova G., Perrakis A., Brush G.S.,
Bessman M.J., Wilson K.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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Pred. No. 30;
2; Mismatches 2; Indels
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SEQUENCE 241 AA; 27329 MW; 61AD2375CC94BDE8 CRC64;
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EMBL; X14845; CAA32953.1; --
EMBL; J02516; AAA32497.1; --
PIR; A04309; KIBD94.
PIR; S04612; S04612.
PDB; IDEK; 11-JAN-97.
PDB; IDEL; 11-JAN-97.
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Best Local Similarity 63.6%;
Matches 7; Conservative
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161 LDKFNSGYDYY 171
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Sequence of an imm Synthetic peptide Malaria antigen fo

Non-immunogenic am Resin-bound Plasmo fdMal protein N-te full and 2 half

fdMal protein

Perfect score: Sequence: Scoring table:

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AABB4362
AAB49997
AAP60804
AAR49980
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AAR70039
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AAB15523
AAR22907
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AAW69278
AAU03175
AAB08105
AAR08362
AAR59808
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AAW29733
AAW61558
AAG63516
AAY91224
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AAP82566
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AAR14261
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 AAR03092;
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 RESULT
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Plasmodium falcipa
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2.860 Million cell updates/sec
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                                                                                                                 January 29, 2002, 10:21:41; Search time 310.82 Seconds
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**SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:**

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**SIDSB/gcgdata/geneseq/geneseqp/genes
               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                       522463 segs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                   protein search, using sw model
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AAR70038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                      Synthetic.
                                                      AAR49981;
                                                                                                                                                                                                                                                                       Comis A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR70038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                        AAR49981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           XEXTX
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                                             δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hybrid surface proteins are claimed in which an active polypeptide (e.g. a surface antigen from a mammalian tunnour cell, sperm or an allergen, bacterium, virus, parasite or fungus) is fused to an anchor region from a surface antigen normally expressed on the cell surface of gram positive bacteria. The anchor segment is pref. derived from a streptococcal M protein (see AAR41780). Sequence AAR41783 is a peptide sequence from the cs protein of p. falciparum (Nature 314:111-114) suitable for development of a vaccine against malaria.
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene encoding hybrid surface protein of gram positive bacteria useful for preparing vaccine compsn. for protecting animals from bacterial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                 Group A Streptococci; surface antigen; anchor region; gram positive bacterium; M protein; fusion protein; immunogen; malaria; circumsporozoite protein; vaccine.
                                                                                                 .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 12;
                                                                            Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
The sequence NANP can be repeated 3-40 times. When conjugated to a tuberculin protein derivative, the product is useful as an anti-malaria vaccine and provides a high antibody response.
                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 12; Conservative 0; Mismatches 0;
                                                                             100.0%; Score 69; DB 11;
ilarity 100.0%; Pred. No. 0.00016;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                 Plasmodium falciparum cs protein antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                             Schneewind 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 53; 85pp; English.
                                                                                                                                                                                         AAR41783 standard; protein; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                      93WO-US02355
                                                                                                                                                                                                                                                                                                                                                                                         92US-0851082
                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                             (UYRQ ) UNIV ROCKEFELLER.
                                                                                                                                                                                                                                                                                                                                                                                                                              Fischetti VA, Pozzi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NANPNANPNANP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1993-303477/38.
                                                                                                                         1 NANPNANPNANP 12
                                                                                                                                   12 AA;
                                                                                  Query Match
Best Local Similarity
Matches 12; Conserv
                                                      12 AA;
                                                                                                                                                                                                                                                                                                                                                                      12-MAR-1993;
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                                                                                                                                                                                                                                  25-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                     16-SEP-1993
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                                                                                                                                                                                                                 AAR41783;
                                                        Sequence
                                                                                                                                                                           7
                                                                                                                                                                           RESULT
AAR41783
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Synthetic peptide antigen analogues of native peptide antigens which are either (1) retro modified, (2) inverso modified or (3) retronances modified with respect to the native antigen can be used to raise antibodies which recognise the native antigen and hence can be used in the treatment and/or prophylaxis of diseases and therapy of disease states. They can be used in the production of vaccines and in assays for antibodies specific for the native antigen. They can have increased stability to degredation after administration and they can be administered orally. This sequence is based on the financodominant epitope of the circumsporozoite coat protein of plasmodium falciparum. The retro-inverso version of this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                 Peptide; retro; inverso; retro-inverso; therapy; disease; vaccine; immunogen; antibody; antibodies; assay; treatment; prophylaxis; plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New retro, inverso and retro-inverso peptide analogues - used as immunogens for the prodn. of antibodies and in diagnosis, therapy and prophylaxis of diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                            Synthetic peptide analogue of P. falciparum used as immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR70038 standard; Protein; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 6; Page 21; 87pp; English.
AAR49981 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tyler MI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92AU-0004374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum. 1 is described in AAR60483.
                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DEAK-) DEAKIN RES LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1994-100849/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-AUG-1992;
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us-09-763-397a-4.rag

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The malaria circumsporozoite protein repeat region is used in an immunogenic composition along with the T-cell epitope derived from malaria. The T-cell epitope elicits an anti-malarial T-cell response in mammals of diverse genetic backgrounds. The composition can be used as a vaccine to confer prophylactic or therapeutic immunity against malaria. They may also be used to inhibit the propagation of a malarial organism in a susceptible animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is a peptide comprising a malarial B-cell epitope, which is contained in the COOH-terminal repeat region of the Plasmodium falciparum circumsporozoite (CS) protein. It is this epitope that stimulates the production of antibodies that specifically recognise and bind to the malarial CS protein. This epitope can be incorporated into a polyoxime with T-cell epitopes to produce a vaccine that is packgrounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenic composition containing T cell epitope of malaria-derived peptide - incorporated into a poly:oxime and optionally B cell epitope, used in vaccines to protect against malaria in subjects of differing genetic background(s)
                                           New immunogenic compositions for malaria – comprise malaria derived peptide comprising universal T-cell epitope which elicits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Circumsporozoite protein; CS; antibody; polyoxime; T-cell epitope;
                                                                                                                                                                                                                                                                                        Score 69; DB 19;
Pred. No. 0.00016;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rose K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA.
                                                                                                    Disclosure; Page 2; 38pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW29731 standard; peptide; 12
                                                                                                                                                                                                                                                                                        100.0%;
                                                                       anti-malarial T-cell response
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nussenzweig RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                          Ouery Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Malarial B-cell epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                 1 NANPNANPNANP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-398801/34.
              WPI; 1998-413810/35.
                                                                                                                                                                                                                                                12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine; malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9830237-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW29731;
                                                                                                                                                                                                                                                Sequence
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    δλ
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                                                                                                                                                                                                                                                                                                                                                                         The protein represents 12 amino acid units of the P. falciparum circumsporozoite protein repeat region (AAR70034), which are sufficient for the production of antibodies reactive against the whole protein. Insertion of the coding sequence into the major coat protein gene VIII of bacteriophage Fd in a region of the protein known to be exposed on the virus surface results in expression of the P. falciparum antigen on the phage surface. Thus, the phage is useful in a vaccine composition against malarla, or as a therapeutic/diagnostic product.
                                                                                                                                                                                                                                                                                     Filamentous bacteriophage engineered to display T- and B-cell epitopes and/or a peptide eliciting HIV neutralising antibodies - useful in vaccines and as a therapeutic/diagnostic prod.
Bacteriophage Fd; phage display; malaria; vaccine; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 69; DB 16; 100.0%; Pred. No. 0.00016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Malaria circumsporozoite protein repeat region.
                                                                                                                                                                                                                  Veronese F, Willis AE;
                                                                                                                                                                                    (CAMB-) CAMBRIDGE BACTERIOPHAGE TECHNOLOGIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 32; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW61556 standard; peptide; 12 AA
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                                                                                                                             94WO-GB01827
                                                                                                                                                         93GB-0017304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                  Perham RN,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NANPNANPNANP 12
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                                                                                                                                                                                                                                             WPI; 1995-098754/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                            N-PSDB; AAQ83024.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 AA;
                                                                                                                             19-AUG-1994;
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                                                                                                                                                         19-AUG-1993;
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                                                                    WO9505454-A
                                                                                                 23-FEB-1995
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                                                                                                                                                                                                                  Appella E,
              diagnostic
                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Length 12; Indels

Gaps

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Indels

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Mismatches

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(first entry)

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Human hepatitis B core protein; HBC; modified; immunodominant; nucleocapsid protein; vaccine; T cell epitope.
                                                                                                                                                                   Plasmodium falciparum polypeptide hapten.
                                                                                                  AAY29734 standard; Protein; 12
12; Conservative
                                        1 nanpnanpnanp 12
                     1 NANPNANPNANP 12
                                                                                                                                                08-NOV-1999
                                                                                                                           AAY29734;
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  Matches
                                                                                          AAY29734
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                                                                                                                                                                                                                                                             Immunogenic composition; viral particle; hybrid protein; expression; immunogen; diagnosis; passive immunisation; vaccination; vaccine; immune response; epitopic site; pathogen; toxin.
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New hybrid protein comprising a particle forming protein and a polypeptide having epitopes, useful as a vaccine -
                                                                         ;
0
                                                 Score 69, DB 19; Length 12; Pred. No. 0.00016;
                                                                         0; Indels
                                                                                                                                                                                                                                            Plasmodium falciparum circumsporozoite core peptide.
                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Column 20; 13pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barr PJ, Kuo G, Valenzuela PDT;
                                                                                                                                                                            AAY41790 standard; peptide; 12 AA.
                                                  ucery Match
Best Local Similarity 100.0%;
Matches 12; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                      85US-0777976.
87US-0128639.
92US-0966291.
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94US-0352989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84US-0650323
                                                                                                                                                                                                                           08-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-579892/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHIR ) CHIRON CORP.
                                                                                                  1 NANPNANPNANP 12
                                                                                                               12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAZ25062
                      12 AA;
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04-DEC-1987;
26-OCT-1992;
23-SEP-1993;
09-DEC-1994;
12-SEP-1984;
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                        Sednence
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                                                                                                                                                                    AAY41790
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The present invention describes a conjugate (A) comprising a catrategically modified hepatitis B core (HBC) protein (I) attached to a trategically modified hepatitis B core (HBC) protein (I) attached to a hapten, where (I) includes amino acids (aas 10-140 of the wild type (II) in the 183 as sequence (given in ANZ29674) and additionally has an insert (II) in the region corresponding to aa's 50-100, where the insert is corresponding to a protective antibody response against corresponding from which the hapten is derived, in humans or other carrians in native HBC protein, increasing the reactivity of aa side chains in native HBC protein, increasing the reactivity Modified HBC can be derivatised in the form of particles by well-defined chemical can be derivatised in the form of particles by well-defined chemical can be derivatised in the form of particles by well-defined chemical corresponding to the cause immunological side-effects. ANX29675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conjugate of hepatitis B core protein, modified to increase reactivity with hapten, used to raise antibodies against the hapten, e.g. in vaccines
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100.0%; Pred. No. 0.00016;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 39; 128pp; English.
                                                                                                                                                                                           99WO-US03055.
                                                                                                                                                                                                                                                             98US-0074537.
                                                                                                                                                                                                                                                                                                                              (IMMU-) IMMUNE COMPLEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.

Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-527340/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 AA;
                                                                                                                                                                                                   11-FEB-1999;
                                                                                                                                                                                                                                                             12-FEB-1998;
                                                                                                                              19-AUG-1999.
                                                                                                                                                                                                                                                                                                                                                                                                         Birkett AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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Length 12;

Score 69; DB 20; Pred. No. 0.00016;

100.0%;

Query Match Best Local Similarity

us-09-763-397a-4.rag

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Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; real-periope; treatment; recal-periope; treatment; circumsporozoite protein; CSP: sporozoite surface protein-2; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; MSP-2; apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody.
                                                                                                                                                                                                                                                                                                                                                                         Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle \,
                                                                                                                                                                                                                                                                                      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 16; 52pp; English.
                                                                                                                                                                                                                                                                                                                 Lal AA, Shi YP, Hasnain SE;
                                                                                                                                                                                                                 99WO-US18869.
                                                                                                                                                                                                                                                                        (NAIM-) NAT INST IMMUNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                              Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NANPNANPNANP 12
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Best Local Similarity
Watches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 AA;
                                                                                                                                                       WO200011179-A1.
                                                                                                                                                                                                               19-AUG-1999;
                                                                                                                                                                                                                                            21-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-SEP-2001
                                                                                                                                                                                   02-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB73753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hepatitis, tuberculosis). The activated T-cells can be used to treat the same conditions by adoptive T-cell transfer therapy.
                                                                                                                        Activated T helper cell; CD4+; cytotoxic T cell; CD8+; liposome; epitope; peripheral blood lymphocyte; antigen-presenting cell; APC; virus; tumour; bacterium; parasite; cytokine; vaccine; cancer; malaria; HIV; hepatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptides AAW67583-W67611 are used to produce activated T helper (CD4+) and cytotoxic (CD8+) T-cells. The activated T cells are produced by treating peripheral blood lymphocytes with liposome-enospaulated peptide antigen to generate Ag-loaded antigen-presenting cells (APC), contacting naive or anergic T-cells with these APC, and isolating the resulting partitionary one derived from a tumour, but also those from viruses, bacteria and other parasites. It can also be used to identify antigens and epitopes able to generate an Ag-specific T-cell response (by assessing proliferation and cytokine release). Also the Ag-loaded APC can be used as cellular vaccines for treating cancer (claimed) or other diseases (e.g. malaria, human immune deficiency virus infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Method of activation of T cells - by exposure to antigen-presenting cells loaded with antigen in liposome, used for, e.g. treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 12;
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                                                                                                                                                                                                                                                                                                                                                                                     Longenecker BM, Reddish MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum CSP antigenic epitope, P519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 69; DB 20;
100.0%; Pred. No. 0.00016;
ive 0; Mismatches 0;
                                                                                              Plasmodium falciparum T-cell activation peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 24; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY70280 standard; peptide; 12 AA.
           AAW67599 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer and microbial infections
                                                                                                                                                                                                                                                                                                  98WO-US09288.
                                                                  02-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUN-2000 (first entry)
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Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   Agrawal B, Krantz MJ,
                                                                                                                                                                                                             Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NANPNANPNANP 12
                                                                                                                                                                                                                                                                                                                                                         (BIOM-) BIOMIRA INC.
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-034715/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 AA;
                                                                                                                                                                                                                                          WO9850527-A1.
                                                                                                                                                                     tuberculosis
                                                                                                                                                                                                                                                                                                 07-MAY-1998;
                                                                                                                                                                                                                                                                                                                             08-MAY-1997;
                                                                                                                                                                                                                                                                     12-NOV-1998
                                                                                                                                                                                                 Synthetic.
                                         AAW67599;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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AAW67599
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The present sequence is the antigenic epitope P519, derived from circumsporozoite protein (CSP) of the sporozoite stage of Plasmodium falciparum. It is used in the construction of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melittin signal peptide, (His)6 tag, T-cell epitope from tetanus toxoid and 21 antigenic epitopes from circumsporozoite protein (CSP), sporozoite surface protein-2 (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apitcal membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of P. falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Circumsporozoite peptide antigen; malaria parasite; epitope; monoclonal antibody; affinity chromatography; DEAE-Sephadex A50 resin; diethylamine-ethyl group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum circumsporozoite peptide antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 69; DB 21; 100.0%; Pred. No. 0.00016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       falciparum in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB73753 standard; peptide; 12 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                              Use of an anion exchange resin (EPM-7) as solid support for peptide, e.g. angiotensin II, synthesis and affinity chromatography .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of MAL1, which is displayed on E2 core surface.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E2 core protein; 2-oxo acid dehydrogenase; multienzyme complex;
                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                       Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 69; DB 22;
100.0%; Pred. No. 0.00016;
ive 0; Mismatches 0;
                                                                                                                                                                         Rodrigues MM
                                                                                                                                                    (CNPQ-) CNPQ CONSELHO NACIONAL DESENVOLVIMENTO.
                                                   /note= "Optionally acetylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB84362 standard; peptide; 12 AA.
                                                                                                                                                                                                                                               Disclosure; Page 6; 17pp; English.
                                                                                                                                                                         Cilli EM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-DEC-2000; 2000WO-GB04720.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99GB-0029151
                                                                                                                20-DEC-2000; 2000WO-BR00160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                    99BR-0006091
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domingo GJ;
                                                                                                                                                                            Ianzer DA,
                Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NANPNANPNANP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-475830/51.
                                                                                                                                                                                                                                                                                                                                                               12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200142439-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine; MAL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified.
                                                                            WO200146216-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-DEC-1999;
                                     Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JUN-2001
                                                                                                                                     22-DEC-1999;
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                                                                                              28-JUN-2001
                                                                                                                                                                            Nakale CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB84362;
                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                   The specification describes a truncated E2 core protein of a 2-oxo acid dehydrogenase multienzyme complex, where the protein assembles into a core structure of the complex. The E2 core protein has an ability to display a variety of different numbers of peptides or polypeptides on single complex, and the ability to display a variety of different peptides or polypeptides on the same complex. The E2 core protein is useful in screening for peptides or polypeptides which bind target proteins of interest or bound by target antibodies, or which have other desirable properties, and for the elicitation of immune responses, e.g. for vaccination. It is also useful for obtaining and/or raising antibodies to the peptides or polypeptides, for evoking an immune response, and in pharmaceutical compositions. The present sequence response, and in pharmaceutical compositions the E2 core protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides a novel method of immunisation involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunization by administering ex vivo a transgene having a hematopoletic cell-specific expression element operationally linked to a polynucleotide encoding one or more heterologous epitopes to a
                      Novel truncated E2 core protein of 2-oxo acid dehydrogenase multienzyme complex, which assembles into a core structure of the complex, useful in screening for polypeptides which bind target proteins of interest -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Somatic transgene immunisation; immune response; haematopoietic cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 69; DB 22; 100.0%; Pred. No. 0.00016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunity; disease treatment; disease prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumour antigen MUC-1 epitope peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 8; Page 70; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB49997 standard; Peptide; 12 AA.
                                                                                                              Disclosure; Page 27; 53pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-024628/03
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WPI; 2001-381670/40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ZANE/) ZANETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200064488-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                  12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Peptide; retro; inverso; retro-inverso; therapy; disease; vaccine; immunogen; antibody; antibodies; assay; treatment; prophylaxis; Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                          New retro, inverso and retro-inverso peptide analogues - used as immunogens for the prodn. of antibodies and in diagnosis, therapy and prophylaxis of diseases
                                                                                                   Synthetic peptide analogue of P. falciparum used as immunogen.
                           AAR49980 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                           Example 6; Page 21; 87pp; English.
                                                                                                                                                                                                                                                                                                                           Fischer P, Tyler MI;
                                                                            (first entry)
                                                                                                                                                                                                                                                                                                   (DEAK-) DEAKIN RES LTD.
                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-100849/12
                                                                                                                                                                                                                                                  27-AUG-1993;
                                                                                                                                                                                                                                                                         27-AUG-1992;
                                                                            10-0CT-1994
                                                                                                                                                                                                 WO9405311-A.
                                                                                                                                                                                                                           17-MAR-1994.
                                                                                                                                                                           Synthetic.
                                                   AAR49980;
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                AAR49980
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the administration of a haematopoietic cell specific expression element to a lymphoid cell. The method is known as somatic transgene immunisation. It is particularly useful in the treatment and prevention of tunours, autoimmune disease, allergy, metabolic disorders, endocrine disorders, pain, blood disorders and dental disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The patentors claim a novel conjugate which comprises AAP60804 and a cartier protein. The conjugates are useful for providing protective immunity against malaria. The conjugates are effective in raising high titres of antibodies in vivo. These antibodies recognise sporozoites and neutralise sporozoite infectivity in vitro by a vigorous CSP reaction. The epitope of the P.falciparum CS protein is
                                                                                                                                        Gaps
                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conjugate of immunogenic peptide - having amino acid sequence corresp. to immuno-dominant epitope of P.falciparum circumsporozoite protein
                                                                                                              Length 12;
                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                          Sequence of an immunodominant epitope of P.falciparum
                                                                                                             ch 100.0%; Score 69; DB 22; Similarity 100.0%; Pred. No. 0.00016; 12; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                               AAP60804 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 18; Page 25; 37pp; English.
                                                                                                                                                                                                                                                                                                                                       circumsporozoite (CS) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                86WO-US00627.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85US-0716960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYNY-) NEW YORK UNIVERSITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zavala FP;
                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum.
                                                                                                                                                                          1 NANPNANPNANP 12
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                                                                                                              Query Match
Best Local Similarity
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                                                                          12 AA;
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93WO-AU00441. 92AU-0004374.

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Synthetic peptide antigen analogues of native peptide antigens which are either (1) retro modified, (2) inverso modified or (3) retro-inverso modified with respect to the native antigen can be used to raise antibodies which recognise the native antigen and hence can be used in the treatment and/or prophylaxis of diseases and therapy of disease states. They can be used in the production of vaccines and in assays for antibodies specific for the native antigen. They can have increased stability to degredation after administration and they can be administrated orally. This sequence is based on the immunodominant epitope of the circumsporozoite coat protein of plasmodium falciparum. The retro-inverso version of this peptide
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Pred. No. 0.00018;
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Job time: 417 sec
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Best Local Similarity
Matches 12; Conserv
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ch 100.0%; Score 69; DB 7; Length 13; 1 Similarity 100.0%; Pred. No. 0.00018; 12; Conservative 0; Mismatches 0; Indels

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Best Local Similarity Matches 12; Conserv

Query Match

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Sequence 4, Appli
Sequence 3, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 35, Appl
Sequence 35, Appl
Sequence 15, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 14, Appli
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Sequence 6, Appli
Sequence 6, Appli
Sequence 8, Appli
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Sequence 4, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 10, Appl
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                                                   Search time 133.18 Seconds
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Compugen Ltd
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US-08-909-551-4
US-08-909-551-3
US-07-987-286-8
US-08-614-626-8
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US-08-614-626-8
US-08-614-626-8
US-08-614-626-8
US-08-614-35
US-08-614-35
US-08-143-3654-13
US-08-143-3654-13
US-08-143-3654-14
US-08-135-14
US-08-135-14
US-08-133-08435-1
US-08-133-08435-1
US-08-133-08435-1
US-08-932-9298-1
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                                                                                                                                                              Total number of hits satisfying chosen parameters:
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GenCore version Copyright (c) 1993 - 2000
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                                                                                                      1 NANPNANPNANP 12
                                                                             US-09-763-397A-4
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Sequence 105, Application US/09248588

Fatent No. 6231864

GENERAL INFORMATION:
APPLICANT: Birkett, Ashley J.
TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and TITLE OF INVENTION: Their Derivatives
FITLE OF INVENTION: Their Derivatives
FITLE REFERENCE: SYN-101 456469529
CURRENT APPLICATION NUMBER: 05/09/248,588

CURRENT FILING DATE: 1999-02-11

EARLIER PAPLICATION NUMBER: 60/074537

EARLIER PILING DATE: 1998-02-12

NUMBER OF SEQ ID NOS: 113

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 105

LENGTH: 12
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Sequence 4, Application US/08909551
Sequence 5.261569
GENERAL INFORMATION:
APPLICANT: COMIS, ALFIO
APPLICANT: FISCHER, PETER
APPLICANT: TYLER, MARGARET I
TITLE OF INVENTION: Retro-, Inverso-
TITLE OF INVENTION: Squthetic Peptide Analogues
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 69; DB 4; Ler
Pred. No. 8.3e-05;
                                        US-08-318-856A-13
US-08-94-818B-1
US-08-94-818B-5
US-08-570-311-8
US-08-33-485-8
US-08-336-308A-10
US-08-336-311-27
US-08-82-324-6
US-08-870-311-10
US-08-570-311-10
US-08-570-311-14
US-08-770-311-14
US-08-770-311-14
US-08-747-137-40
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nilarity 100.0%;
Conservative 0;
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PAGES: 1436-1440
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  TYPE: PRT
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LOCATION: 1..2
COTHER INFORMATION: /label= A
OTHER INFORMATION: /note= "RESIDUE 1 IS AN EXTRA CYSTEINE
OTHER INFORMATION: FESTIDUE ADDED TO THE N-TERMINUS OF THE
OTHER INFORMATION: PEPTIDE"
DUBLICATION: PEPTIDE"
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                                                                                                                     CUMPUTER KENDABLE FORM:
WEDULM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENTIN RELEASE #1.0, Vers. #1.25
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/909,551
FILING DATE: 12-AUG-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/AU93/0041
FILING DATE: 27-FEB-1995
APPLICATION NUMBER: PCT/AU93/0041
FILING DATE: 27-FEB-1995
APPLICATION NUMBER: AN 4374
FILING DATE: 27-AUG-1993
APPLICATION NUMBER: AN 4374
FILING DATE: 37-AUG-1993
APPLICATION NUMBER: AN 4374
FILING DATE: 37-AUG-1993
APPLICATION NUMBER: AN 4374
FILING DATE: 37-AUG-1993
APPLICATION NUMBER: BASSIERATION NUMBER: BASSIERATION NUMBER: BASSIERATION NUMBER: GHCZUSA
MAME: BAS MATY E.
REFERENCE/DOCKET NUMBER: GHCZUSA
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US-07-987-286-8

US-07-987-286

Sequence 8, Application 07/987286

Patent No. 550036

Patent No. 1FORMATION:
GENERAL INFORMATION:
APPLICANT: GECZY, ANDREW F

TITLE OF INVENTION:
TITLE OF INVENTION:
UMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
                Pennsylvania
United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Plasmodium falciparum
DEVELOPMENTAL STAGE: SPOROZOITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
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TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO FRAGMENT TYPE: 1 ORIGINAL SOURCE:
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US-08-909-551-3
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APPLICANT: FISCHER, PETER
APPLICANT: TYLER, MARGAET I VETER
TITLE OF INVENTION: Synthetic Peptide Analogues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., P.O. Box 457
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cutr., P.O. Box 457
                                                                                                                                                                                                                                       CUMPUTER KEADABLE FORM;
MEDULM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: Patentin Release #1.0, Vers. #1.25
SOFTWARE: Patentin Release #1.0, Vers. #1.25
CURRENT APPLICATION DATA:
FILING DATE: 12-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/387,932
FILING DATE: 27-FEB-1995
APPLICATION NUMBER: PCT/AU93/00441
FILING DATE: 27-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU 4374
FILING DATE: 27-AUG-1993
ATTORNEY/AGENT INVORMATION:
AMANE: OAK AMANE: DATA:
AMANE: OAK AMANE: DATA: DATA: AMANE: DATA: DATA: DATA: AMANE: DATA: D
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100.0%; Pred. No. 8.3e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            URGANISM: Plasmodium falciparum
PUBLICATION INFORMATION:
DOCUMENT NUMBER: AU PL4374
FILING DATE: 27-AUG-1992
US-08-909-551-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFRENCE/POCKEY NUMBER: GHC2USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-5818
                                                                                                                               STATE: Pennsylvania
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 %3-08-909-551-3
; Sequence 3, Application US/08909551
; Patent No. 651569
; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NANPNANPNANP 12
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                                                                                                    Spring House
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N
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Sequence 35, Application US/08455625
Patent No. 593218
GENERAL INFORMATION:
APPLICANT: Berzofsky, Jay A.
APPLICANT: Ahlers, Jeffrey D.
APPLICANT: Anners, Peter
APPLICANT: Anners, Peter
TITLE OF INVENTION: COMPOSITE SYMTHETIC PEPTIDE CONSTRUCT
TITLE OF INVENTION: COMPOSITE SYMTHETIC PEPTIDE CONSTRUCT
TITLE OF INVENTION: LYMPHOCYTES AGAINST HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
5219987-4
;Patent No. 5219987
; APPLICANT: VERDINI, ANTONIO S.;PESSI, ANTONELLO;BONELLI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 69; DB 2; I 100.0%; Pred. No. 0.00012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 69; DB 6; 100.0%; Pred. No. 0.00017;
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ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
                             FILING DATE: 17-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 40 PK2361
FILING DATE: 18-SEP-1990
ATTORNEY/ACENT INFORMATION:
NAME: BENY. STEPHEN A.
RECISTRATION NUMBER: 29,768
RECISTRATION NUMBER: 29,768
TELEPHONE: 202 672 5300
TELEPHONE: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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        JMBER: PCT/AU91/00429
17-SEP-1991
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NUMBER OF SEQUENCES: 7

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/227,364

FILING DATE: 02-AUG-1988
                                                                                                                                                                                                                                  TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.(
Best Local Similarity 100.(
Matches 12; Conservative
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Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NANPNANPNANP 12
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                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA

COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/614,626
                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 07/987,286
FILING DATE: 16-MAR-1993
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                     PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU91/00429
FILING DATE: 17-5EP-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: AU PK2361
FILING DATE: 18-5EP-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENTY, STEPHEN A
REGISTRATION NUMBER: 29,768
REFERENCE/FOCKET NUMBER: 16786/175/CHAC
TELECOMMUNICATION INFORMATION:
TELEFONE: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/08614626
Patent No. 5928644
GENERAL INFORMATION:
APPLICANT: RUSSELL-JONES, GREGORY J
APPLICANT: GECZY, ANDREW F
TITLE OF INVENTION: T-CELL EPITOPES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K STREET, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/987,286
FILING DATE: 16-MAR-1993
ADDRESSEE: FOLGY & CORRECT, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: FOLEY & LAF
STREET: 3000 K STREET,
CITY: WASHINTON, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                WASHINTON, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-07-987-286-8
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HELPER T-LYMPHOCYTE, CYTOTOXIC T LYMPHOCYTE AND NEUTRALIZING ANTIBODY RESPONSES AGAINST HIV-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 69; DB 4; Length 66 100.0%; Pred. No. 0.00052; Live 0; Mismatches 0; Indels
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THAT ELICIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/060,988A
FILING DATE: 14-MAY-1993
                                                                                                                                                                                                                                                                                                                                                      08830/022003
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,685
FILING DATE: 31-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/060,988
FILING DATE: 14-MAY-1993
APPLICATION NUMBER: 07/847,311
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/751,998
FILING DATE: 29-AUG-1991
APPLICATION NUMBER: 07/148,692
FILING DATE: 26-JAN-1988
ATTORNEY/AGENT INFORMATION:
NAME: Beattie, Ingrid A.
RECISTRATION NUMBER: P-42,306
RECISTRATION NUMBER: P-42,306
RECISTRATION NUMBER: 08030/0221
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 617/542-8906
TELEFAX: 200154
TIELERX: 200154
TIELERX: 200156:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 35, Application US/08060988A
Fatent No. 6294322
GENERAL INFORMATION:
APPLICANT: Berzofsky, Jay A.
APPLICANT: Pendleton, C. David
APPLICANT: Pendleton, C. David
APPLICANT: Paral Mura, Peter
APPLICANT: Shirai, Mutsunori
TITLE OF INVENTION: MULTIDETERMINANT
TITLE OF INVENTION: HAT ELICIT
TITLE OF INVENTION: HELPER T-IXPHPHOC:
TITLE OF INVENTION: NEUTRALIZING ANT:
HUMBER OF SEQUENCES: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLACEALTY
FILING DATE: 14-Mai APPLACEATION DATE: 07/847,311
APPLICATION NUMBER: 07/847,311
APPLICATION NUMBER: 06-MAR-1992
APPLACEATION NUMBER: 07/751,998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/751,998
FILING DATE: 29-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: peptide US-08-455-685-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NANPNANPNANP 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-060-988A-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
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APPLICANT: Shira, Peter
APPLICANT: Shira, Mutsunori
TITLE OF INVENTION: MULTIDETERMINANT PEPTIDES THAT ELICIT
TITLE OF INVENTION: HELPER T-LYMPHOCYTE, CYTOTOXIC T LYMPHOCYTE AND
TITLE OF INVENTION: NEUTRALIZING ANTIBODY RESPONSES AGAINST HIV-1
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1..66; Jabel= peptide; OTHER INFORMATION: /note= "peptide from P. falciparum CS antigen" US-08-455-625-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Score 69; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 0.00052;
Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                       COMPUTER: INPY CLASS AND COMPUTER: INPY CANDALLINE
COMPUTER: INPY COMPATINE
COMPUTER: PATENTINE RC-DOS/MS-DOS
SOFTWARE: PATENTIN RALEASE #1.0, Version #1.25
CURRING APPLICATION DATA:
APPLICATION NUMBER: US/08/455,625
CLASSIFTCATION: 435
PRIOR APPLICATION ADATA:
APPLICATION NUMBER: US 08/060,988
FILING DATE: 14-MAY-1993
ATTONNEY AGENT INFORMATION:
ATTONNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 35, Application US/08455685 Patent No. 6214347 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BETZOFSKY, Jay A. APPLICANT: Ahlers, Jeffrey D. APPLICANT: Pendleton, C. David
                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30330
REFERENCE/DOCKET NUMBER: 1173
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8050
TELEFAX: 703-205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 35: SEQUENCE CHARACTERISTICS:
                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH: 66 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clr.
STATE: MACCOUNTRY: US
COUNTRY: US
79. 02110-2804
                        Falls Church
Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1111111111
22 NANPNANPNANP 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                         COUNTRY:
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Gaps
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/label= peptide
/note= "peptide from P. falciparum CS antigen"
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                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: LOWell, George H
TITLE OF INVENTION: IMMUNO-POTENTIATING SYSTEMS FOR
TITLE OF INVENTION: DEPERATION OF IMMUNOGENIC MATERIALS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street
                                                                                    Length 66
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                                                                                                                    0; Indels
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100.0%; Pred. No. 0.00052;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                       Sequence 13, Application US/08143365A Patent No. 5726292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 12; Conservative 0;
                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
; OTHER INFORMATION:
; OTHER INFORMATION:
PCT-US94-05142-35
                                                                                                                                                        1 NANPNANPNANP 12
                                                                                                                                                                        11111111111
22 NANPNANPNANP 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fairfax
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STATE: VA
COUNTRY: US
ZIP: 22031
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US-08-143-365A-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: COMPOSITE SYNTHETIC PEPTIDE CONSTRUCT
TITLE OF INVENTION: ELICITING NEUTRALIZING ANTIBODIES AND CYTOTOXIC T
TITLE OF INVENTION: LYMPHOCYTES AGAINST HIV
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIrch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CONTRY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Relasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05142
FILING DATE: 13:MAX-1994
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                                                                                                                                                                                                                                                                                                                             100.0%; Score 69; DB 4; Length 66; 100.0%; Pred. No. 0.00052; Vative 0; Mismatches 0; Indels
              FILING DATE: 26-JAN-1988
ATTORNEY/AGENT INFORMATION:
NAME: Beatlie, Ingrid A.
REGISTRATION NUMBER: P-42,306
REFERENCE/DOCKET NUMBER: 08830/022001
TELECHOMUNICATION INFORMATION:
TELEFOHONE: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Svensson, Leonard R.
RECISTRATION NUMBER: 30330
REFERCE/DOCKET NUMBER: 1173-434P
TELECOMMUNICATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/060,988
FILING DATE: 14-WAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US94-05142-35; Sequence 35, Application PC/TUS9405142
GENERAL INFORMATION:
APPLICANT:
 07/148,692
                                                                                                                                 TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
TYPE: amino acids
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INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
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amino acid
GY: linear
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                     ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-060-988A-35
 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                 1 NANPNANPNANP 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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; Pred. No. 0.001;
0; Mismatches 0; Indels
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APPLICANT: Ding, Zhi-Ming
TITLE OF INVENTION: Targeted Nucleic Acid Delivery into
TITLE OF INVENTION: Liver Cells
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WEDION TYPE: El-DPPy disk COMPUTER: El-DPPy disk COMPUTER: El-DPPy disk COMPUTER: El-DPPy disk COMPUTER: EBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/021,625D FILING DATE: 16-FEB-1993 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Highlander, Steven L. REGISTRATION NUMBER: 37,642 REFERENCE/DOCKET NUMBER: UTSC:410/HYL TELECOMMUNICATION: NORMATION:
SYSTEM: PC-DOS/MS-DÖS
PatentIn Release #1.0, Version #1.30
                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSC:410/HYL
TELECOMMUNICATION INFORMATION:
                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/395,602A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08021625D Patent No. 5976851
GENERAL INFORMATION:
                                                                                                                                                                                                                         TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (512) 418-3000
(713) 789-2679
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
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Best Local Similarity 100.
Matches 12; Conservative
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MEDIUM TYPE: Floppy
                                                                                 FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
US-08-021-625D-4
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TOPOLOGY:
US-08-395-602A-4
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                                                                                                         Process for Producing Hydrophobic Polypeptides and Proteins, and Fusion Proteins for Use in Producing Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kuo, M. Tien
APPLICANT: Ding, Zhi-Ming
TITLE OF INVENTION: Targeted Nucleic Acid Delivery into
TITLE OF INVENTION: Liver Cells
NUMBER OF SQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold, White & Durkee
STREET: PO. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,348A
FILING DATE: 29-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: EP 93110755.1 FILING DATE: 06-JUL-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Parise, John P. REGISTRATION NUMBER: 34,403
REFERENCE/DOCKET NUMBER: 4105/157
                                                                                                                                                                                                                   Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08395602A
Patent No. 5766899
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
        APPLICANT: Dobeli, Heinz
APPLICANT: Draeger, Nicholas
APPLICANT: Trottman, Gerda H
APPLICANT: Jakob, Peter
APPLICANT: Stuber, Dietrich
TITLE OF INVENTION: Process for
TITLE OF INVENTION: Prolypeptid
TITLE OF INVENTION: Producing shumber of SEQUENCES: 12
                                                                                                                                                                                                               ADDRESSEE: HOIIMann --- careet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (201) 235-6326
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                             STREE1.
CITY: Nutley
STATE: New Jersey
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US-08-395-602A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: F
STATE:
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Gaps

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RESULT 15

US-08-268-348A-8

| Sequence 8, Application US/08268348A
| Sequence 9, Application 9, Application 9, Applicant 9, Applicant Draeger, Nicholas Applicant Draeger, Nicholas Applicant Trotumen, Gerda H
| Applicant 3tobel, Peter 9
| Applicant 3tobel, Peter 9
| Applicant 3tobel, Peter 9
| TITLE 0F INVENTION: Process for Producing Hydrophobic 7 TITLE 0F INVENTION: Polypeptides and Proteins, and Fusion Proteins for Use in TITLE 0F INVENTION: Producing Same NUMBER 0F SEQUENCES: 12
| CORRESPONDENCE ADDRESS: ADDRESSE: Hoffmann-La Roche Inc. | CITY: Nutley | STATE: New Jersey | CONNEY 10.5.A. | COMPUTPE | CITY: U.S.A. | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Query Match 100.0%; Score 69; DB 2; Length 126; Best Local Similarity 100.0%; Pred. No. 0.001; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAPPTER TRADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATION
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,348A
FLING DATE: 09-JUN-1994
FLING APPLICATION NUMBER: EP 93110755.1
FILING DATE: 06-JUL-1993
ATYONREY/AGENT INFORMATION:
NAME: PALISE: JOHN P:
REGISTRATION NUMBER: 34,403
REFRENCE/DOCKET NUMBER: 34,403
REFRENCE/COCKET NUMBER: 34,403
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELECOMMUNICATION ON 8:
SEQUIBORE CIRRAACTERISTICS:
LENGTH: 133 amino acids
TOPPLICATION acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: January 29, 2002, 10:24:02
Job time: 508 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-268-348A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NANPNANPNANP 12
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C;Accession: A39756 R;Lal, A.A.; Goldman, I.F. J. Biol. Chem. 266, 6686-6689, 1991 A;Title: Circumsporozoite protein gene from Plasmodium A;Reference number: A39756; MUID:91201303 A;Accession: A39756 망 QY A;Cross-references: GB:M60972; NID:g160228; PIDN:AAA29561.1; PID:g160229 C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat howers;312-366/Domain: thrombospondin type 1 repeat homology <THR1> C;Species: Plasmodium reichenowi C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 20-Aug-1999 RESULT A39756 A; Molecule type: DNA A; Residues: 1-388 <LAL> A; Status: preliminary circumsporozoite protein - Plasmodium reichenowi Matches Query Match 196 Local l Similarity 12; Conserva Conservative 207 100.0%; 0 Score 69; DB 2; Pred. No. 0.002; Mismatches ? 0; Length 388, Indels reichenowi, a repeat homology 0 Gaps chimpanzee malar 0

R:Caspers, P.; Gentz, R.; Matile, H.; Pink, J.R.; Sinigaglia, F. Mol. Biochem. Parasitol. 35, 185-190, 1989
A;Title: The circumsporozoite protein gene from NF54, a Plasmodium A;Reference number: A45527; MUID:8936498
A;Accession: A45527

falciparum isolate

A; Molecule type: DNA A; Residues: 1-405 <CAS>

A; Status: preliminary

A;Cross-references: GB:M22982; GB:J04650; NID:g160168; PIDN:AAA29527.1; PID:g160169

Nucleic Acids Res. 17, 5854, 1989
A; Title: DNA sequence of the gene encoding A; Reference number: S05428; MUID:89345189
A; Accession: S05428

D

Plasmodium falciparum malaria candidate

A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-405 <CAM>
A;Cross-references: EMBL:X15363
A;Cross-references: EMBL:X15363

circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate NF54) C;Species: Plasmodium falciparum C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jun-2000 C;Accession: S05428; A45527; I60657 R;Campbell, J.R.

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C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Date: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jun-2000
C;Accession: A03388
R;Dame, J.B.; Williams, J.L.; McCutchan, T.F.; Weber, J.L.; Wirtz, R.A.; Hochmeyer, W.T.
Science 225, 593-599, 1984
A;Fitle: Structure of the gene encoding the immunodominant surface antigen on the sporoz A;Reference number: A03388
A;Hocession: A03388
A;Accession: A03388
A;Molecule type: DNA
A;Residues: 1-412 <DAM>
A;Residues: 1-412 <DAM>
A;Residues: 1-412 <DAM>
A;Cross-references: GB:K02194; NID:g160160; PIDN:AAA29524.1; PID:g160161
A;Experimental source: clone 7G8
C;Comment: There are 41 copies of a 4-residue repeating unit in the middle domain of the C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
F;336-390/Domain: thrombospondin type 1 repeat homology <THRI>
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Mol. Biochem. Parasitol. 37, 275-280, 1989
A;Title: Wild isolates of Plasmodium falciparum show extensive polymorphism in A;Reference number: A60657; MUID:90114334
A;Accession: I60657
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A; Residues: 319-336,354-373 < LOC>
A; Residues: 319-336,354-373 < LOC>
C; Superfamily: circumsporozoite protein; thrombospondin
F; 329-383/Domain: thrombospondin type 1 repeat homology
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                                                                                                                                                                                                                                                                                                                    circumsporozoite protein - malaria parasite (Plasmodium falciparum) (Strain T4, C;Species: Plasmodium falciparum C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000 C;Accession: A54533
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                                                                                                   A;Cross-references: GB:M19752; NID:g160216; PIDN:AAA29555.1; PID:g160217 C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat how F;348-402/Domain: thrombospondin type 1 repeat homology <THRI>
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Mol. Biochem. Parasitol. 24, 289-294, 198
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A; Residues: 1-442 <L
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                  3.4.22.37) precursor
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R;Theologis, A; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Talloker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: A86322
A;Accession: A86322
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Mol. Biochem. Parasitol. 22, 101-108, 1987
A;Title: Strain variation in the circumsporozoite protein gene of A;Reference number: A54529; MUID:87115616
A;Accession: A54529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; not compared with conceptual translation
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                                                                                                                                                                                                                                                                                  A; Cross-references: GB: AE005172; NID: g6730703; PIDN: AAF27098.1;
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A; Residues: 1-387 <STO>
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R;de la Cruz, V.F.; Lal, A.A.; McCutchan, T.F.
J. Biol. Chem. 262, 11935-11939, 1987
A;Title: Sequence variation in putative functional domai A;Reference number: A92609; MUID:87308186
A;Accession: B29795
A;Molecule type: DNA
A;Residues: 1-161 <DEL>
A;Cross-references: GB:M17802; GB:M17803; GB:M17806
A;Title: W11d isolates of Plasmodium falciparum show ext
A;Reference number: A60657; MUID:90114334
A;Accession: A60657
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C;Date: 05-Mar-
C;Accession: S4
R;Aduse-Opoku,
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                                                                                                                                                                                                                                                             circumsporozoite protein - malaria parasite (Plasmo C; Species: Plasmodium falciparum C; Date: 18-Oct-1989 #sequence_revision 21-Jul-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-171 <DELA>
C; Superfamily: circumsporozoite
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R;de la Cruz, V.F.; Lal, A.A.; McCutchan,
J. Biol. Chem. 262, 11935-11939, 1987
A;Title: Sequence variation in putative fi
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R; de la Cruz, V.F.; Lal, A.
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C;Keywords:
                           A; Status: preliminary; not compared
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A; Residues: 1-1526 <ADU>
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                A; Molecule
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C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999
C;Accession: T13065
                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1528 <STO>
                                                                                                                                                                                                                                                                                                                                                hypothetical protein ypjA [imported] - Escherichia coli (strain 0157:H7) C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                    A; Reference number: A; Accession: D85912
                                                                                                                                                                                                                                                                  R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                             C; Accession: D85912
R; Perna, N.T.; Plun
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A; Residues: 1-1171 <SUR>
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Neuron 21, 225-234,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
                                                                                                                             A;Cross-references: GB:AE005174; NID:g12517083; PIDN:AAG57760.1; GSPDB:GN00145; UWGP:A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                       A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7 A; Reference number: A85480; MUID:21074935; PMID:11206551
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8; Conserv
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8; Conser
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9; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.5%;
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Pred.
                  Score 49;
Pred. No.
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K.; Apoda
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1196

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A; Residues: 1-1732 <BAR>
A; Cross references: EMBL:U42210; NID:g1314325; PID:g1314326; R; Slakeski, N.; Cleal, S.M.; Reynolds, E.C. submitted to the EMBL Data Library, October 1996 A; Reference number: Z20896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 17-Nov-2000 C;Accession: T30836; T30837; T30526; A53113 R;Barkocy-Gallagher, G.A.; Han, N.; Patti, J.M.; Whitlock, J.; Progulske-Fox, J. Bacteriol. 178, 2734-2741, 1996 A;Title: Analysis of the prtP gene encoding porphypain, a cysteine proteinase A;Reference number: Z20895; MOID:96213011 A;Accession: T30836
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C; Keywor
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A; Residues: I-1704 <PAV>
A; Residues: I-1704 <PAV>
A; Cross references: GB:U15282; NID:g557067; PIDN:AAA69539.1; PID:g557068
A; Cross references: GB:U15282; NID:g557067; PIDN:AAA69539.1; PID:g557068
A; Pike, R.; McGraw, W.; Potempa, J.; Travis, J.
J. Biol. Chem. 269, 406-411, 1994
A; Title: Lysine- and arginine-specific proteinases from Porphyromonas gi
A; Reference number: A53113; MUID:94103245
A; Accession: D53113
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A;Title: Molecular cloning and structural characterization of the Arg-gingipain proteina A;Reference number: A55426; MUID:95138080
A;Accession: A55426
                                                                        A:Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1350,'N',1352-1363,'Y',1365-1447,'H',1449-1732 <I
A;Cross-references: EMBL:AF017059; NID:g2738802; PID:g2738803;
R;Pike, R.; McGraw, W.; Potempa, J.; Travis, J.
                                                                                                                                                                                                                               A;Title: IS195, an insertion sequence-like element associated with protease A;Reference number: Z20844; MUID:98298016 A;Accession: T30526
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-795,'1',797-1389,'N',1391-1478,'Y',1480-1732 <SLA>
A;Cross-references: EMBL:U75366; NID:g2182811; PID:g2182812; PIDN:AAB60809.1
R;Lewis, J.P.; Macrina, F.L.
Infect. Immun. 66, 3035-3042, 1998
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A; Residues: 228-249 < PIK>
                        R;Pike, R.; McGraw, W.; Potempa, J. Biol. Chem. 269, 406-411, 1994
A;Title: Lysine- and arginine-spe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: T30837
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A; Residues: 1-1732 <
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N;Alternate names: lysine-specific cysteine proteinase 1, 60K
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number:
and arginine-specific proteinases er: A53113; MUID:94103245
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3; PIDN:AAC26523
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues; 1-2628 <HANN
A;Cross-references: EMBL:U41807; NID:g1552410; PID:
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C;Species: Porphyromonas gingivalis
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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T28651
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C;Keywords: cysteine
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A;Molecule type: protein
A;Residues: 229-249 <PIK>
                                                                          C; Superfami.
C; Keywords:
                                                                                                                                                                                                                                                                                                                               transcription factor Vpl - common ice plant
C;Species: Mesembryanthemum crystallinum (common ice plant)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_ch
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                                                                                                                                                 A; Cross-references: EMBL: AB015183
                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-790 <FUK>
                                                                                                                                                                                                                                         A;Description: Expression of Vp1
A;Reference number: Z17452
                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, June 1998
                                                                                                                                                                                                                                                                                              C; Accession: T12203
R; Fukuhara, T.; Bohnert, H.J.
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Best Local S
                                                                                         Superfamily: rice transcription factor VP1
                                                                                                                                Genetics:
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Query Match
Best Local Similarity
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                                                                        DNA binding; transcription regulation
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66.7%;
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72.78;
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Search completed: January 29, 2002, 10:26:35
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55.1 423 1 YHJ3_YEAST 55.1 431 1 PGD1_YEAST 55.1 448 1 AAC2_DICD1 55.1 510 1 GAT1_YEAST 55.1 1297 1 PUR4_VIBCH 55.1 1297 1 PUR4_VIBCH 53.6 191 1 LEP_STAAU 53.6 198 1 SECG_HELPJ 53.6 199 1 SECG_HELPJ 53.6 199 1 SECG_HELPJ 53.6 241 1 HFB1_HAEIN	ALIGNMENTS	PLAFL CSP_PLAFL CSP_PLAFL CSP_PLAFL CSP_PLAFL CSP_PLAFL O1-NOV-1988 (Rel. 09, Created) O1-NOV-1988 (Rel. 09, Last sequence update) O1-NOV-1988 (Rel. 28, Last annotation update) CIRCUMSPOROZOITE PROTEIN (CS) (FRGMENT). Plasmodium falciparum (isolate le5). Eukaryota; Alveolata; Apicomplexa; Haemosporida;	SEQUENCE FROM N.A. MEDLINE-87308186; PubMed-2442154; MEDLINE-87308186; PubMed-2442154; la Cruz V.F., Lal A.A., McCutchan T.F.; "Sequence variation in putative functional domains of the circumsporozoite protein of Plasmodium falciparum. Implications for vaccine development."; J. Biol. Chem. 262:11935-11939(1987). -!- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE MALARTA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE VETTERRATE HOST). -!- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	EMBL; M17802; AAA29538.1; Malaria; Sporozoite; Repeat. NON_TER 1 1 40 X 4 AA TANDEM REPEATS NON_TER 315 315 NON_TER 315 A3, 33649 WW; A334DB11FA7FD777 CRC64 SEQUENCE 315 AA; 33649 WW; A334DB11FA7FD777 CRC64 TY MATCh 100.0%; Score 69; DB 1; Lengt t Local Similarity 100.0%; Pred. No. 0.0013; t Local Similarity 100.0%; Pred. No. 0.0013;	12	STANDARD; PRT; 388 AA.
34 35 36 36 37 38 39 39 40 41 42 44 44 37 45 37		ESULT 1 CSP_PLAFL LD CSP_PLAFL STANDARD AC P05601, DT 01-NOV-1988 (Rel. 09, C. 01-NOV-1988 (Rel. 09, L. 01-NOV-1988 (Rel. 28, L. 05) DT 01-FEB-1994 (Rel. 28, L. 05) C EUKATYOTA; Alveolata; Al	L LI LLD MEDLINE-873 La Cruz V.F. "Sequence v. circumsporo vaccine dev. J. Biol. Ch. -!- FUNCTIO -!- FUNCTIO SURFACE MALARIA VERTEBR. -!- MISCELL. ANCHORI	This SWISS- between th the Europea use by no modified an entities re	EMBL; M1780 Malaria; Sp MON_TER DOMALN NON_TER SEQUENCE SEQUENCE Query Match Best Local Sim	8 – 8 - 8	RESULT 2 CSP_PLARE ID CSP_PLARE AC P26694;
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Nucleic Acids Res. 17:5854-5854(1989).
                                                                                                                                                                                      MEDLINE=91201303; PubMed=2016283;
MEDLINE=91201303; PubMed=2016283;
Lal A.A., Goldman I.F.;
"Circumsporozoite protein gene from Plasmodium reichenowi, a chimpanzee malaria parasite evolutionarily related to the human malaria parasite Plasmodium falciparum.";
J. Biol. Chem. 266:6686-66801991).
-;- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
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Malaria; Sporozoite; Repeat; Signal.
SIGNAL 17 388 CIRCUMSPOROZOITE PROTEIN.
CHAIN 120 267 62 X 4 AA TANDEM REPEATS OF N-A-N-P.
COMAIN 120 267 W; C031EEFBEZE35604 CRC64;
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P19597: Q25798;
01-FEB-1991 (Rel. 39, Last sequence update)
20-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CIRCUMSPORSOZITE PROTEIN PRECURSOR (CS).
Plasmodium falciparum (isolate NF54).
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                               Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5854;
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         01-AVG-1992 (Rel. 23, Created)
01-AVG-1992 (Rel. 23, Last sequence update)
01-AVG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A39756; A39756.
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
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PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
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Matches 12; Conservative
                                                                                                     Plasmodium reichenowi.
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                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-89364998; Pubmed=2671723;
MEDLINE-89364998; Pubmed=2671723;
MEDLINE-89364998; Pubmed=2671723;
Caspers P., Gentz R., Matile H., Pink J.R., Sinigaglia F.;
Caspers P., Gentz R., Matile H., Pink J.R., Sinigaglia F.;
Caspers P., Gentz R., Matile H., Pink J.R., a Plasmodium falciparum isolate used in malaria vaccine trials.";
Mol. Biochem. Parasitol. 35:185-190(1989).
-!- FUNCTION: THE CIRCUMSPORZOITE PROPEIN IS THE IMMUNODMINANT
SURFACE ANTIGEN ON THE SPORZOITE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
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-!- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
-!- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
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43 X 4 AA TANDEM REPEATS OF N-A-N-P.
A -> ANPNANNA (IN REF. 4).
9E81146F59EBCEA3 CRC64;
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                                                              [3]
SEQUENCE FROM N.A.
MEDLINE-92155298; PubMed-1346766;
Davis J.R., Cortese J.F., Herrington D.A., Murphy J.R., Clyde D
Thomas A.W., Baqar S., Cochran M.A., Thanassi J., Levine M.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 69; DB 1; Length 397; 100.0%; Pred. No. 0.0016;
                                                                                                                                                                                                                               Hackett C.S.; "plasmodium falciparum: in vitro characterization and human "plasmodium falciparum: in contrivity of a cloned line."; Exp. Parasitol. 74:159-168(1992).
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Campbell J.R.; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
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21-JUL-1986 (Rel. 01, Last sequence update)
20-AUG-2001 (Rel. 06, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    412 AA
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SIGNAL 1 16 PROBABLE.
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InterPro; IPR003067; Cromsprzoite.
InterPro; IPR000884; TSP1.
Pfam; PF00090; tSP1.
SMRTNTS; PR01303; CROMSPRZOITE.
SMART; SM00209; TSP1, 1.
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EMBL; M83886; AAA29521.1; --
EMBL; M22982; AAA29527.1; --
PIR; S05428; S05428.
PIR; A45527; A45527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NANPNANPNANP 12
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THE REPEAT SEQUENCES

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MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A54529; A54529
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CSP_PLAFW
P08307;
                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                       CSP_PLAFW
                                                                                                                                                                                                                                                                                                                                                                     ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                        InterPro; i..

InterPro; i..

R Pfam; PF00090; tsp_1; 1.

R PRINT; PR01303; CRCMSPRZOITE.

DR SMART; SM01303; CRCMSPRZOITE.

DR SMART; SM0209; TSP1; 1.

KW Malaria; Sporozoite; Repeat; Signal.

T 412 CIRCUMSPOROZOITE PROTEIN.

SIGNAL 17 412 CIRCUMSPOROZOITE PROTEIN.

17 412 CIRCUMSPOROZOITE PROTEIN.

A12 CIRCUMSPOROZOITE PROTEIN.

A12 CIRCUMSPOROZOITE PROTEIN.

A12 CIRCUMSPOROZOITE PROTEIN.

TA AA TANDEM REPEATS OF P-N-A-N.

AM; IEEEED3DE90965F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                        MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR MACHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURRACE ANTIGEN OF THE ORGANISM.
SIMILARITY: CONTAINS I TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOI. Biochem. Parasitoí. 24:289-294(1987).
-1- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT
SURFAC ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
VERTEBRATE HOST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           del Portillo H.A., Nussenzweig R.S., Enea V.;
"Circumsporozoite gene of a Plasmodium falciparum strain from Thailand.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum (isolate t4 / Thailand).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 69; DB 1; Length 412; 100.0%; Pred. No. 0.0017; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                424 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                         PIR; A03388; OZZQAF.
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-87315205; Pubmed-3306373;
del Portillo H.A., Nussenzweig R.
                                                                                                                                                                                                                                                                                                                                EMBL; K02194; AAA29524.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 NANPNANPNANP 159
                                                                                                                                                                VERTEBRATE HOST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NANPNANPNANP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 12; Conserv
           NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=5846;
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P13814;
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CSP_PLAFT
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                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a alloense agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-87115616; PubMed-3543671;
LOCKyer M.J., Schwarz R.T.;
"Strain variation in the circumsporozoite protein gene of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CIRCUMSPOROZOITE PROTEIN.
45 X 4 AA TANDEM REPEATS OF N-A-N-P.
710AB14238786CD9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 401. Blochem. Parasitol. 22:101-108(1987).
-!-FUNCTION: THE CIRCUMSPORZOTTE PROTEIN IS THE IMMUNODOMINANT
SUREACE ANTIGEN ON THE SPORZOTTE (THE INFECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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NCBL_TaxID=5848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
ANCHORING THE PROTEIN TO THE CELL MEMBRANE. TH WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM. SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 69; DB 1;
; Pred. No. 0.0017;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1988 (Rel. 08, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum (isolate Wellcome).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Malaria; Sporozoite; Repeat; Signal.
SIGNAL 1 16 PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A54533; A54533.
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR00084; TSP1.
Pfam; PF00090; Lsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45610 MW;
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M19752; AAA29555.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M15505; AAA29554.1; -.
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     424 AA;
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Wilson D.B.;
                                                                                                      01-MAY-1992
                                                                      GUNZ_THEFU
                                                                                        P26222;
                                                     GUN2_THEFU
                                                                                      THE STATE OF STATES AND STATES AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                              Gaps
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Pfam; PP01364; Peptidase_C25; 5.
Hemagglutinin; Virulence; Hydrolase; Thiol protease; Signal; Repeat.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIRCUMSPOROZOITE PROTEIN.
47 X 4 AA TANDEM REPEATS OF N-A-N-P.
BD57A9A152B85E03 CRC64;
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0
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Pred. No. 8.6;
                                                                                                                                                                                                                        100.0%; Score 69; DB 1; Length 442; 100.0%; Pred. No. 0.0018; Pred. No. 0. 10018; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEMAGGLUTININ A.
PEPTIDASE C25-LIKE 1.
PEPTIDASE C25-LIKE 2.
PEPTIDASE C25-LIKE 3.
PEPTIDASE C25-LIKE 4.
PEPTIDASE C25-LIKE 5.
MW; 61C4DE32540C99DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; CFB group; Bacteroidaceae; Porphyromonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 2628 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
Pfam; Pr00090; Lsp_1; 1.
SMRINTS; PR01303; CRCMSPRZOITE.
SMRT; SM00209; TSP1; 1.
Malaria; Sporozoite; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97047672; PubMed=8926061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                       442 AA; 47402 MW;
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-AUG-2001 (Rel. 40, Last
HEMAGGLUTININ A PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                              Query Match 100.

Best Local Similarity 100.

Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NANPNANPNANP 12
                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                       1 NANPNANPNANP 12
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Matches 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-381;
                                                                                                                                                                                                                                                                                                                                                                                                                                       HAGA_PORGI
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DOMAIN
DOMAIN
SEQUENCE
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SEQUENCE
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| R PIR; A42360; A42360.
| R PDB; 1TML; 31-JAN-94.
| R InterPro; IPR001919; CBD_2.
| R InterPro; IPR001524; Glyco_hydro_6.
| R InterPro; IPR001524; Glyco_hydro_6.
| R Pfam; PF01341; Glyco_hydro_6; 1.
| R PR01341; Glyco_hydro_6; 1.
| R PRODOM; PD003733; GLYCOSYL_HYDROL_6.
| R PROSTIE; PS00656; GLYCOSYL_HYDROL_F6_1; 1.
| R PROSTIE; PS00655; GLYCOSYL_HYDROL_F6_2; 1.
| R PROSTIE; PS00656; GLYCOSYL_HYDROL_F6_2; 1.
                                                                                                                                          01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ENDOGLUCANASE E-2 PRECURSOR (EC 3.2.1.4) (ENDO-1,4-BETA-GLUCANASE E-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SIMILARITY: BELONGS TO CELLULASE FAMILY B (FAMILY 6 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochemistry 32:9906-9916(1993).
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-GLUCOSIDIC
-!- CATALACES IN CELLULOSE.
-!- PATHWAY: CELLULOSE DEGRADATION.
-!- SIMILARITY: CONTAINS 1 BACTERIAL-TYPE CELLULOSE-BINDING DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=YX;
Jung E.D., Lao G., Irwin D., Barr B., Benjamin A., Wilson D.B.;
Submitted (MAY-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 32-317.
MEDLINE=94002001; PubMed=8399160;
Spezio M., Wilson D.B., Karplus P.A.;
"Crystal structure of the catalytic domain of a thermophilic endocellulase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptosporangineae; Thermomonosporaceae;
Thermobifida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-91258320; PubMed=1904434;
Lao G., Ghangas G.S., Jung E.D., Wilson D.B.;
"DNA sequences of three beta-1,4-endoglucanase genes from
AA.
441
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Meth. Enzymol. 160:314-323(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Bacteriol. 173:3397-3407(1991)
                                                                                                            (Rel. 22, Created)
                                                                                                                                                                                                                                                                                                                                     (CELLULASE E-2) (CELLULASE EŻ)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M73321; AAC06388.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REVISIONS, SEQUENCE FROM N.A.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermomonospora fusca
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermomonospora fusca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 32-47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYDROLASES).
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                                        CIRCUMSPOROZOITE-PROTEIN RELATED ANTIGEN FB60C8250BC0B589 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-85215483; PubMed-2582354;
MEDLINE-85215483; PubMed-2582354;
Hope I.A., McKay M., Hyde J.E., Goman M., Scalfe J.;
Hope I.A., McKay M., Hyde J.E., Goman M., Scalfe J.;
Hope in a exported antigen of the malaria parasite Plasmodlum falciparum cloned and exported antigen of the malaria parasite Plasmodlum falciparum cloned and expressed in Escherichia coll.";
Nucleic Acids Res. 13:369-379(1985).
-!- MISCELLANEOUS: THIS PROPABLY IN THE PARASITOPHOROUS VACUOLE MEMBRANE.
-!- MISCELLANEOUS: THIS ANTIGEN AND THE CIRCUMSPOROZOITE PROTEIN
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
BEDLINES-87218564; Pubmed-2438130;
Simmons D., Woollett G., Bergin-Cartwright M., Kay D., Scaife J.;
"A malaria protein exported into a new compartment within the host
                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falcipàrum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
         Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                           Score 41; DB 1; Length 162;
Pred. No. 8.1;
                                                                                                                                                                                                                                                                                                                                                                                      EXP1_PLAFA STANDARD; PRT; 162 AA.
P04926; P06718;
113-AUG-1987 (Rel. 05, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
MALARIA PROTEIN EXP-1 PRECURSOR (EXPORTED ANTIGEN AG 5.1).
                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                  PROBABLE.
                                                                                                                                                                                                                                                                 17349 MW;
                                                                                                                                                                                                                                                                                           59.4%;
                                                                                                                                                                                                                       EMBL; M11145; AAA29523.1; -. PIR; A25780; A25780.
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                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 50.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBO J. 6:485-491(1987).
                                                                                                                                                                                                                                                  16
162
 Plasmodium falciparum.
                                                                                                                                                                                                                                                                   162 AA;
                                  SEQUENCE FROM N.A.
         Eukaryota; Alveo.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=5833;
                                                                                                                                                                                                                                         Signal; Malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     erythrocyte.
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                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
EXP1_PLAFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-7GG-1987 (Rel. 05, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CIRCUMSPOROZOITE-PROTEIN RELATED ANTIGEN PRECURSOR (CRA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         87218E4537092AE5 CRC64;
                CELLULOSE-BINDING.
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                                 PROTON DONOR
                                         NUCLEOPHILE
CATALYTIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43;
Pred. No.
                                                                   POTENTIAL.
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70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Conservative
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                                 ||| ||| || || || 321 NPNPNPNPTP 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         441 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 7; Conserv
CRA_PLAFA
P04923;
        DOMAIN
DOMAIN
ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
DISULFID
DISULFID
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CRA_PLAFA
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           between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its burnepan Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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TISSUB-COLTION

MEDIATR=95148760; PubMed=7846182;

MEDIATR=95148760; PubMed=7846182;

MEDIATR=95148760; PubMed=78.4.;

MACKENZIE S.J.;

Bhella R.S., Mackenzie S.L.;

glycerol-3-phosphate acyl transferase.";

plant Physiol. 106:1713-1714(1994).

-I-FUNCTION: ESTERIFIES ACYL-GROUP FROM ACYL-ACP TO THE SN-1 POSITION

G GLYCEROL-3-PHOSPHATE. THE ENXYME FROM CHILLING-RESISTANT PLANTS

DISCRIMINATE AGAINST NON-FIUID PALMITIC ACID AND SELECT OLEIC ACID

WHEREAS THE ENXYME FROM SENSITIVE PLANTS ACCEPTS BOTH FATTY ACIDS.

-I-CATALYTIC ACTIVITY: ACYL-COA + SN-GLYCEROL 3-PHOSPHATE =

COA + 1-ACYL-SN-GLYCEROL 3-PHOSPHATE.

COA + 1-ACYL-SN-GLYCEROL 3-PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- PATHWAY: FIRST STEP IN DE NOVO PHOSPHOLIPID BIOSYNTHESIS. IT MAY ALSO FUNCTION IN THE REGULATION OF MEMBRANE BIOGENESIS.
-i- SUBCELLULAR LOCATION: CHLOROPLAST STROMA.
-i- SIMILARITY: BELONGS TO THE PLANT GPAT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
GLYCEROL.3-PHOSPHATE ACTIRANSFERASE PRECURSOR (EC 2.3.1.15) (GPAT).
Carthamus tinctorius (Safflower).
Subtrayory viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicoryledons; core endicots;
Asteridae; euasterids II; Asterales; Asteraceae; Cardueae; Carthamus.
NCBL_TaxID=4222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                               POTENTIAL.

EPITOPE (DEDUCED).

D -> G (IN 5.1 NEGATIVE STRAINS).

P -> T (IN STRAINS PALO ALTO17 & 3D7).

V -> A (IN REF. 2).

AFGB57446E4AA212 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                MALARIA PROTEIN EXP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       463 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB Pred. No. 8.1;
                                                                                                                                                                                                                                                                                             Transmembrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                   APPEAR TO HAVE A COMMON EPITOPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                17450 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.4%;
                                                                                                                                                                                                     EMBL; X05074; CAA28735.1; -.
                                                                                                                                                                                                                                            A04553; CAA00366.1; -.
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                                                                                                                                                                                                                         EMBL; X01745; CAA25881
                                                                                                                                                                                                                                                            PIR; A23052; YAZQ51.
PIR; A26769; A26769.
                                                                                                                                                                                                                                                                                                   Malaria; Sporozoite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                162 AA;
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                       CHAIN
TRANSMEM
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                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                  EMBL;
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COMPLEX IS REQUIRED FOR THE INDUCED EXPRESSION OF A LARGE NUMBER
COMPLEX IS REQUIRED ALTERS CHROMATIN STRUCTURE TO FACILITATE
OF GENES. THIS COMPLEX ALTERS CHROMATIN STRUCTURE TO FACILITATE
BINDING OF GENE-SPECIFIC DEDICATED TRANSCRIPTION FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINES 89057455: PubMed=3143101; O'Hara P.J., Horowitz H., Eichinger H., Young E.T.; O'Hara P.J., Horowitz H., Eichinger H., Young E.T.; O'Hara P.J., ADR6 gene encodes homopolymeric amino acid sequences and potential metal-binding domain."; potential metal-binding domain.";
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, U33335; AAB68089.1; -.
EMBL, X12493; CAA31013.1; -.
PIR, S05728; TMNYR6.
TRANSPAC; T01279; -.
SGD, S0005937; SW11.
InterPro; IPR001606; ARID.
Fram; PF01388; ARID; 1.
SMART; SW00591; BRIGHT; 1.
Transcription regulation; Activator; DNA-binding; Nuclear protein;
                                                                                                                              463 GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE.
50834 MW; 5792E933068A534D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
TRANSCRIPTION REGULATORY PROTEIN ADR6 (SWI/SNF COMPLEX COMPONENT ADR6) (REGULATORY PROTEIN (REGULATORY PROTEIN SWII) (REGULATORY PROTEIN GAM3).
ADR6 OR SWII OR GAM3 OR YPL016W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                 DB 1; Length 463;
23;
                                                                                                                                                                                                                                                                                                          2; Indels
               InterPro; IPR002123; Acyltransferase.
Phospholipid biosynthesis; Transferase; Acyltransferase;
                                                                                                         CHLOROPLAST (POTENTIAL)
                                                                                                                                                                                                                                                    Score 41; DB 1
Pred. No. 23;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1314 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION.
MEDLINE-92154671; PubMed=1339306;
                                                                                 Transit peptide; Chloroplast.
TRANSIT 1 91
                                                                                                                                                                                                                                                          59.4%;
                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50.v.
6; Conservative
EMBL; L33841; AAA74319.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                         1 NANPNANPNANP 12
                                                                                                                                                                                                                                                                                                                                                                                                                               NANPRVSPSSSP 29
                                                                                                                                                                     SEQUENCE 463 AA;
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us-09-763-397a-4.rsp

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Treich I., Cairns B.R., de Los Santos T., Brewster E., Carlson M.;
"Srelich I., Cairns B.R., de Los Santos T., Brewster E., Carlson M.;
"Srelil, a new component of the yeast SNF-SWI complex that interacts
with a conserved region of SNF2.",
Mol. Cell. Biol. 15:4240-4248(1995).
-!- FUNCTION: INVOLVED IN TRANSCRIPTIONAL ACTIVATION. THE SWI/SNF
-COMPLEX IS REQUIRED FOR THE INDUCED EXPRESSION OF A LARGE NUMBER
OF GENES. THIS COMPLEX ALTERS CHROMATIN STRUCTURE TO FACILITATE
                                                                                                                                                                                                                                                                        BINDING OF GENE-SPECIFIC DEDICATED TRANSCRIPTION FACTORS.
-!- SUBUNIT: COMPONENT OF THE SWI/SNF GLOBAL TRANSCRIPTION ACTIVATOR
              SNF11 OR YDR073W OR D4411.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi; Ascomycota: Saccharomycotina: Saccharomycetes;
Saccharomycetales; Sacchromycetaceae; Saccharomyces.
                                                                                         SEQUENCE FROM N.A.
STRANH=S288C / FY1679;
COSTET F., Jonniau J.-L., Goffeau A.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NANPNANPNAN 11
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                           CHARACTERIZATION.
                                                                  NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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REPEAT
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REPEAT
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PROB_BACSU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
TRANSCRIPTION REGULATORY PROTEIN SNF11 (SWI/SNF COMPLEX COMPONENT
                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
Sukaryota: Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inoue T., Yoshida Y., Isaka Y., Tagawa K.;
Isolation of mitochondrial cyclophilin from bovine heart.";
Blochem. Blochys. Res. Commun. 190:857-863(1993).
-!- FUNCTION: PETAESE ACCELERATE THE FOLDING OF PROTEINS.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
-!- SIMILARIY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
PIR; PC1237; PC1237.
                                                                                                                                                                                                                                                        01-APR-1993 (Rel. 25, Last sequence update)
20-AUC-2001 (Rel. 40, Last annotation update)
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, MITOCHONDRIAL (EC 5.2.1.8)
(PPIASE) (ROTAMASE) (CYCLOPHILIN F) (FRAGMENTS).
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                                                                                          Length 1314;
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                                                     F442D5A82013CDBD CRC64;
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Pred. No. 4.5;
); Mismatches
                                                                                                                                                                                                                                    64 AA.
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                                                                                         Score 41; DB
Pred. No. 64;
1; Mismatches
                ASN/THR-RICH.
GLN-RICH.
C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro: IPR002130; CSA_PPIASE.
Pfam; PF00160; pro_isomerase; 1.
PROSITE: PS00170; CSA_PPIASE_1; PARTIAL.
PROSITE: PS50072; CSA_PPIASE_2; PARTIAL.
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                                                                                                                                                                                                                                    PRT;
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MEDLINE-93176190; PubMed-7679902;
                5 65
337 385
1241 1258
1314 AA; 147938 M
                                                                                         59.4%;
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63.6%;
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Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                         223 NTNSNSTPNAN 233
                                                                                                                                            1 NANPNANPNAN 11
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                                                                                         Query Match
Best Local Similarity
Matches 7; Conserv
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Zinc-finger.
DOMAIN
DOMAIN
3.
ZN_FING
12.
SEQUENCE
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P38956;
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P30404;
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                                                                                                                                                                            ...vator; Nuclear protein; Repeat.
6 X 4 AA TANDEM REPEATS OF N-[AT]-[NT]-A.
31 1-1.
35 1-2.
39 1-4.
1 1-5.
1 -5.
2 X 5 AA PF-
2 2-1.
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P39820: 034562;
01-FEB-1995 (Rel. 31, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FC626E373C32C2C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                     regulation; Activator;
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                                                                                                                                                                            EMBL; 246796; CAA86795.1; -.
EMBL; 274369; CAA98991.1; -.
EMBL; X82086; CAA57601.1; -.
EMBL; X82086; CAA57600.1; -.
PIR; S48760; S48760.
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ilarity 72.7%;
Conservative
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                                                                                                                                                                                                                                                                                     Devine K.M.;
"Sequence of the Bacillus subtilis genome between xlyA and ykoR.";
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE = ADP + L-GLUTAMATE
5-PHOSPHATE (PRODUCT RAPIDLY CYCLIZES TO 5-OXOPROLINE AND ORTHOPHOSPHATE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R EMBL; AJ002571; CAA05591.1; -
R EMBL; AJ002571; CAA05591.1; -
R EMBL; AJ002571; CAA05591.1; -
R EMBL; AJ002571; CAA05591.1; -
R EMBL; AJ002571; CAA05591.1; -
R UnterPro; IPR0104048; Pakinase.
R InterPro; IPR0010478; Pub.
InterPro; IPR001057; Glut_5_kinase.
R Pfam; PF00472; Pub.
R Pfam; PF00472; Pub.
R Pfam; PF00472; Pub.
R PRINTS; PR00474; GLUSKINASE; 1.
R PROSTTE; PR00902; GLUTAMATE, KINASE; 1.
R PROSTTE; PS00902; GLUTAMATE, KINASE; 1.
R CONFLICT 51 51 7 P -> A (IN REF. 1).
T CONFLICT 54 54 R. -> A (IN REF. 1).
T CONFLICT 181 185 NPEAR -> ILSE (IN REF. 1).
CONFLICT 54 55 AA; 39457 MW; 042871624A0A7291 CRC64;
                                                                                                                                          Ogura M., Kawata-Mukai M., Itaya M., Takio K., Tanaka T.;
"Multiple copies of the proB gene enhance degS-dependent
extracellular protease production in Bacillus subtilis.",
1 Bacteriol. 176:5673-5680(1994).
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                   -1- PATHWAY: FIRST STEP IN PROLINE BIOSYNTHESIS PATHWAY.
-1- SUBCELLULAR LOCATION: CYTOPLASMIC.
-1- SIMILARITY: BELONGS TO THE GLUTAMATE 5-KINASE FAMILY.
        Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
NCBL_TaxID=1423;
                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
                                                                                                                              MEDLINE=94364946; PubMed=8083159;
                                                                                                                  STRAIN=168
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175 DANPNENPEA 184

; 0

Gaps

.; 0

58.0%; Score 40; DB 1; Length 365; 70.0%; Pred. No. 25; 2; Indels iive 1; Mismatches 2; Indels

Query Match 58.0 Best Local Similarity 70.0 Matches 7; Conservative

1 NANPNANPNA 10 à

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Search completed: January 29, 2002, 11:13:38 Job time: 814 sec

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Run on:

Sequence:

Searched:

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Q9m9v1 arabidopsis
Q9z2u3 mus musculu
Q9z2u3 mus musculu
Q9z9zBy porphyromon
Q51839 porphyromon
Q9v9y2 drosophila
Q9v9y2 drosophila
Q97140 dictyosteli
Q61732 drosophila
Q9178 arabidopsis
Q9178 arabidopsis
Q9178 arabidopsis
Q9178 arabidopsis
Q9176 porphyromon
Q9znb5 porphyromon
Q9znb5 porphyromon
             arabidopsis
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Zheng C., Xie P., Chen Y.;
Zheng C., Xie P., Chen Y.;
Zheng C., Xie P., Chen Y.;
Molecular cloning and expression of circumsporozoite protein gene from Plasmodium falciparum FCC-1/HN strain in mycobacterium.";
Submitted (CCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF315469; AAG37074.1: -
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR003084; TSP1.
Pfam; PF00090; Lsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
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O54817 mus m
O88933 mus m
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Q51817
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Plasmodium falciparum.
Eukaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID-5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 383;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 69; DB 5; L
Pred. No. 0.0018;
Mismatches 0;
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Q99255;
01-NOV-1996 (TrEMBLrel. 01, Created)
Q9DH26
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Q9Z2U3
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 Local Similarity 100.
ses 12; Conservative
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1687
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                                                                                        Search time 285.36 Seconds
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            GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
                                                                                       January 29, 2002, 11:12:09

    protein search, using sw model

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sp_bacteria:*
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MEDLINE=84250215; PubMed=6204383;
Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A., Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D., Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.;
"Structure of the gene encoding the immunodominant surface antigen on the sporozoite of the human malaria parasite Plasmodium falciparum."; Science 225:593-599(1984).
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MEDLINE-BASS0215; PubMed-6204383;
Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A.,
Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D.,
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5839;
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NCBI_TaxID=5833;
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Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
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44829 MW; D3EF560B2D368DE9 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Best Local Similarity 100.
Matches 12; Conservative
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INTERPROTEIN TO THROUGH TO THE TRANSMER TO THE ORGANISM.

INTERPROTEIN PROUGH TO THE TRANSMER TO THE ORGANISM.

PAGMI, PROUGH TO THE TRANSMER TO THE TRANS
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-1- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT
SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
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   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (CS) PRECURSOR, VARIANT 1 (FRAGMENT).
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NCBI_TaxID=5833;
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SEQUENCE FROM N.A.
STRAIN-SANTA LUGIA, SAL1;
Oari S.H., Lal A.A.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U20969; AAA63153.1;
Thterpro; IPR00084; TSP1.
Therero; IPR0003067; Cremsprzoite.
Pfam; PF00090; tSp_1; 1.
Pfam; PF00090; TSP_1; 1.
SPINTS; PR01303; CREMSPRZOITE.
SMART; SM00209; TSP1; 1.
SEQUENCE 408 AA; 43871 MW; A545BE517822515C CRC64;
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                                                                                                              Plasmodium falciparum.
Eukaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium
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SIGNAL 16 POTENTIAL.
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393 AA;
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                                                                                                                                                                                                                                                                                                                                                                                          protein gene."
                                                                                                                                                                                                                                                                                                                                   Lockyer M.J.;
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SEQUENCE
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InterPro; IPR003067; Crcmsprzoite.
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Best Local Similarity 100.0%; Pr
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                      Query Match
Best Local Similarity 100.0%;
Matches 12; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                   CIRCUMSPOROZOITE PROTEIN.
                                                                                                                                                                                                                                                         PRELIMINARY;
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SEQUENCE FROM N.A.
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MEDLINE-84250215; PubMed-6204383;
Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A.,
Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D.,
Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.;
"Structure of the gene encoding the immunodominant surface antigen on
the sporozoite of the human malaria parasite Plasmodium falciparum.";
Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.; "Structure of the gene encoding the immunodominant surface antigen on the sporozoite of the human malaria parasite Plasmodium falciparum."; Science 225:593-599(1984)
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                                                                                                                                               la Cruz V.F.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
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Mol. Blochem. Parasitol. 0:0-0(0).
EMBL; M03161; AA249.7-11; -.
InterPro; IPR000084; TSP1.
InterPro; IPR003067; Crcmsprzoite.
Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
SEQUENCE 420 AA; 45155 MW; 3A85B92432C2893C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00209; TSP1; 1.
SEQUENCE 420 AA; 45318 MW; F7F70F1C4939DEA7 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Mol. Biochem. Parasitol. 0:0-0(0).
EMBL: M83174; AAA29552.1; -
InterPro: IPR000884; TSP1.
InterPro: IPR03067; Crcmsprzoite.
PRIMTS: PR01303; CRCMSPRZOITE.
PROSITE: PS50092: TSP1; 1.
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Best Local Similarity 100.
Matches 12; Conservative
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUV-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (CS) PRECURSOR, VARIANT 2 (FRAGMENT).
Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TAXID=5833;
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NCBI_TaxID=5833;
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Length 420;
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Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; M83169; AAA29547.1; -.
EMBL; M83149; AAA29562.1; -.
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PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
SEQUENCE 424 AA; 45592 MW; F20CEB60636DB9BE CRC64;
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Last annotation update)
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Pred. No. 0.0019;
; Mismatches 0;
Score 69; DB 5;
Pred. No. 0.0019;
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EMBL; M83168; AAA29546.1; -.
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01-JUN-2001
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MEDLINE-84250215; PubMed-6204383;
Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A.,
Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D.,
Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.;
"Structure of the gene encoding the immunodominant surface antigen on
the sporozoite of the human malaria parasite Plasmodium falciparum.";
Science 225:593-599(1984).
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WOULD BE THE SURRACE ANTIGEN OF THE ORGANISM.

EMBL, M57499; AAA63422.1; -
INTERPO; IPR000884; TSP1.
INTERPO; IPR000867; Crcmsprzoite.
Fram, PF00090; tsp_1: 1.
Fram, PF00090; tsp_1: 1.
Fram, PF00090; TSP1: 1.
Malaria, Repeat; Sporozoite, Signal.
Malaria, Repeat; Sporozoite, Signal.

INTERPORTED TO THE REPEAT SEGUENCE

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                                                            protein gene.";
Mol. Biochem. Parasitol. 45:179-182(1991).
-!- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT
-SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
VERTEBRATE HOST).
                                   ockyer M.J.; 'clonal variation in the Plasmodium falciparum circumsporozoite
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NCBl_TaxID=5833;
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Jongwitiwes S., Tanabe K., Kanbara H.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; M83155; AAA29568.1; -
EMBL; M83152; AAA29565.1; -
EMBL; M83158; AAA29577.1; -
EMBL; M83166; AAA29544.1; -
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Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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                 MEDLINE=91270295; PubMed=2052038;
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Q27246;
01-NOV-1996 (TrEMBLrel. 01, Cz
01-NOV-1996 (TrEMBLrel. 01, La
01-JUN-2001 (TrEMBLrel. 17, La
CIRCUMSPOROZOITE PROTEIN.
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Best Local Similarity 100.
Matches 12; Conservative
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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InterPro; IPR000884; TSP1.
InterPro; IPR003067; Crcmsprzoite.
Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMRAT; SW00209; TSP1; 1.
SEQUENCE 432 AA; 46414 MW; 8787E6005578873A CRC64;
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MOI. Biochem. Parasitol. 0:0-0(0).
EMBL; MBAIGS; AAA29543.1; -
InterPro: IPR000884; TSP1.
InterPro: IPR000804; TSP1.
PRINTS; PR00130; CRCMSPRZOITE.
PRINTS; PR01303; CRCMSPRZOITE.
SMARR; SM00209; TSP1; 1.
SEQUENCE 432 AA; 46385 MW; 2CE8D9A68B
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01-NOV-1996 (TrEMBLrel. 01, Created)
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Matches 12; Conserv
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MEDLINE=84250215; PubMed=6204383;
Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A.,
Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D.,
Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.;
"Structure of the gene encoding the immunodominant surface antigen of the sporozoite of the human malaria parasite Plasmodium falciparum.' Science 225:593-599(1984).
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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     Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
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                                                                                                         Jongwilles S., Tanabe K., Kanbara H.;
Mol. Blochem. Parasitol. 0:0-0(0).
EMBL; M83167; AAA39545.1;
InterPro; IPR000884; TSP1.
InterPro; IPR003067; Crcmsprzoite.
Pfam: PF00090; tsp.1.1;
PRINTS; PR01303; CRCMSPRZOITE.
PROSITE: PS50092; TSP1; 1.
SWART; SM00209; TSP1; 1.
SEQUENCE A36 AA; 46875 MW; F102683C5C1DC85A CRC64;
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SEQUENCE 442 AA; 47414 MW; BFAF9D939D7862FF CRC64;
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Mol. Biochem. Parasitol. 0:0-0(0).
EMBL, M83173; AAA29551.1; -
InterPro; IPR000884; TSP1.
InterPro; IPR003067; Crmsprzoite.
Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
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Best Local Similarity 100.
Matches 12; Conservative
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 NANPNANPNANP 159
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                                                            SEQUENCE FROM N.A.
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01-JUN-2001
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                                                                                        STRAIN=842;
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                                                                                                                                                                                                                                                                                                         Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A., Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D., Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.; "Structure of the gene encoding the immunodominant surface antigen on the sporozoite of the human malaria parasite Plasmodium falciparum."; Science 225:593-599(1984).
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MEDLINE-8425015; PubMed-6204383;
MEDLINE-8425015; L., McCutchan T.F., Weber J.L., Wirtz R.A.,
Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D.,
Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.;
Structure of the gene encoding the immunodominant surface antigen on
the sporozolite of the human malaria parasite Plasmodium falciparum.";
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                                                                                                                                   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jongwitiwes S., Tanabe K., Kanbara H.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; M83164; AAA295421;
EMBL; M83163; AAA295631;
EMBL; M83163; AAA29576.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       la Cruz V.F.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           436 AA; 46688 MW; 5B42FF3348B68655 CRC64;
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Last annotation update)
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InterPro; IPR03067; Crcmsprzoite.
Jefan; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                                                MEDLINE-84250215; Pubmed-6204383;
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2001 (TrEMBLrel. 17,
                                                         CIRCUMSPOROZOITE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CIRCUMSPOROZOITE PROTEIN.
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                            Plasmodium falciparum.
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SEQUENCE FROM N.A.
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Bukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A., Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D., Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.; "Structure of the gene encoding the immunodominant surface antigen on the sporozoite of the human malaria parasite Plasmodium falciparum.";
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MEDILINE-20196006; PubMed=10731132;
Adams M.D., Cellniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                  Last sequence update)
Last annotation update)
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                                                 452 AA
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Mol. Biochem. Parasitol. 0:0-0(0).
EMBL; M83156; AAA29569.1;
InterPro; IPR000884; TSP1.
InterPro; IPR003067; Crcmsprzoite.
Pfam; PF00090; tsp_1; 1.
                                                                                                            Created)
                                                 PRT;
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MEDLINE-84250215; PubMed-6204383;
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PROSITE; PS50092; TSP1; 1.
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Conservative (
                                                                                                         (TrEMBLrel. 01, (TrEMBLrel. 01, (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 225:593-599(1984).
                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 1 CIRCUMSPOROZOITE PROTEIN.
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                                                    PRELIMINARY;
                                                                                                                                                                                                                                                           Plasmodium falciparum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 NANPNANPNANP 151
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Best Local Similarity
Matches 12; Conserv
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                                                                                                         01-NOV-1996
01-NOV-1996
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Q9V650;
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RESULT 14
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Search completed: January 29, 2002, 11:12:09 Job time: 765 sec

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George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen. L.X.,

Ray Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfelffer B.D.,

Ray Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,

Ray Ballew R.M., Basu A., Barendale J., Bayraktaroglu L., Beasley E.M.,

Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolahakov S.,

Burtis R.C., Busam D.A., Bullor H., Cadieu E., Center A., Chandra I.,

Ray Gerson K.Y., Deuchen M.R., Bouck J., Enoksteln P., Brottier P.,

Burtis R.C., Busam D.A., Bullor H., Cadieu E., Center A., Chandra I.,

Ray Gerson C., Gabrielian R.E., Dewnes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Ray Goson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Ray Goson K., Doup L.E., Downes M., Dugan-Rocha S., Pleischmann W.,

Ray Harris N.L., Harvey B., Heiman T.J., Wei M.-H., Ibegwam C.,

Ray Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,

Ray Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,

Ray Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,

Ray Lisko P., Lei Y., Levitsky A.A., Li J., McPherson D.,

Ray McMimel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Lu X., Mattel B., Morintosh T.C., Morison D.M., Resen M.

Ray Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Ray Rolon D.R., Ney M., Murphy B., Nuspeki M.P., Saith H.,

Ray Ray C., Siden-Kamos I. Sinpson M., Strong R., Sinch R.,

Ray C., Siden-Kamos I. Sinpson M., Strong R., Sinth H.,

Ray C., Siden-Kamos I. Sinpson M., Strong R., Sinth H.,

Ray Ray C., Web R., Pitch R., Sander E., Wang S., Zho O., Zhen G., Sheng L., Sheng C., Siden-Kamos I., Singson M., Strong R., Weh R.-F., Zaveri J.S., Zhan M., Zhong W., Zhong G., Zheo O., Zhen Gibbs R.A, Myeres E.W., Rodoger T., Worley C., Wu D., Yang G., Zhoo O., Zhen C., Stene C., Strongele E., Sheng K., Zhon M., Zhong W., Zhong S., Zhon Y., Zhong Y., Zhon W., Zhong Y., Zhon W., Zhong Y., Zhon W., Zhong Y., Zhon W., Zhong Y., Zhon W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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90.9%;
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Pfam; PF02017; CIDE-N; 1
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WPI; 2000-237654/20
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NS1_81-RLfAuth + (
NS1_81(NANP)4RLfAu
NS1_81(NVDP)4RLfAu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region of P.falcip
Circumsporozoite a
Circumsporozoite a
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NS1_81-RLfdelta9.
NS181RLFAuth plasm
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                                                                                                                                        (without alignments)
3.098 Million cell updates/sec
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                                                                                                               January 29, 2002, 10:21:41; Search time 310.82 Seconds
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| SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                       522463 seqs, 74073290 residues
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Listing first 45 summaries
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AAR07289
AAP60412
AAR13175
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AAR13177
AAR13177
AAR13178

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                      1 KHKKLKQPGDGNP 13
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Maximum DB seq length: 2000000000
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                                                                            OM protein
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Sequence encoded b
Sequence of R prot
SIVmac239 vpr gene
HIV-2/SIV Vpr prot
IDI plasmodium sur
Human secreted pro
M24-M5-M6-M19-M3-M
S. pyogenes octava
P. vivax circumspo
Circumsporozoite a
                                                                                                                                                     C-terminal amidati
Membrane targeted
Human secreted pro
Drosophila gustato
    Sequence encoded b
CS protein of mala
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                                                                                                                      Lambda gt10ch2 enc
Lambda gt10ch101 e
Porcine PAM-8. Su
                                                                                                                                      C-terminal amidati
Lambda gt10ch201 e
Equine C-terminal
                         Sequence corresp.
PAGE1 polypeptide.
PAGE-4 polypeptide
                                                                                                                 Human 5' EST secre
                                         Human secreted pro
                                                                                                                                                                          H. pylori GHPO 173
Recombinant vaccin
                                                                                                       Sequence encoding
Plasmodium vivax
                                                                                                                                                                                          ALIGNMENTS
                                                                             AAG02761
AAR51001
AAB03124
AAR37974
AAR07288
                                                                                                       AAP70708
AAR30609
                                                                                                                 AAY12447
AAR06400
AAR06379
AAR29770
AAR20026
AAR11113
                    AAR71653
AAP61001
                                                        AAR22369
AAW99813
                                                                   AAW89317
AAR12308
          AAP60416
AAP80835
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4444

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10.000044444444

10.00004444444

10.00000444444
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Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; T-cell epitope; tetanus toxoid; antigenic epitope; treatment; circumsporozoite protein; CSP; sporozoite surface protein-1; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; MSP-2; apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody. Plasmodium falciparum CSP antigenic epitope, P592. AAY70281 standard; peptide; 13 AA. (first entry) Plasmodium falciparum

WO200011179-A1.

99WO-US18869

98US-0097703

(NAIM-) NAT INST IMMUNOLOCY. (USSH) US DEPT HEALTH & HUMAN SERVICES.

Lal AA, Shi YP, Hasnain SE;

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The present sequence is the antigenic epitope P592, derived from circumsporozoite protein (CSP) of the sporozoite stage of plasmodium fallogrum. It is used in the construction of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melittin signal peptide, (His)6 tag, Trecal epitope from tetanus toxoid and 21 antigenic epitopes from circumsporozoite protein (CSP), sporozoite surface protein-2 (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (BBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the can used for treatment and prevention of malarial cativity and can used for treatment and prevention of malarial
     Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle
                                                                                                                  Claim 2; Page 16; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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0; Gaps ; 100.0%; Score 75; DB 21; Length 13; 100.0%; Pred. No. 1.6e-05; Indels 0; 0; Mismatches P. falciparum in biological samples 13; Conservative 1 KHKKLKQPGDGNP 13 Query Match Best Local Similarity 13 AA; Matches අ ŏ

AAP82541 standard; peptide; 19 AA. 12-DEC-1990 (first entry) AAP82541; AAP82541 RESULT

Region of P.falciparum circumsporozoite protein with linker attached. $^{(}$ P.falciparum circumsporozoite protein; malaria;

synthetic.

DE3723583-A.

16-JUL-1987; 28-JAN-1988.

87DE-3723583. 86IT-0021144 16-JUL-1986;

(ENIE) ENIRICERCHE SPA.

Bernardi A, Bonelli F,

New immunogenic polypeptide for malaria vaccine - contg. sequences derived from P. falciparum circumsporozoite protein, WPI; 1988-030026/05.

Pessi A, Verdini AS;

Claim 1; Page 2; 13pp; German.

also useful for antibody assay

46

g

δλ

AAR07289

RESULT

This is the N-terminal of an immunogenic polypeptide useful as a malaria vaccine. It comprises a fragment of the P-falciparum cicumsporozoite protein (CSP) and one copy of a peptide linker, which is pref. present in 3-10 copies, which links the preceding

ö ö Gaps Gaps The protein was produced by expression of a synthetic gene. The analogue comprises AAs 68-123 of the native P. falciparum CS protein, followed by four repeat sequences (three "B"s, i.e. NANP) and one "A", i.e. NVDP), followed by AAs 289-392 of the native protein. Reduction of the immunological dominance of the repeats relative to the epitopes in the regions flanking the repeats enhances sporozoite neutralising activity. ; 0 sequence to a 2nd (C-terminal) sequence comprising tetrapeptide units of CSP. See AAP82542. ; 0 100.0%; Score 75; DB 11; Length 180; 100.0%; Pred. No. 0.00023; ive 0; Mismatches 0; Indels (Recombinant plasmodium circumsporozoite analogues - lacking one or more repeat epitope(s) for use as a malaria sub-unit Length 19; Indels 100.0%; Score 75; DB 9; I 100.0%; Pred. No. 2.3e-05; 0; Mismatches CS protein; plasmodium; malaria; vaccine Circumsporozoite analogue Falciparum 4. AAR07290 standard; protein; 180 AA. Gibson HL; Claim 10; Fig 10; 22pp; English. 90EP-0303907. 89US-0336288 (first entry) Query Match 100. Best Local Similarity 100. Matches 13; Conservative Query Match 100. Best Local Similarity 100. Matches 13; Conservative Barr PJ, Bathurst IC, 1 KHKKLKQPGDGNP 13 1 KHKKLKQPGDGNP 13 See also AAR07287-91 WPI; 1990-314486/42. N-PSDB; AAQ06153. (CHIR-) CHIRON CORP. 180 AA; AA; 11-APR-1990; 11-APR-1989; 28-JAN-1991 17-0CT-1990. EP392820-A. Synthetic. Sequence AAR07290, vaccine. Sequence RESULT AAR07290 ò q 22 X 88

AAR07289

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The peptides may be synthesised in pure form and used to generate an immune response in vaccination against malaria. The featured repeat units are claimed and must be present in copies of 2-1000, in the P.falciparum genome, the first is coded for 37 times. See also AAN60362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1..81
/label= N-terminal of NS1
/note= "Influenza virus nonstructural protein 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenic determinant; circumsporozoite; CS; vaccine; malaria; hybrid; influenza virus; non-structural protein 1; fusion.
                                                                                                                                                                                                                                                                            New immunologically active pure synthetic peptide(s) - used for protection against infection by malaria parasite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /noce= "Region 1 contg. flanking region less
/note= "Region 1 contg. flanking region less
signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                     Schneider I;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= AAs 297-412 of CS protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82..87
/label= synthetic linker
                                                                                                                                                                                                                     Dame JB, Williams JL,
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/note= "see comments"
 /label= Repeat unit
/note= "of claim 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR13175 standard; Protein; 309 AA.
                                                                                                                                                                                                                                                                                                                      Claim 7; Page 40-41; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum.
Influenza virus (A/PR/8/34/).
                                                                                                   85EP-0107794.
                                                                                                                              84US-0624564.
                                                                                                                                                            OF COMMERCE.
                                                                                                                                                                          GOVERNMENT.
SEC OF THE ARMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KHKKLKQPGDGNP 13
                                                                                                                                                                                                                                                WPI; 1986-008635/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                        250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NS1_81-RLfdelta9.
                                                                                                                                                            SEC
                                                                                                                                                                                                                     McCutchan TF,
                                                                                                   24-JUN-1985;
                                                                                                                              26-JUN-1984;
                                                                                                                                                         (USDC ) US S
(USGO ) US G
(USSA ) US S
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                                                                        02-JAN-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hybrid;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The protein was produced by expression of a synthetic gene. The analogue comprises AAs 43-123 of the native P. falciparum CS protein, followed by four repeat sequences (three "B"s, i.e. NANP) and one "A", i.e. NVDP), followed by AAS 289-374 of the native protein. Reduction of the immunological dominance of the repeats relative to the epitopes in the regions flanking the repeats enhances sporozoite neutralising activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 75; DB 11; Length 184; 100.0%; Pred. No. 0.00023;
                                                                                                                                                                                                                                                                                                                                                                                            Recombinant plasmodium circumsporozoite analogues - lacking one or more repeat epitope(s) for use as a malaria sub-unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic peptide antigenic for the malaria parasite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                  CS protein; plasmodium; malaria; vaccine.
                                                                                     Circumsporozoite analogue Falciparum 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
18..21
/label- Repeat unit
/note- "of claim 1"
22..26
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                                                                                                                                                                                                                                                                                                                      Gibson HL;
AAR07289 standard; protein; 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Fig 8; 22pp; English.
                                                                                                                                                                                                                                 90EP-0303907
                                                                                                                                                                                                                                                            89US-0336288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-JUN-1991 (first entry)
                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sporozite; vaccination.
                                                                                                                                                                                                                                                                                                                      Bathurst IC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KHKKLKQPGDGNP 13
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                                                                                                                                                                                                                                                                                        (CHIR-) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 AA;
                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ06152.
                                                                                                                                                                                                                                 11-APR-1990;
                                                                                                                                                                                                                                                            11-APR-1989;
                                                       28-JAN-1991
                                                                                                                                                                                                   17-0CT-1990
                                                                                                                                                                        EP392820-A.
                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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Barr PJ,

vaccine.

AAP60412;

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RESULT AAP60412

õ 8 Key Region

Region

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Gaps

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N-PSDB; AAQ06580
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                                                                                               01-MAY-1990;
                                                                                                                                    03-MAY-1989;
                                                         22-NOV-1990
                    EP398540-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR13176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR13176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
    Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The polypeptide is prepd. by genetic engineering of genes encoding the P. falciparum circumsporozoite (CS) protein [Dame et al., Science 225 : 593 (1984)], and the influenca virus non-structural protein 1 (NS1), [Baeze et al., Nucleic Acids Research, 8 : 5845 (1980)]. The DNA encoding the 1st 81 AAs of the N-terminal of NS1 (NS1 81) is linked via a synthetic sequence to DNA encoding Region I contg. flanking regionless the 18 AA signal region, which in turn is fused to DNA encoding Region II-contg. flanking region I less the first nine N-terminal AAs. This CS fusion is designated RLfdelta9. The Pro residue separating the ASP (at the C-terminal of the linker) from RLfdelta9 is an artifact of a filled in BamHI site. The peptide can be used in a vaccine for protection against
                                                                                                                                                                                                                                                                                                                                                                             Polypeptide comprising immunogenic determinants from P falciparum for vaccine against malaria infection in humans.
/note= "Region II flanking region minus 9 N-term-
inal AAs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 75; DB 12; 1
100.0%; Pred. No. 0.0004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.81
/label= NS181 protein fragment
/note= "from plasmid pMG-1"
89..193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  See also AAR12306-R12311 and AAR13176-R13179.
                                                                                                                                                                                                                                                                                                       Hollingdale MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR07945 standard; protein; 319 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 7; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NS181RLFAuth plasmid product
                                                                                                                                                                                     89US-0447746
                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM. (USSA ) US SEC OF THE ARMY. (BIOM-) BIOMEDICAL RES INST
                                                                                                                                            90EP-0313257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-FEB-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.

Best Local Similarity 100.

Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. KHKKLKQPGDGNP 13
                                                                                                                                                                                                                                                                                                         Gross MS, Gordon DM,
                                                                                                                                                                                                                                                                                                                                          WPI; 1991-179771/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Malaria; vaccine.
                                                                                                                                              06-DEC-1990;
                                                                                                                                                                                       08-DEC-1989;
                                                                                                           19-JUN-1991
                                                                      EP432965-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR07945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
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Gaps
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/label= N-terminal of NS1
/note= "Influenza virus nonstructural protein 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunogenic determinant; circumsporozoite; CS; vaccine; malaria; hybrid; influenza virus; non-structural protein 1; fusion.
                                                                                                                                                                                                                                     New polypeptide used in malaria vaccine - comprises immunogenic determinants from 1st and 2nd flanking regions of plasmodium surface protein and intermediate repeat domain
                                                                                                                                                                                                                                                                                                                                                                    The product is useful in preparation of vaccines for treatment a prophylaxis of plasmodium sporozite infection. It may be easily produced in large pure quantities from a transformed E.coli expression system.
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89..193
/label= AAs 19-123 of CS protein
/note= "Region 1 contg. flanking region less
signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 75; DB 11; Length 319; 100.0%; Pred. No. 0.00041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= artifact
/note="see comments"
195.319
/label= AAS 288-412 of CS protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82..87
/label= synthetic linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "see comments"
                                                                                                                                                                                                                                                                                                                                   Example 2; Page 11-12; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR13176 standard; Protein; 319 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= artifact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum.
Influenza virus (A/PR/8/34).
90EP-0304720.
                                          89US-0346863.
                                                                                    (SMIK ) SMITHKLINE BEECHAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
"a+rhes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KHKKLKQPGDGNP 13
                                                                                                                                   Gross MS, Young JF;
                                                                                                                                                                             WPI; 1990-350299/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 AA;
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WPI; 1991-179771/25.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUN-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                 EP432965-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gross MS,
                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
AAR13178
                                                        Region
                                                                                                                                                                                                                                                                                                                                   Region
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                                                                                                                                                                                                       Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The polypeptide is prepd. by genetic engineering of genes encoding the P. falciparum circumsporozoite (CS) protein [Dame et al., Science 225: 593 (1984)], and the influenza virus non-structural protein [NSI), [Baez et al., Nucleic Acids Research, 8: 5845 (1980)]. The DNA encoding the 1st 81 AAs of the N-terminal of NSI (NSI_81) is linked via a synthetic sequence to DNA encoding Region I contg. flanking regionless the 18 AA signal region, which in C turn is fused to DNA encoding Region II-contg. flanking regions Region II-contg. flanking region of the Asp (at the C-terminal of the linker) from Rifauth is an artifact of a filled in BamHI site; the Gly separating Region II-contg. CS flanking regions is an artifact of a filled in BamHI site; the Gly separating Region II-contg. CS flanking regions is an artifact of a synthetic protection against malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                         Polypeptide comprising immunogenic determinants from P falciparum - for vaccine against malaria infection in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenic determinant; circumsporozoite; CS; vaccine; malaria; hybrid; influenza virus; non-structural protein 1; fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Influenza virus nonstructural protein 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complete nucleotide and AA sequences are given in EP-304720,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 75; DB 12; Length 319; 100.0%; Pred. No. 0.00041; tive 0; Mismatches 0; Indels (
               /note= "Region II flanking region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  See also AAR12306-R12311 and AAR13175-R13179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1..81
/label- N-terminal of NS1
                                                                                                                                                                                                                                                                                                           Gross MS, Gordon DM, Hollingdale MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Page 10; 18pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR13177 standard; Protein; 327
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Influenza virus (A/PR/8/34/).
                                                                                                                                      90EP-0313257.
                                                                                                                                                                               89US-0447746.
                                                                                                                                                                                                                    (SMIK ) SMITHKLINE BEECHAM.
(USSA ) US SEC OF THE ARMY.
(BIOM-) BIOMEDICAL RES INST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                WPI; 1991-179771/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 AA;
                                                                                                                                    06-DEC-1990;
                                                                                                                                                                               08-DEC-1989;
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Region
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The polypeptide is prepd. by genetic engineering of genes encoding the P. falciparum circumsporozoite (CS) protein [Dame et al., Science 225: 593 (1984)], and the influenza virus non-structural protein 1 (NS1), [Baez et al., Nucleic Acids Research, 8: 5845 (1980)]. The DNA encoding the 1st 81 AAS of the N-terminal of NS1 (NS1_81) is linked via a synthetic sequence to DNA encoding Region I conty, flanking region less the 18 AAS signal region. This is linked to a synthetic sequence encoding two repeat units from the mmunodominant region, which in turn is fused to DNA encoding Region II.conty. flanking region. The Pro residue separating the C terminal of the linker) from the Region I-conty. C separating the repeat units and the Region II-conty. CS flanking region is an artifact of a filled-in BamHI site; the Gly separating the repeat units and the Region II-conty. CS flanking region is an artifact of a synthetic FOKI/TthIII I linker. The peptide can be used in a vaccine for protection against malaria.
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                                                                                                                                                                                                                                /note= "Region 1 contg. flanking region less
signal sequence"
                                                                                                                                                                                                                                                                                                                                 /label- immunodominant repeat region
/note= "two tetrapeptide repeat units"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Region II flanking region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label- AAs 288-412 of CS protein
                                                                                                                                                                                                    protein
                                                                                                                                                                                             AAs 19-123 of CS
82..87
/label= synthetic linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hollingdale MR;
                                                                                             /label= artifact
/note= "see comments"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="see comments"
203..327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR13178 standard; Protein; 335 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /label- artifact
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(USSA ) US SEC OF THE ARMY.
(BIOM-) BIOMEDICAL RES INST.
                                                                                                                                                              89..193
/label= #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 13; Conservative
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335 AA;

Sednence

S

us-09-763-397a-5.rag

AAR13178;

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Plasmodium falciparum.
Influenza virus (A/PR/8/34).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90EP-0313257.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM.
(USSA ) US SEC OF THE ARMY
(BIOM-) BIOMEDICAL RES INST
                                                                                                                                                                                                                                                                                                                                                                                                           29-AUG-1991 (first entry)
                                                                                                                                                195 khklikqpgdgnp 207
                                                                                                                 1 KHKKLKQPGDGNP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NS1_81(NVDP)4RLfAuth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1991-179771/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUN-1991.
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                                                                                                                                                                                                                                                                                                                                                           AAR13179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
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                                                                                                                                                                                                                                                     11
                                                                                                                                                                                                                                                        RESULT 1
AAR13179
                                                                                                                                                                      g
                                                                                                                         δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polypeptide comprising immunogenic determinants from P falciparum for vaccine against malaria infection in humans.
                                                                                                                                                                                                                                                                                          1..81
/label- N-terminal of NS1
/note= "Influenza virus nonstructural protein 1"
                                                                                                Immunogenic determinant; circumsporozoite; CS; vaccine; malaria; vybrid; influenza virus; non-structural protein 1; fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Region 1 contg. flanking region less signal sequence"
                                                                                                                                                                                                                                                                                                                                                                 82.97
/label= immunodominant repeat region
/label= immunodominant repeat units"
/note= "four tetrapeptide repeat units"
/label= synthetic linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="see comments"
211..335
Tabbl= AAs 288-412 of CS protein
/note="Region II flanking region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "see comments"
105..209
| Jabel= AAs 19-123 of CS protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gross MS, Gordon DM, Hollingdale MR;
                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; Page 11; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= artifact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= artifact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM.
(USSA ) US SEC OF THE ARMY.
(BIOM-) BIOMEDICAL RES INST.
                                                                                                                                                                                    Plasmodium falciparum.
Influenza virus (A/PR/8/34).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90EP-0313257.
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29-AUG-1991 (first entry)
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                                                     NS1_81(NANP)4RLfAuth
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polypeptide comprising immunogenic determinants from P falciparum - for vaccine against malaria infection in humans.
                                                                                                                                                                                                                                                                    1..81
/label= N-terminal of NS1
/note= "Influenza virus nonstructural protein 1"
                                                                                                                                                                                            Immunogenic determinant; circumsporozoite; CS; vaccine; malaria; hybrid; influenza virus; non-structural protein 1; fusion.
                                                                                                                                                                                                                                                                                                 82.97
/label- immunodominant repeat region
/note- "four variant tetrapeptide repeat units"
                    ;
0
                                                                                                                                                                                                                                                                                                                                                                            /note- ~~~
105..209
/label= AAs 19-123 of CS protein
/note= "Region 1 contg. flanking region less
signal sequence"
Length 335;
                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               /label= artifact
/note="see comments"
/label= AAS 288-412 of CS protein
/note= "Region II flanking region"
Query Match
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 13; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                               98..103
/label= synthetic linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gordon DM, Hollingdale MR;
                                                                                                                                                                                                                                                                                                                                                              /label= artifact
/note= "see comments"
                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                AAR13179 standard; Protein; 335 AA.
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WPI; 2000-237654/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-AUG-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP278940-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP83144;
                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; really aptrope; treatment; tetanus toxold; antigenic epitope; treatment; classical experience; creatment; classical expectation of the surface protein-2; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; MSP-2; aptroatmentrane antigen-1; AMA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody;
the P. falciparum circumsporozoite (CS) protein [Dame et al., Science 225: 593 (1984)], and the influenza virus non-structural protein 1 (NSI), [Baez et al., Nucleic Acids Research, 8: 5845 (1980)]. The DNA encoding the 1st 81 AAS of the N-terminal of NSI (1981) is linked to a synthetic sequence encoding four repeat units (the variant form) from the immunodominant region, which in turn is linked via a synthetic sequence to DNA encoding Region II-contg. Cantg. flanking region less the 18 AA signal region. This is contg. flanking region II-contg. flanking region is an artifact of a filled-the Region I-contg. CS flanking region is an artifact of a filled-the Region I-contg. CS flanking region is an artifact of a filled-the Region I-contg. CS flanking region is an artifact of a flanking regions is an artifact of a synthetic Fokl/TthiII I
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Recombinant multivalent malarial vaccine"
                                                                                                                                                                                                                                                                 ;;
                                                                                                                                                                                                                                       100.0%; Score 75; DB 12; Length 335; 100.0%; Pred. No. 0.00043; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1..22
/label= Melittin_signal_peptide
/note= "Derived from Honey bee"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.350
/label- Mature_CDC/NIIMALVAC-1
                                                                                                                                                                                See also AAR12306-R12311 and AAR13175-R13178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NAIM-) NAT INST IMMUNOLOGY.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant vaccine CDC/NIIMALVAC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          AAY70278 standard; Protein; 350 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric - Apis sp.
Chimeric - Clostridium tetani.
Chimeric - Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shi YP, Hasnain SE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0097703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US18869
                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUN-2000 (first entry)
                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                              195 khkklkqpgdgnp 207
                                                                                                                                                                                                                                                                                        1 KHKKLKQPGDGNP 13
                                                                                                                                                                                                       335 AA;
                                                                                                                                                                   against malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200011179-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        honey bee.
                                                                                                                                                                                                                                                                                                                                                                                                 AAY70278;
                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lal AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                              AAY70278
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The present sequence is that of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melittin signal peptide, (His) 6 tag, T-cell epitope from tetanus toxoid and 21 antigenic epitopes from circumsporozoite protein (CSP), sporozoite surface protein-2 (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical membrane antigen-1 (MAA-1), erythrocyte binding antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, PfG27. These epitopes were obtained at different stages of the life cycle of Plasmodium falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting P. falciparum in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                         Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 75; DB 21; Length 350;
; Pred. No. 0.00045;
0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Repeat region, repeat unit = NANP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence encoded by the circumsporozoite (CS) gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaccine; antigen; immunogen; probe; hybridisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP83144 standard; protein; 411 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       De Wilde M, Harford N;
                                                                                                                                                                                                  Claim 3; Page 43-44; 52pp; English.
                                                                                                                                 plasmodium falciparum life cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KHKKLKQPGDGNP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum
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N-PSDB; AAZ51336.
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AAP80835
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                                                                                         Sequence of the CS gene (AAN81108) is from lambda-mpfl. A recombinant DNA molecule is claimed, comprising functional DNA coding sequence fused, in phase, to a portion of the Pre-S2 region of a hepatitis B virus (HBV) Pre-S2-S protein coding sequence. The functional DNA coding sequence comprises the Pre-S2 coding sequence, Pre-S1 coding sequence, the CS protein coding sequence or entire Plasmodium, or a HIV coding sequence such as an HIV coding sequence such as an HIV envelope gene sequence, e.g. HIV C7 protein coding region, HIV Peptide 121 coding region, or HIV Dreesman peptide coding region.
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Plasmodium CS gene was used to isolate peptides capable of inducing an immune response to the parasite. Peptide antigens may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - used for
                              DNA encoding hepatitis B virus antigens and hybrids contg. them used for expression in yeast to obtain vaccines and bivalent
                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                  Score 75; DB 9; Length 411; pred. No. 0.00053; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New immunologically active pure synthetic peptide(s) protection against infection by malaria parasite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schneider I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McCutchan TF, Dame JB, Williams JL,
                                                                          Example; Fig 3Aa-3Af; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
124..127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124..12/
/label= Repeat unit
                                                                                                                                                                                                                                                                                                                                                     AAP60416 standard; Protein; 412 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 2; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   CS protein of malaria parasite.
                                                                                                                                                                                                                                     100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (USDC ) US SEC OF COMMERCE.
(USGO ) US GOVERNMENT.
(USSA ) US SEC OF THE ARMY.
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                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sporozoite; vaccination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum.
                                                                                                                                                                                                                                                                                          1 KHKKLKQPGDGNP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1986-008635/02.
N-PSDB; AAN60362.
   WPI; 1988-229751/33.
N-PSDB; AAN81108.
                                                                                                                                                                                                        411 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUN-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUN-1984;
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                                                                                                                                                                                                                                                                                                                                                                                               13-JUN-1991
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                                                                                                                                                                                                                                                                                                                                                                         AAP60416;
                                                                                                                                                                                                         Sequence
                                                        vaccines
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plasmid WR201 was obtained from the Walter Reed Army Institute of Research, and results from insertion of a 2.3 kb EcorI fragment from lambda mpfl encoding the complete CS protein gene P. falciparum into vector pUCB. A recombinant DNA vector is claimed, which comprises a DNA sequence contg. the coding sequence of the CS P. falciparum operatively linked to an expression control sequence. Prefd. expression control sequences include the yeast glyceraldehyde-3P-dehydrogenase gene (TDH3) promoter and the yeast confithine carbamoyl transferase gene (ARG3) transcription termination region. A suitable coding sequence comprises the 1215bp Stul-Rsal fragment of WR201 contg. the P. falciparum CS protein coding sequence, minus its first 50bp. Also claimed is a
                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Circumsporozoite gene; Plasmodium falciparum; lambda mPfl; vaccine; yeast glyceraldehyde-3P-dehydrogenase gene (TDH3) promoter; yeast ornithine carbamoyl transferase gene (ARG3); repeat region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence encoded by the circumsporozoite (CS) gene of Plasmodium falciparum in lambda mPfl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Expression of P. falciparum circumsporozoite protein by yeast using recombinant DNA vector having coding sequence linked to expression control sequence
                                                                                                                                                                                                                                                 ;
0
be synthesised in pure form and used to generate an immune response in vaccination against malaria. The featured repeat units are claimed and must be present in copies of 2-1000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 ..147
/note="repeat region, repeat unit=NANPNVDP"
148 ..207
                                                                                                                                                                                          Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="repeat region, repeat unit=NANP"
212..287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212.287
/note="repeat region, repeat unit=NANP"
                                                                                                                                                                                          100.0%; Score 75; DB 7; L
100.0%; Pred. No. 0.00053;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAP80835 standard; protein; 412 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 2a; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87US-0008791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88WO-BE00002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SMIK ) SMITH KLINE RIT SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        De Wilde M, Gathoye AM;
                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum
                                                                                                                                                                                                                                                                                                              1 KHKKLKQPGDGNP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1988-235171/33.
N-PSDB; AAN81781.
                                                                                                                                                                                                                               Best Local Similarity
Matches 13; Conser
                                                                                                                       412 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-SEP-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-SEP-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAP80835;
                                                                                                                       Sequence
                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
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transformed host cell, a method of culturing the cell to produce CS, the protein, and a vaccine. The vector comprises a 192 bp Sau3A fragment coding for 16 tetrapeptide repeats of the P. falciparum CS protein coding form Sau3A digestion of a 1215 bp Stul Rsal fragment of WR201 containing the P. falciparum CS protein coding sequence minus cc approx. Its first 50 bp, or two, three, four or more tandem copies of XX Sequence 412 AA;
```

Ouery Match 100.0%; Score 75; DB 9; Length 412; Best Local Similarity 100.0%; Pred. No. 0.00053; Matches 13; Conservative 0; Mismatches 0; Indels Qy 1 KHKKLKQPGDGNP 13

Db 109 khklkqpgdgnp 121

Search completed: January 29, 2002, 10:21:42 Job time: 418 sec

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Gaps

; 0

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 29, 2002, 10:26:35; Search time 144.96 Seconds (without alignments) 6.831 Million cell updates/sec

US-09-763-397A-5 75 1 KHKKLKQPGDGNP 13 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

pir_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	circumsporozoite p	circumsporozoite p	circumsporozoite p		circumsporozoite p	circumsporozoite p		gene R protein - h	vpr protein - simi	transcription fact	hypothetical prote	conserved hypothet	pyruvate dehydroge	circumsporozoite p	circumsporozoite p		V1 protein - tobac	probable membrane	opsin, green-sensi	RH2 opsin - green	circumsporozoite p	ribosomal protein	hypothetical prote	circumsporozoite p	ATP-dependent heli	hypothetical prote	hypothetical prote	peptidylglycine mo	KIAA0645 protein -
SUMMARIES	DI	OZZQAF	A54533	A54529	B29795	S05428	A29795	A39756	S03067	ASLJR3	A32993	T18627	B82143	C59237	A29319	A32068	A48571	A42452	H71259	A42347	151319	OZZQAK	H69042	S74326	OZZQAB	T05883	T21431	E81804	URHUAP	T00376
	DB	-	7	~	~	7	~	~	~	-	7	7	7	~	7	2	~	~	7	~	~	-	~	~	-	7	7	~	-	~
	Length	412	424	442	189	405	171	388	97		304		179	978	343	367	386	102	320	355	355	363	96	97	378	633	739	803	974	1572
dР	Ouery Match	100.0	100.0	100.0	95.0	92.0	90.7	68.0	61.3	_	57.3	57.3	26.0	56.0	55.3	55.3	55.3	54.7	54.7	54.7	54.7	54.7	53.3	53.3	53.3	ന	53.3	m	53.3	53.3
	Score	75	75	75	69	69	89	51	46	46	43	43	42	42	-	┑	41.5	41	41	41	41	41	40	40	40	40	40	40	40	40
	Result No.	7	7	m	4	S.	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

30 39.5 52.7 478 2 JO2034 31 39 52.0 101 2 S08439 32 39 52.0 101 2 S08439 34 39 52.0 452 2 L064583 35 52.0 685 2 R08506 36 52.0 872 1 URBOAP 37 39 52.0 972 1 URBOAP 38 50.7 195 2 E0146 41 38 50.7 395 2 A41156 42 38 50.7 395 2 C0446 44 38 50.7 455 2 D96525	RNA-directed RNA p	vpr protein - huma	cytochrome P450 Rv	hypothetical prote	stress-induced pro	conjugal transfer	lipoxygenase (EC 1	peptidylglycine mo	pregnancy-associat	N-terminus of phag	rRNA (guanine-N1-)	homeotic protein H	circumsporozoite p	hypothetical prote	OXA1 homolog - hum	protein TlN15.19 [
500.0000000000000000000000000000000000	JQ2034	S08439	H70921	D64583	T48150	B82606	T10085	URBOAP	S65464	E70446	E82129	A56553	A41156	C84809	138079	D96525
500.0000000000000000000000000000000000	~	~	П	~	~	7	~	-	~	~	~	~	~	~	~	7
0,	478	101	400	452	558	685	877	972	1627	195	278	327	395	435	435	455
30.5 31.33 32.33 33.4 33.4 33.4 33.6 33.6 33.6 33.6 44.0 33.6 44.0 44.0 44.0 44.0 44.0 44.0 44.0 44	52.7	52.0	52.0	52.0	52.0	52.0	52.0	52.0	52.0	50.7	50.7	50.7	50.7	50.7	50.7	50.7
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	39.5	39	39	39	39	39	39	39	39	38	38	38	38	38	38	38
	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 OZZQAF Circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate IMTM22) C;Species: Plasmodium falciparum C;Date: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jun-2000	C;Accession: A03388 R:Dame, J.B.; Williams, J.L.; McCutchan, T.F.; Weber, J.L.; Wirtz, R.A.; Hochmeyer, W Science 225, 593-599, 1984 A;Title: Structure of the gene encoding the immunodominant surface antigen on the spo A;Reference number: A03388; MUID:84250215 A;Accession: A03388	A.Molecule type: DNA A.Residues: 1-412 < CDAN> A.Residues: 1-412 < CDAN> A.Cross-references: GB.K02194; NID:g160160; PIDN:AAA29524.1; PID:g160161 A.Experimental source: clone 7G8 C.Comment: Residues 1-16 are the probable signal sequence. C.Comment: Residues 1-16 are 41 copies of a 4-residue repeating unit in the middle domain of C.Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology F;336-390/Domain: thrombospondin type 1 repeat homology	Query Match Best Local Similarity 100.0%; Score 75; DB 1; Length 412; Best Local Similarity 100.0%; Pred. No. 4.4e-05; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RE O O C C C C C C C C C C C C C C C C C	A P S S R C	A A A A D D D E	5-2

109 KHKKEKQPGDGNP 121 1 KHKKLKQPGDGNP 13 ò

q

7 RESULT A54533

Circumsporozoite protein - malaria parasite (Plasmodium falciparum) (strain T4, Thail Cispecies: Plasmodium falciparum C; Species: Plasmodium falciparum C; Species: Plasmodium falciparum C; Species: Plasmodium falciparum C; Species: Plasmodium falciparum C; Accession: A54533
R; del Portillo, H.A.; Nussenzweig, R.S.; Enea, V.
R; del Portillo, H.A.; Nussenzweig, R.S.; Enea, V.
A.; Title: Circumsporozoite gene of a Plasmodium falciparum strain from Thailand.
A; Reference number: A54533
A; Accession: A54533
A; Accession: A54533
A; Status: preliminary
A; Mollocule type: DN
A; Residues: 1-424 < CDEL.
A; Cross-references: GB:M19752; NID:g160216; PIDN:AAA29555.1; PID:g160217
C; Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology F; 348-402/Domain: thrombospondin type 1 repeat homology

0; Gaps Ouery Match 100.0%; Score 75; DB 2; Length 424; Best Local Similarity 100.0%; Pred. No. 4.5e-05; Matches 13; Conservative 0; Mismatches 0; Indels

q ò

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circumsporozoite protein - malaria parasite (Plasmodium falciparum) (strain B11) (fra circumsporozoite protein - malaria parasite (Plasmodium falciparum) (species: Plasmodium falciparum) (species: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 09-Jun-2000 (spacession: A29795 Ride la Cruz, V. V.F.; Lal, A.A.; McCutchan, T.F. J. Biol. Chem. 262, 11935-11939, 1987 A; Title: Sequence variation in putative functional domains of the circumsporozoite pr A; Reference number: A92609; MUID:87308186
                                                                                                                                                                                                                                                                                                              R;Caspers, P.; Gentz, R.; Matile, H.; Pink, J.R.; Sinigaglia, F.
Mol. Biochem. Parasitol. 35, 185-190, 1989
A;Title: The circumsporozoite protein gene from NF54, a Plasmodium falciparum isolate
A;Reference number: A45527; MUID:89364998
A;Accession: A45527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:M22982; GB:J04650; NID:g160168; PIDN:AAA29527.1; PID:g160169
R;Lockyer, M.J.; Marsh, K.; Newbold, C.I.
Mol. Blochen. Parasitol. 37, 275-280, 1989
A;Title: Wild isolates of Plasmodium falloparum show extensive polymorphism in T cell A;Reference number: A60657; MUID:90114334
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jun-2000 C;Accession: S05428; A45527; I60657 R;Campbell, J.R. Nucleic Acids Res. 17, 5854, 1989 A;Title: DNA sequence of the gene encoding a Plasmodium falciparum malaria candidate A;Reference number: S05428; MUID:89345189 A;Accession: S05428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 319-336, 354-373 <LOC>
A;Residues: 319-336, 354-373 cLOC>
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
F;329-383/Domain: thrombospondin type 1 repeat homology <THR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-171 <DELA>
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
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C;Species: Plasmodium reichenowi
C;Species: Plasmodium reichenowi
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 20-Aug-1999
C;Accession: A39756
R;Lal, A.A.; Goldman, I.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 0.00028;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 69; DB 2; Length 405;
Pred. No. 0.00045;
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92.3%;
                                                                                                                                                                                                              A; Status: translation not shown A; Molecule type: DNA
                                                                                                                                                                                                                                                                    A; Residues: 1-405 <CAM>
A; Cross-references: EMBL:X15363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 90.7
Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 92.0
Best Local Similarity 92.3
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-405 <CAS>
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A39756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              circumsporozoite protein - malaria parasite (Plasmodium falciparum) (strain LE5) (fragme C; Species: Plasmodium falciparum C; Species: Plasmodium falciparum (c; Date: 18-Oct-1898) #sequence_revision 21-Jul-1995 #text_change 09-Jun-2000 C; Accession: B29795; A60657. A.; McCutchan, T.F. R. de La Cruz, V.F.; Lal, A.A.; McCutchan, T.F. J. Biol. Chem. 262, 11935-11939, 1987 A. fritle: Sequence variation in putative functional domains of the circumsporozoite prote A; Reference number: A92609; MuID:87308186
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                                                                                                                                                                                                                                          circumsporozoite protein - malaria paraşite (Plasmodium falciparum) (strain Wellcome) C;Species: Plasmodium falciparum falciparum (C;Species: Plasmodium falciparum falciparum (C;Species: Plasmodium falciparum 12;Species: 28-Oct-1994 #text_change 09-Jun-2000 C;Scecession: A54529 R:Lockyer, M.J.; Schwarz, R.T. Mol. Biochem. Parasitol. 22, 101-108, 1987 Mol. Biochem. Parasitol. 22, 101-108, 1987 A;Title: Strain variation in the circumsporozoite protein gene of Plasmodium falciparum. A;Reference number: A54529; MuID:87115616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate NF54) C;Species: Plasmodium falciparum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA A;Residues: 1-442 <LOC>
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pred. No. 0.00021;
0; Mismatches 1; Indels
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92.3%;
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Best Local Similarity 92...
Local 12; Conservative
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Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                109 KHKKLKQPGDGNP 121
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                                                                      1 KHKKLKQPGDGNP 13
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A.Molecule type: mRNA
A.Residues: 1-304 <EVA>
A.Residues: 1-304 <EVA>
A.Cross-references: GB:Md2009; NID:g212628; PIDN:AAA49055.1; PID:g212629
A.Cross-references: GB:Md2009; NID:g212628; PIDN:AAA49055.1; PID:g212629
C.Superfamily: transcription factor GATA-1; GATA-type zinc finger homology
C.Keywords: DNA binding; nucleus; transcription factor; transcription regulation; zin
F:107-1160/Domain: GATA-type zinc finger homology <GZF1>
F:101-134/Megion: zinc finger GATA motif
F:161-214/Domain: GATA-type zinc finger homology <GZF2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 4
A;Introns: 18/2; 75/3; 119/2; 350/3; 475/2; 487/3; 521/2; 601/3; 641/3; 749/2; 870/1
                                                                                                                                                                                                                                  N.Alternate names: transcription factor Eryfl
C; Species: Gallus gallus (chicken)
C; Date: 29-Dec-1989 #sequence_revision 29-Dec-1989 #text_change 26-Aug-1999
C; Date: 29-Ber 1989 #sequence_revision 29-Dec-1989 #text_change 26-Aug-1999
C; Accession: A32993
R; Evans, T.; Pelsenfeld, G.
Cell 56, 877-885, 1989
A; Title: The erythroid-specific transcription factor Eryfl: a new finger protein.
A; Reference number: A32993; MUID:89376538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted to the EMBL Data Library, February 1996
A.Reference number: 21899
A.Accession: T18637
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-944 <WIL>
A.Kolecule streferences: EMBL:Z69634; PIDN:CAA93451.1; GSPDB:GN00022; CESP:B0001.2
A.Experimental source: clone B0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18627
R;Sims, M.
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29;
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Pred. No.
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61.5%; Pred. No.
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72.78;
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Best Local Similarity 72.73
انتخاص 8; Conservative
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309 KHRKLFQAGDG 319
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Matches 8; Conserv
                                                              1 :: [|| [||
79 HSRIGQPGGGNP
                                   2 HKKLKQPGDGNP
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J. Biol. Chem. 266, 6686-6689, 1991
A;Title: Circumsporozoite protein gene from Plasmodium reichenowi, a chimpanzee malaria
A;Reference number: A39756; MUID:91201303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guyader, M.; Alizon, M.; Daniel, M.D.; Desrosiers, R.C.; Tiollais, P.
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1987
C;Superfamily: AIDS vpr protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Chakrabarti, L.; Guyader, M.; Alizon, M.; Daniel, M.D.; Desrosiers, R.C.; Tiollais, Nature 328, 543-547, 1987
A:Title: Sequence of simian immunodeficiency virus from macaque and its relationship A;Reference number: A28887; MUID:87287230
A;Accession: E28887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Hahn, B.H.; Kong, L.I.; Lee, S.W.; Kumar, P.; Taylor, M.E.; Arya, S.K.; Shaw, G.M. Nature 300, 184-186, 1987
A;Title: Relation of HTLV-4 to simian and human immunodeficiency-associated viruses. A;Reference number: S03065
A;Reference number: S03067
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                                                                                                                             A; Molecule Lype: DNA
A; Residues: 1-388 <-LALD
A; Cross references: GB: M60972; NID: q160228; PIDN: AAA29561.1; PID: q160229
C; Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
F; 312-366/Domain: thrombospondin type 1 repeat homology <-THR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Wolecule type: DNA A;Residues: 1-97 <HAH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene R protein - human T-cell lymphotropic virus type 4, HTLV-4
C;Species: human T-cell lymphotropic virus type 4, HTLV-4
C;Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N.Alternate names: orf-R protein
C.Species: similan immunodeficiency virus, SIV
C.Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
C.Accession: E28887
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                                                                                                                                                                                                                                                                                                                          Score 51; DB 2; Length 388;
Pred. No. 0.51;
                                                                                                                                                                                                                                                                                                                                                                              2; Indels
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0.91;
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Pred. No. 0.91
2; Mismatches
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58.3%;
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75.0%;
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58.3%;
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Best Local Similarity 75.0
Matches 9; Conservative
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Best Local Similarity 58.3
Matches 7; Conservative
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 KHNKLKQPGNDN 120
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79 HSRIGQPGGGNP 90
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C;Superfamily: AIDS vpr
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                                                                                                       A; Status: preliminary
                                                                                 A; Accession: A39756
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A; Molecule type: DNA
A; Residues: 1-367 <ARNY
A; Cross-references: GB:M20670; GB:J04090; NID:g160183; PIDN:AAA29534.1; PID:g552194
C; Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
E;292-345/Domain: thrombospondin type 1 repeat homology <THR1>
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56.2%; Pred. No. 20;
:ive 1; Mismatches
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Job time: 647 sec
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Best Local Similarity 56.2.
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Best Local Similarity
Matches 9; Conserv
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C; Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 17-Mar-1999
C; Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 17-Mar-1999
C; Accession. 329319; A44187, Welsh, J.A.; McCutchan, T.F.
S; de la Cruz, V.F.; Lal, A.A.; Welsh, J.A.; McCutchan, T.F.
J. Biol. Chem. 262, 6464-6467, 1987
A; Title: Evolution of the immunodominant domain of the circumsporozoite protein gene frc
A; Reference number: A29319; MUID:87194878
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CiSpecies: Thiobacillus ferrooxidans
CiSpace: OS-May-2000
CiSpecies: The good Esquence_revision 05-May-2000
CiSpace: OS-May-2000
Cispace: OS-May-
                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-179 <HBI>
A;Cross-references: GB:AE004265; GB:AE003852; NID:g9656424; PIDN:AAF95040.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype E1 Tor
C;Genetics:
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A;Residues: 1-343 <DEL>
R;McCutchan, T.F.; Lal, A.A.; de la Cruz, V.F.; Miller, L.H.; Maloy, W.L.; Charoenvit,
Science 230, 1381-1383, 1985
                                                R.J.
C;Accession: B$2143
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, J.R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
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A; Cross-references: GB:U81808; GB:L75931; NID:q1750277; PIDN:AAB41628.1; PID:g1750280
A; Experimental source: strain ATCC 33020
                                                                                                                                                                                                  A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Pred. No. 45;
1; Mismatches
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C;Superfamily: Escherichia coli ycfP protein
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70.0%;
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Best Local Similarity 58.3%;
Matches 7; Conservative
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Best Local Similarity 70.0°
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C;Keywords: oxidoreductase
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51 HKAIEQSGDPNP 62
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301 HRKSDQPGDG 310
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                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
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Length 367;

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A; Title: Sequence of the immunodominant epitope for the surface protein on sporozoite A; Reference number: A44187; MUID:86070222
A; Accession: A44187
A; Accession: A44187
A; Molecule type: DNA
A; Residues: 1-98 < MCC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Arnot, D.E.; Barnwell, J.W.; Stewart, M.J.
Proc. Natl. Acad. Sci. U.S.A. 85, 8102-8106, 1988
A;Title: Does biased gene conversion influence polymorphism in the circumsporozoite
A;Reference number: A32068; MUID:89042133
                                                                                                                                                                                         A;Cross-references: GB:J02751
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
F;268-321/Domain: thrombospondin type 1 repeat homology <THR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  circumsporozoite protein - Plasmodium vivax (strain North Korean) (fragment)
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C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 20-Aug-1999
C;Accession: A32068
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Pred. No. 19;
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56.2%;
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A company

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CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper 6 Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Sequence 12, Appl
Patent No. 5178861
Sequence 13, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 5, Appli
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2.197 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                      January 29, 2002, 10:24:02
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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1 KHKKLKQPGDGNP 13
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Maximum DB seq length: 200000000
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                          Run on:
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Sequence 21, Appl
Sequence 21, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 4, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 59, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: VERGARA, ULISES; RUIZ, ANDRES; FERREIRA, ARTURO;
NUSSENGWEIG, RUTH S.; NUSSENGWEIG, VICTOR N.
TITLE OF INVENTION: CROSS-REACTIVE AND PROTECTIVE EPITOPES
OF CIRCUMPOROZOITE PROTEINS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,241
FILING DATE: 22-01N-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 115,544
FILING DATE: 26-07-1987
FILING DATE: 26-07-1987
FILING DATE: 12-SEP-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Jessell, Thomas M. and Avihu Klar
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 75; DB 6; I
llarity 100.0%; Pred. No. 2.4e-05;
Conservative 0; Mismatches 0;
US-08-462-679-21
US-08-466-210A-21
US-08-467-147A-21
US-08-469-014-21
PCT-US93-10506A-21
PCT-US93-10506-21
US-08-188-582-16
US-08-646-715-16
US-08-045-806-4
US-08-366-051B-4
US-08-227-536-2
                                                                                                                                                                                                                                                                                            US-08-450-257-59
US-08-450-246-59
US-08-450-098-59
US-08-451-233-59
US-08-450-236-59
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Length 232;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
: SEED and BERRY
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                      Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43; DB 3;
Pred. No. 9.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41.5; DE
Pred. No. 28;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Rosenman, Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 481112.405C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/175,112
FILING DATE: 30-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 754,645
FILING DATE: 9-JUL-1985
APPLICATION NUMBER: 115,634
FILING DATE: 26-OCT-1987
APPLICATION NUMBER: 649,903
FILING DATE: 12-SEP-1984
                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,271 FILING DATE: 15-SEP-1997 CLASSIFICATION: 424
                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.3%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 56.2'
Conservative
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Best Local Similarity 61.5
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-937-271-22
                                                                                          ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KHKKLKQPGDGNP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington
                                      Seattle
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                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO:7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
5171843-9
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Best Local Similarity 100.0%; Score 75; DB 1; Length 412;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Pacent No. 5178861
; Pacent No. 5178861
; APPLICANT: VERGARA, ULISES; RUIZ, ANDRES; FERREIRA, ARTURO; NUSSENZWEIG, VICTOR N.
; NUSSENZWEIG, RUTH S.; NUSSENZWEIG, VICTOR N.
; TITLE OF INVENTION: CROSS-REACTIVE AND PROTECTIVE EPITOPES
; OF CIRCUMPOROZOITE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.7%; Score 56; DB 6; Length 13; 100.0%; Pred. No. 0.011; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22, Application US/08937271
Sequence 22, Application US/08937271
Fatent No. 6063386
GENERAL INFORMATION:
APPLICANT: Lederer, James B.
APPLICANT: Lederer, James B.
TITLE OF INVENTION: RECOMBINANT MULTIVALENT M PROTEIN
TITLE OF INVENTION: ACCINE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
      PatentIn Release #1.0, Version #1.30
                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,288B
FILING DATE: January 5, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
TELEDHONE: (212) 278-0400
TELEPHONE: (212) 391-0526
TELESA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 18
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,241
FILING DATE: 22-JUN-1989
PRIOR APPLICATION NUMBER: 115,634
FILING DATE: 26-CT-1987
APPLICATION NUMBER: 649,903
                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 12-SEP-1984
                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 74.7
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: peptide US-08-313-288B-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 KHKKLKQPGDGNP 121
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                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 13
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US-08-937-271-22
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5178861-17
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us-09-763-397a-5.rai

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ENZYME PARTICIPATING IN C-TERMINAL
AMIDATION, AND METHOD OF PREPARING SAME AND USE THEREOF
21
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53.8%; Pred. No. 2e+02;
tive 2; Mismatches 4; Indels
              TITLE OF INVENTION: EMAINE FAMILITY IN CITEMALM TITLE OF INVENTION: AMIDATION, AND METHOD OF PREPARING NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: Wagner, Cantor, Mueller & Player, P.C.
STREET: 1233 20th Street, N.W.
CITY: Washington
STATE: D.C.
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036 4918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/070,301
FILING DATE: 24-MAY 1991
CLASSIFICATION NUMBER: JP 1-209687
FILING DATE: 15-AUG-1989
PRIOR APPLICATION NUMBER: JP 1-181933
FILING DATE: 26-MAR-1990
PRIOR APPLICATION NUMBER: JP 2-76331
FILING DATE: 24-MR-1990
PRIOR APPLICATION NUMBER: JP 2-106412
FILING DATE: 24-MR-1990
PRIOR APPLICATION NUMBER: JP 2-106412
FILING DATE: 24-MR-1990
PRIOR APPLICATION NUMBER: JP 2-106412
FILING DATE: 24-MR-1990
PRIOR APPLICATION NUMBER: JP 2-205475
FILING DATE: 24-MR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-450-22830
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Patent No. 5871995
GENERAL INFORMATION
APPLICANT: IIDA, Toshio
APPLICANT: KAMINUMA, Toshihiko
APPLICANT: FUSE, Yuka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: P-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-040
TELEFAX: (202) 835-0605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAJIMA, Masahiro
YANAGI, Mitsuo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 440706
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OKAMOTO, Hiroshi
KISHIMOTO, Jiro
IFUKU, Ohji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1020 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Player, William E. REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 53.3
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | | :|:|| | |
| 899 KQKLIKEPGSGVP 911
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-070-301-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: VERGARA, ULISES; RUIZ, ANDRES; FERREIRA, ARTURO; NUSSENZWEIG, RUTH S.; NUSSENZWEIG, VICTOR N.
TITLE OF INVENTION: CROSS-REACTIVE AND PROTECTIVE EPITOPES; OC CIRCUMPOROZOITE PROTEINS
NUMBER OF SEQUENCES: 18
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/370,241
FILING DATE: 22-010*-1989
PRIOR APPLICATION NUMBER: 115,634
FILING DATE: 26-07-1987
PFLING DATE: 26-07-1987
FILING DATE: 12-SEP-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 6; Length 378;
    APPLICANT: NUSSENZWEIG, VICTOR TITLE OF INVENTION: IMMUNOGENIC POLYPEPTIDE AND METHOD FOR PURIFYING IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.7%; Score 41; DB 6; Length 27; 70.0%; Pred. No. 4.2; 1.4e 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41.5; D
Pred. No. 45;
1; Mismatches
                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/175,112
FILING DATE: 30-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 754,645
FILING DATE: 9-JUL-1985
APPLICATION NUMBER: 115,634
FILING DATE: 26-07-1987
APPLICATION NUMBER: 649,903
FILING DATE: 12-SEP-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KAMINUMA, TOSHIO
APPLICANT: KAMINUMA, TOSHIOKO
APPLICANT: FUSE, YUKE
APPLICANT: TAJIMA, MASAHIO
APPLICANT: YANKGI, MILSUO
APPLICANT: OKAMOTO, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-070-301-3

Sequence 3, Application US/08070301

Patent No. 5871995

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAJIMA, Masahiro
YANAGI, Mitsuo
OKAMOTO, Hiroshi
KISHIMOTO, Jiro
IFUKU, Ohji
KATO, Ichiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 55.3
Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : |||||| || || 89 RENKLKQPGDRADGQP 104
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Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                           NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 KLKQPGDGNP 13
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5178861-4
;Patent No. 5178861
;Patent No. 5171843
                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; SEQ ID NO:4:
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APPLICANT:
APPLICANT:
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Sequence 10. 572351
Sequence IV. Application US/08318856A
Patent No. 5972351
GENERAL INFORMATION:
APPLICANT: Adrian V.S. Hill, et al.
TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-
TITLE OF INVENTION: RESTRICTED CTL EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAGE
TITLE OF INVENTION: ANTIGENS (AS AMENDED)
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb
~MEDIUM TYPE: IBM PC Compatible
                                                                                                                                                                                                    E: Floppy disk, 3.5 inch, 1.44 mb
IBM PC compatible
                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 2;
                                                                                                                                                                                                                                                                                                                FILING DATE: October 3, 1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 08 068.8
FILING DATE: APPLICATION NUMBER: GB 92 08 068.8
FILING DATE: APILI 3, 1992
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: GB 92 17 704.7
FILING DATE: AUGUST 20, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB93/00711
FILING DATE: APILI 5, 1993
ATTORNEY/AGENT INPORMATION:
NAME: Lee Cheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 4.7
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 263-PPIR1577US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPorfect 5.1+
CURRENT APPLICATION DATA:
FILING DATE: October 3, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 amino acid residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (202) 721-8200
TELEFAX: (202) 721-8250
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WordPerfect 5
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Best Local Similarity 100.0
Local 6; Conservative
                                                                                                                ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Flore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: WordPer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington STATE: D.C.
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                              Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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Patent No. 5972351
GENERAL INFORMATION:
APPLICANT: Adrian V.S. Hill, et al.
APPLICANT: Adrian V.S. Hill, et al.
TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-
TITLE OF INVENTION: RESTRICTED CTL EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAGE
TITLE OF INVENTION: ANTIGENS (AS AMENDED)
                          TITLE OF INVENTION: ENZYME PARTICIPATING IN C-TERMINAL TITLE OF INVENTION: AMIDATION, AND METHOD OF PREPARING SAME AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
APPLICATION NUMBER: US/08/070,301
FILING DATE: 12-AMA-1991
CLASSIFICATION NUMBER: US 1999
PRIOR APPLICATION NUMBER: JP 1-181933
FILING DATE: 31-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-76331
FILING DATE: 26-WAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 2-106412
FILING DATE: 26-WAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 2-106412
FILING DATE: 26-WAR-1990
PRIOR APPLICATION NUMBER: US 2-106412
FILING DATE: 22-WAR-1990
PRIOR APPLICATION NUMBER: PD 2-205475
FILING DATE: 100-2-MG-1990
ATPONEY/AGENT INFORMATION:
WANNEY: NUMBER: 02-AMG-1990
ATPONEY/AGENT INFORMATION:
WANNEY: NUMBER: 02-AMG-1990
ATPONEY/AGENT INFORMATION:
WANNEY: MANNEY: 102-AMG-1990
ATPONEY/AGENT INFORMATION:
                                                                                                                        ADDRESSEE: Wegner, Cantor, Mueller & Player, P.C. STREET: 1233 20th Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB 2;
Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Player, William E., REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: P-450-22830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202) 887-040
TELEFAX: (202) 835-0605
TELEEX: 440706
INFOREMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.0%;
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 53.8
Matches 7; Conservative
     KATO, Ichiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | | :|:|| | | 867 KQKLVKEPGSGVP 879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Bovine
                                                                                                                                                                                                                               COUNTRY: U.S.A. ZIP: 20036-8218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-08-318-856A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-070-301-14
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Gaps

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APPLICANT: Morin, Patrice
APPLICANT: Morin, Patrice
APPLICANT: Vogelstein, Bert
APPLICANT: Sparks, Andrew
TITLE OF INVENTION: Beta Catenin, TCF-4, and APC
TITLE OF INVENTION: Interact to Prevent Cancer
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FSSLESD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,687A
                                                   1107.05064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1107.05064
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STREET: 1001 G Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/821,355
FILING DATE: 20-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32,145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 5, Application US/09003687A
; Patent No. 5998600
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32,145
REFERENCE/DOCKET NUMBER: 1107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELER: 97430 BMB UT
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 442 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 1107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 97430 BMB UT
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 442 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clevers, Hans
Korinek, Vladimir
                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: No. 5851775e
US-08-821-355A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 49.3
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Barker, Nick APPLICANT: Clevers, Hans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | |: ||||: |
| 405 KRKRDKQPGETN 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KHKKLKQPGDGN 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-003-687A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.3%; Score 37; DB 2; Length 9; 100.0%; Pred. No. 1.6e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Morin, Patrice
APPLICANT: Kinzler, Kenneth
APPLICANT: Kinzler, Kenneth
APPLICANT: Vogelstein, Bert
APPLICANT: Sparks, Andrew
TITLE OF INVENTION: Interact to Prevent Cancer
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: DISKetter
COMPUTER: IBM Compatible
COPERATING SYSTEM: DOS
SOFTWARE: FastESO for Windows Version 2.0
CURRIN APPLICATION DATA:
APPLICATION NUMBER: US/08/821,355A
FILING DATE: 20-MAR-1997
CLASSIFCATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                  PRILING DATE: October 3, 1994
PRIOR PAPELICATION NUMBER: 05008/318, 856A
PRIOR PAPELICATION DATA: 1994
APPLICATION NUMBER: GB 92 08 068.8
FILING DATE: April 3, 1992
PRIOR APPLICATION DATA: APPLICATION DATE: ABPLICATION NUMBER: GB 92 17 704.7
FILING DATE: August 20, 1992
PRIOR PAPLICATION NUMBER: WO PCT/GB93/00711
APPLICATION NUMBER: WO PCT/GB93/00711
APPLICATION NUMBER: 40, 949
REGISTRATION NUMBER: 40, 949
REGISTRATION NUMBER: 40, 949
REFERENCE/DOCKET NUMBER: 263-PPIR1577US
TELEPONMUNICATION INFORMATION: TELEPHONE: (202) 721-8200
INFORMATION POR SEQ 1D NO: 14: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-821-355A-5; Sequence 5, Application US/08821355A; Patent No. 5851775; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 9 amino acid residues TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Barker, Nick
APPLICANT: Clevers, Hans
APPLICANT: Korinek, Vladimir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 49.3
Best Local Similarity 100.
Matches 7; Conservative
      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington
STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KHKKLKQ 7
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APPLICANT: He, Tong-Chuan
APPLICANT: He, Tong-Chuan
APPLICANT: Kinzler, Kenneth
APPLICANT: Kinzler, Kenneth
APPLICANT: VOGELstein, Bert
TITLE OF INVENTION: Berea Catenin, TCF-4, and APC Interact to
TITLE OF INVENTION: Prevent Cancer
FILE REFERENCE: 1107.75741
CURRENT APPLICATION NUMBER: US/09/136,605A
CURRENT FILING DATE: 1998-08-20
EARLIER PILICATION NUMBER: 08/821,355
EARLIER FILING DATE: 1999-08-20
EARLIER FILING DATE: 1998-01-06
BARLIER FILING DATE: 1998-01-06
MUMBER FILING DATE: 1998-01-06
MUMBER FILING DATE: 1998-01-06
MUMBER FILING DATE: 1998-01-06
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                                                                                                         Score 37; DB 2; Length 442;
Pred. No. 2.5e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49.3%; Score 37; DB 4; Length 442
58.3%; Pred. No. 2.5e+02;
Live 2; Mismatches 3; Indels
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APPLICANT: MILLER, WALTER L.

APPLICANT: MILLER, WALTER L.

APPLICANT: BLACK, STEPHEN M.

APPLICANT: BLACK, STEPHEN M.

TITLE OF INVENTION: CHOLESTEROL DISPOSAL FUSION ENZYMES

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM STREET: FIVE PALO ALTO SQUARE CITY: PALO ALTO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/075,193
                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09136605A
Patent No. 6140052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-075-193-2
; Sequence 2, Application US/08075193
; Patent No. 5547868
; TOPOLOGY: linear ,
; MOLECULE TYPE: No. 5998600e
US-09-003-687A-5
                                                                                                              49.3%;
58.3%;
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Best Local Similarity 58.5.
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Best Local Similarity 58.3
Matches 7; Conservative
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405 KRKRDKQPGETN 416
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ORGANISM: Homo sapiens
US-09-136-605-5
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405 KRKRDKQPGETN 416
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OPSG_CHICK
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CSP_PLACH
AND_HUMAN
RRPL_DUGBV
VPR_HV2D2
C141_MYCTU
AMD_BOVIN
HXD1_MOUSE
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P19021 homo sapien
Q66431 dugbe virus
P15837 human immun
P18632 mycobacteri
P10731 bos taurus
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Query Match
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y is copyright. It is nostitute of Bioinforms rematics Institute. The institutions as long attement is not removed license@ibrsib.ch). Cromsprzoite. TSP1. Cromsprzoite. TSP1. Repeat; Signal. PROBABLE CIRCUMSPOROZ. 12 CIRCUMSPOROZ. 13 CIRCUMSPOROZ. 14 A A TAL	'K L ZBH 24002"	AL PRT [uen. ota	OPSD_RAJER OPSD_SCYCA OPSB_GEGGE C11A_HUMAN MOP_DESGI AMD_MOUSE VG78_BRAL5 2SSE_BRANA MPD1_YEAST OPS1_ASTFA BRN4_HUMAN BRN4_MOUSE
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Plasmodium falciparum (isolate t4 / Thailand).
Eukaryota; Alveolata; Apicomplexa; Haemosporida;
  Plasmodium falciparum Eukaryota; Alveolata; NCBI_TaxID=5848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement entities requires a license
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del Portillo H.A., Nussenzweig R.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=5846;
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InterPro; IPR000884; TSP1.
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13; Conser
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Sporozoite; Repeat; Signal.

1 16
PROBABLE.
17 424
CIRCUMSPOROZOITE PROTEIN.
17 424
123 300
45 X 4 AA TANDEM REPEATS
17 4AA: 45610 MW; 710AB14238786CD9 CRC64;
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                       Apicomplexa; Haemosporida; Plasmodium.
                                            (isolate Wellcome)
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                                                                                                                                                                                                                                                                                                                                                                                                                Score 75; DB 1;
Pred. No. 1.4e-05;
                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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RESULT 4
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Best Local :
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P05691;
01-NOV-1988
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Malaria;
SIGNAL
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the European Bioinformatics Institute. There as
use by non-profit institutions as long as i
modified and this statement is not removed. Us
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SEQUENCE FROM N.A.
MEDLINE=87115616; PubMed=3543671;
                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum
Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M15505; AAA29554.1; PIR; A54529; A54529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                              01-NOV-1988 (Rel.
01-NOV-1988 (Rel.
01-FEB-1994 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Strain variation in the circumsporozoite protein falciparum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lockyer M.J., Schwarz
                                         <del>:</del>
                                                                                                                                                                                       circumsporozoite protein of Plasmodium
                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=87308186; PubMcd=2442154;
Partial Cruz V.F., Lal A.A., McCutchan T.F.;
1a Cruz V.F., Lal A.A. mccutchan T.F.;
"Sequence variation in putative functional domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00090;
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InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003067;
                                                                                                                                                                  vaccine development."
                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=5840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119
                                                                                                                                                Biol.
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                                BIO1. Chem. 262:11935-11939(1987).
FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS SURFACE ANTIGEN ON THE SPOROZOITE (THE INF. MALARIA PARASITE THAT IS TRANSMITTED FROM VERTEBRATE HOST).
MISCELLANEOUS: THE C-TERMINAL REGION IS PROME THAT IS THE CONTROL OF THE CONTROL
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ANCHORING THE PROTEIN TO THE CELL WOULD BE THE SURFACE ANTIGEN OF TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KHKKLKQPGDGNP
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SM00209; TSP1; 1.
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13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                        09, Created)
09, Last sequence up
28, Last annotation
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                                         THE C-TERMINAL REGION IS PROBABLY USED FOR
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Apicomplexa;
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47 X 4 AA TANDEM REPEATS;
BD57A9A152B85E03 CRC64;
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Pred. No. 1.4
); Mismatches
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                                                                                                                                                                                                                                                                                                                                      Haemosporida; Plasmodium
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                                                                                   INFECTIVE
ROM THE MOS
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                     THE REPEAT SEQUENCES
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L outstation -
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Best Local Similarity
Matches 12; Conser
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P19597; Q25798;
01-FEB-1991 (Rel. 17, Created)
30-MAY-2000 (Rel. 39, Last sequence updat
20-AUG-2001 (Rel. 40, Last annotation upd
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                "DNA sequence of the gene encoding a Plasmodium candidate vaccine antigen.";
Nucleic Acids Res. 17:5854-5854(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M17802; AAA29538.1; -. Malaria; Sporozoite; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
                                                                                                                                  MEDLINE-89364998; PubMed-2671723;
Caspers P., Gentz R., Mattle H., Pink J.R.
"The circumsporozoite protein gene from Ni
                                                                                                                                                                                                                                       Thomas A.W., Bagar Hackett C.S.;
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-92155298; PubMed-1346766;
                                                                                                                                                                                                                                                                                                                            Campbell
                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                               Davis J.R., Cortese
                                                                                                                                                                                                                                                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                                           REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                        Campbell J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-89345189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=5843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum
Eukaryota; Alveolata;
                                                                                                               isolate used in malaria vaccine trials.";
Mol. Biochem. Parasitol. 35:185-190(1989)
                                                                                                                                                                                                              "Plasmodium falciparum:
infectivity of a cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
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                                               Blochem. Parasitol. 35:185-190(1307).
FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOM SUFFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO VERTEBRATE HOST).
           MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAU WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.

SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
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315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                            N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,
                                                                                                                                                                                                   74:159-168(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=2668895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270
315
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                                                                                                                                                                                                                                                   S., Cochran M.A.,
                                                                                                                                                                                                                                                   J.F., Herrington D.A., Murphy S., Cochran M.A., Thanassi J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.0%;
92.3%;
                                                                                                                                                                                                                                                                                                                 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (isolate NF54
                                                                                                                                                                                                              in vitro characterization line.";
                                                                                                                                                                                                                                                                                                                 the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
Pred.
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4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemosporida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA TANDEM REPEATS OF P-N-A-N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
0.00011;
                                                                                                                                     .R., Sinigaglia F.;
NF54, a Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₽
                                                                                                  THE IMMUNODOMINANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          falciparum malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                           and human
                                                                                                                                                                                                                                                            J.R., Clyde D.F.,
                                                                                                                                                                                                                                                    Levine M.M.
                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           restrictions
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                                                   FOR
                                                                         TO OF
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                                                                                                                                     falciparum
                                     SEQUENCES
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                                                                           THE
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _PLARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
CONFLICT
SEQUENCE
                                                                                                                                                                                                          "Circumsporozoite protein gene from Plasmodium reichenowi, a chimpanzee malaria parasite evolutionarily related to the human malaria parasite Plasmodium falciparum.";

J. Biol. Chem. 266:6686-6689(1991).

-i- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE VERTEBRATE HOST).
                                                                                                                                                                                                                                                                                                                                                                                                                       P26694.

01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updat
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
                                                                   the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X15363; CAA33421.1; -.
EMBL; M83886; AAA29521.1; -.
EMBL; M22982; AAA29527.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rik; A43327; A43327.
InterPro; IPR001067; Crcmsprzoite
InterPro; IPR000884; TSP1.
Pfam; PF00090; tsp_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                        MEDLINE=91201303; PubMed=2016283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CSP_PLARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR01303; CRCMS
SMART; SM00209; TSP1;
             EMBL; M60972; AAA29561.1;
                                                                                                               between
                                                                                                                                                                                                                                                                                                                         Lal A.A., Goldman I.F.;
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=5854;
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium reichenowi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KHKKLKQPGDGNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                     MISCELLANDOUS: THE C-TERMINAL REGION IS PROBABLY USED ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT WOULD BE THE SURFACE ANTICEN OF THE ORGANISM.
SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S05428; S05428.
A45527; A45527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KHKKLKQPADGNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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194
397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRCMSPRZOITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102
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397
272
194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42646 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat;
                                                                                                                                                                                                                                                                                                                                                                                              Apicomplexa;
                                                      agreement (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal.
PROBABLE.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CIRCUMSPOROZOITE PROTEIN.
43 X 4 AA TANDEM REPEATS
A -> ANPNANPNA (IN REF. 4
; 9E81146F59EBCEA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No ;
                                                                                                                                                                                                                                                                                                                                                                                              Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  388
                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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0.00014;
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                                                                                                                                                                                  THE REPEAT SEQUENCES
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                                                                      and
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SORRER REPORT OF THE PROPERTY 
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Query Match
Best Local S
Matches 8
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
GANTICEN FAMILY C 1 PROTEIN (PROSTATE-ASSOCIATED (PAGE-4) (PAGE-1) (JM27) (GAGE-9).
GAGEC1 OR PAGE4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formatical content is modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mamumalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGC1_HUMAN
060829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003067; Crcmsprzoite
InterPro; IPR003084; TSP1.
Pfam; PF00090; tsp_1; 1
PRINTS; PR01303; CRCMSPRZOITE.
                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=98393718; PubMed=9724777;
                                                                                                                                                                                                                                              or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (APR-1998) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strom T.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brinkmann U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART;
                                                                                                                                                                                                                                                                   entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "PAGE-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KHKKLKQPGDGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: UNKNOWN.

TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN NORMAL MALE AFFEMALE REPRODUCTIVE TISSUES, PROSTATE, TESTIS, FALLOPIAN TUBE.
                                                                                                                                                                                                                                                                                                                                                                                                                     UTERUS, AND PLACENTA, AS WELL AS IN PROSTATE CANCER, AND UTERINE CANCER.
SIMILARITY: BELONGS TO THE GAGE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KHNKLKQPGNDN 120
                                                                                                                                   300287;
                                                                                                                                                 AF275258; AAF88037.1; -. AJ005894; CAA06751.1; -. AF238380; AAF62541.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; PR01303; CRCMS
SM00209; TSP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . Similarity
9; Conserv
  Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sporozoite; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an X chromosome-linked GAGE-like gene that
nd neoplastic prostate, testis, and uterus.'
tl. Acad. Sci. U.S.A. 95:10757-10762(1998).
                                                                                                                                                                                                                                         requires a license agreement (See an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17
120
388 AA;
                                                                                                            102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nyakatura G., Hellebrand H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vasmatzis G.,
                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12
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267 6
42245 MW;
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                                                                                                          11153
                  62.7%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68
75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
                                                                                                            MW;
Pred. No. 0.22
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal.
PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CIRCUMSPOROZOITE PROTEIN.
62 X 4 AA TANDEM REPEATS OF N-A-N-P.
; C031EEFBE2E35604 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 51; DB 1; Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                          CESD07AFBF73301B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yerushalmi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102
                                         DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drescher B., Rosenthal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hominidae;
                                         1;
                                                                                                                                                                                                                                                              http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uterus.";
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RESULT 8
VPR_SIVM1
ID VPR SAC P0599
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P05957;
01-NOV-1988
01-NOV-1988
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P05958;
01-NOV-1988
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01-OCT-1989
VPR PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we use by non-profit institutions as long as its content is in no we
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Simian immunodeficiency virus (K6W isolate) Viruses; Retroid viruses; Retroviridae; Len
SEQUENCE FROM N.A.

MEDLLINE=87287230; PubMed=3649576;

Chakrabarti L., Guyader M., Alizon M.

Tiollais P., Sonigo P.;

"Sequence of simian immunodeficiency
relationship to other human and simia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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(R ORF PROTEIN).
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(R ORF PROTEIN).
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01-AUG-1990 (Rel. 15, Las
20-AUG-2001 (Rel. 40, Las
ERYTHROID TRANSCRIPTION F
PROTEIN) (NF-ElA).
                                                       umichinski J.G., Clore G.M., Schaad O., Appella E., Stahl S.J., Gronenborn A.M.;
"NMR structure of a specific DNA companion of GATA-1.";
Science 261.430
STRUCTURE BY NMR OF 158-223.
MEDLINE-97448676; PubMed-9303001;
Tjandra N., Omichinski J.G., Gronenborn A.M.,
"Use of dipolar 1H-15N and 1H-13C couplings in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P17678;
                                                                                                                                                                 "Activity and tissue-specific NF-El multigene family.";
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                                                                                                                                                          Genes Dev.
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                           Archosauria;
                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
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an email to license@isb-sib.ch):
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InterPro; IPR000679; ZnF_GATA.
InterPro; IPR001164; Znf_GCS.
Pfam; PF00320; GATA; 2.
PRINTS; PR00619; GATAXNFINGER.
SMART; SM00401; ZnF_GATA; 2.
PROSITE; PS00344; GATA_ZN_FINGER_1; 2.
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PIR; A32993; A32993.

PDB; 1GAT; 31-OCT-93.

PDB; 2GAT; 28-JAN-98.

PDB; 3GAT; 28-JAN-98.

PDB; 1GAU; 31-OCT-93.

TRANSFAC; T00267; -
                                                                                            CSP_PLAVS
P13826;
01-JAN-1990
01-JAN-1990
20-AUG-2001
Plasmodium vivax (str.
Eukaryota; Alveolata;
NCBI_TaxID=5856;
                                              01-JAN-1990 (Rel. 13, Last sequence updat. 20-AUG-2001 (Rel. 40, Last annotation upd. CIRCUMSPOROZOITE PROTEIN (CS) (FRAGMENT). Plasmodium vivax (strain Salvador I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TURN
STRAND
HELIX
TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         determination of magnetically oriented macromolecules in solution at Struct. Biol. 4:732-738(1997).

-i- FUNCTION: TRANSCRIPTIONAL ACTIVATOR WHICH PROBABLY SERVES GENERAL SWITCH FACTOR FOR ERVTHROID DEVELOPMENT. IT BINDS SITES WITH THE CONSENSUS SEQUENCE (A/T)GATA(A/G) WITHIN RESIDENCE (A/T)GATA(A/G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zinc-finger;
                                                                                                                                                                                                                                                                                                             218
                                                                                                                                                                                                                                                                                                                                                           1 KHKKLKQPGDGNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACHIEVE SPECIFIC, STABLE DNA BINDING. THE FIRST FINGER IS NECESSARY ONLY FOR FULL SPECIFICITY AND STABILITY OF BINDING, WHEREAS THE SECOND ONE IS REQUIRED FOR BINDING (BY SIMILARITY). SIMILARITY: CONTAINS 2 GATA-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: ERYTHROCYTE.

DOMAIN: THE TWO FINGERS ARE FUNCTIONALLY DISTINCT AND COOPERATE ACHIEVE SPECIFIC, STABLE DNA BINDING. THE FIRST ETWON TO NECESSARY .....
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8; Conserv
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(Rel.
(Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATA_ZN_FINGER_2; 2.
GATA_ZN_FINGER_2; 2.
julation; Activator; DNA-binding; Erythrocyte;
lear protein; 3D-structure.
134
GATA-TYPE 1.
134
GATA-TYPE 2.
                                                                                              13,
13,
40,
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61.5%;
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                          Apicomplexa;
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                                                                                                                                                                                             PRT;
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                          Haemosporida;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 304;
                             Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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VDS TO DNA
REGULATORY
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RESULT 12
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Best Local S
Matches S
ARROL D. E., Barnwell J.W., Stewart M.J.;

ARROL D. E., Barnwell J.W., Stewart M.J.;

"Does biased gene conversion influence polymorphism in the circumsporozoite protein-encoding gene of Plasmodium vivax?";

Proc. Natl. Acad. Sci. U.S.A. 85:8102-8106(1988).

-i- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURPACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                                                                                                                                                     CSP_PLAVB
P08677;
01-JAN-1988
                                                                                                                                                                                                                                                                   CIRCUMSPOROZOITE PROTEIN PRECURSOR Plasmodium vivax (strain Belem). Eukaryota; Alveolata; Apicomplexa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-87194878; PubMed-2437120;
de la Cruz V.F., Lal A.A., Welsh J.A., McCutchan T.F.;
de la Cruz V.F., Lal A.A., Welsh J.A., McCutchan T.F.;
"Evolution of the immunodominant domain of the circumsporozoite
protein gene from Plasmodium vivax. Implications for vaccines.";
J. Biol. Chem. 262:6464-6467(1987).
-1- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT
SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THI
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THI
VERTEBRATE HOST).
                                                                                     MEDLINE=89042133; PubMed=3054880; Arnot D.E., Barnwell J.W., Stewar
                                                                                                                                           "Circumsporozoite protein of Plasmodium characterization of the immunodominant Science 230:815-818(1985).
                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=86044510;
                                                                                                                                                                                                                                                                                                             01-FEB-1996
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
MEDLINE-86070222; PubMed=2416057;
                                                                                                                     REVISIONS
                                                                                                                                                                                                   Arnot D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sporozoite;
                                                                                                                                                                                                                                                         NCBI_TaxID=31273;
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                                                                                                                                                                       "Circumsporozoite
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISCELLANEOUS: THE C-TERMINAL REGION IS PROI ANCHORING THE PROTEIN TO THE CELL MEMBRANE. WOULD BE THE SURFACE ANTIGEN OF THE ORGANISS SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                   RENKLKQPGDRADGQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00090; tsp_1; 1.
1; SM00209; TSP1; 1.
ETE; PS50092; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 56.
9; Conservative
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                                                                                                                                                                                                     Barnwell
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                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -DGNP
                                                                                                                                                                                                                                                                                                         06, Created)
33, Last sequence update)
40, Last annotation update)
                                                                                                                                                                                                  PubMed=2414847;
ell J.W., Tam J.
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                                                                                                                                                       of Plasmodium vivax: mmunodominant epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41.5; E
Pred. No. 7.2;
1; Mismatches
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; 308EFD5BBC15DFC3 CRC64;
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                                                                                                                                                                                                  J.P.,
                                                                                                                                                                                                                                                                   Haemosporida;
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" p., Wistar '
                                                                                                                                                                                                Nussenzweig V., Nussenzweig
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istar R. Jr.,
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                                                                                                                                                           gene
                                                                                                                                                                                                                                                                   Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 343;
                                                                                                                                                                     cloning and
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Hoffman
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Best Local S
Matches 9
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CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                  vivax-like monkey malaria parasite.";
Mol. Biochem. Parasitol. 57:177-180(1993).
-i- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE VERWINDEARS AND LOCAL.
                                                                                                                                                                                                                                                                   01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
                                                                                                                                        Goldman I.F., Qari S.H., Millet P.G., Collins "Circumsporozoite protein gene of Plasmodium vivax-like monkey malaria parasite.";
                                                                                                                                                                                                                               Plasmodium simium.
Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
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modified and this statement is not removed.
entitles requires a license agreement (See l
or send an email to license@isb-sib.ch).
                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=93149205; PubMed=8426613;
                                                                                                                                                                                                                    NCBI_TaxID=5859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00090; tsp_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A26256; OZZQAV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M11926; AAA29526.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                88
                                                                                                                                                                                                                                                                                                                                                                                                                      1 KHKKLKQPG---DGNP
                          MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY ANCHORING THE PROTEIN TO THE CELL MEMBRANE THE ROULD BE THE SURPACE ANTIGEN OF THE ORGANISM.
SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
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ANCHORING THE PROTEIN TO THE CELL MEMBRANE.
WOULD BE THE SURFACE ANTICEN OF THE ORGANISM.
SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                            VERTEBRATE HOST).
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9; Conservative
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97
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AAA29529.1; ALT_SEQ
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92; TSP1;
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378
267
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96
295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CIRCUMSPOROZOITE P
19 X 9 AA TANDEM R
G-Q-P.
G -> E (IN REF. 1)
G -> R (IN REF. 1)
E -> A (IN REF. 1)
R -> S (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41.5; E
Pred. No. 8;
1; Mismatches
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                                                                                                                                                                  Collins
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, a Plasmodium
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Best Local :
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                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sentitles.com/discourses/sentitles/
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InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
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the Euro
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Viruses; ssDNA
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                                                                                                                                                                  InterPro; IPR002621; Gemini_mov.
Pfam; PF01708; Gemini_mov; 1.
                                                                                                                                                                                                                              EMBL; M81103; AAA47947.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92188538; PubMed=1546458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssDNA vi
NCBI_TaxID=31599;
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                                                                                                       Hypothetical protein SEQUENCE 102 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         infecting monocotyledonous plants.";
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viruses; Geminiviridae; Mastrevirus.
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RY MEDLINE-95371134; PubMed-7643409;

RA KAWAMUTA S., Yokoyama S.;

RT "Paralogous origin of the rhodopsinlike opsin genes in lizards.";

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PRINTS; PR00237; GPCRHODOPSN.
PRINTS; PR00238; OPSIN.
PRINTS; PR00579; RHODOPSIN.
PROSITE; PS00337; G_PROTEIN_RECEP_F1_1;
PROSITE; PS00238; G_PROTEIN_RECEP_F1_2;
PROSITE; PS00238; OPSIN; 1.
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01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
BLUE-SENSITIVE OPSIN (BLUE PHOTORECEPTOR PIGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis
NCBI_TaxID-28377;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Photoreceptor; Re
Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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InterPro; IPR001760; Opsin.
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113
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252
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4 (POTENTIAL).
EXTRACELLULAR.
5 (POTENTIAL).
CYTOPLASMIC.
6 (POTENTIAL).
EXTRACELLULAR.
7 (POTENTIAL).
                                                                                                                                                                                                                                                   2 (POTENTIAL).
EXTRACELLULAR.
3 (POTENTIAL).
                                                                                                                                                                                         CYTOPLASMIC.
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2 (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR
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                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G-PROTEIN
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Lipoprotein; Palmitate.
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FT DOMAIN

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355

CYTOPLASMIC...) (POTENTIAL).

FT CARBOHYD

15

15

N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD

200

N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD

200

N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD

210

N-LINKED (GLCNAC...) (POTENTIAL).

FT BINDING

226

227

FT LIPID

322

322

PALMITATE (BY SIMILARITY).

FT LIPID

323

323

PALMITATE (BY SIMILARITY).

FT LIPID

323

323

PALMITATE (BY SIMILARITY).

SQ SEQUENCE

355

AA;

39983

MW;

555B671A4DE96EA6 CRC64;

Ouery Match

Best Local Similarity

87.5%;

PIEG. No. 9.1;

Matches

7;

CONSERVATIVE

1;

Mismatches

0;

Indels

0;

Gaps

0;

Qy

1 KHKKLKQP

1 KHKKLRQP

1 KHKKLRQP

1 KHKKLRQP

1 Search completed: January

29, 2002, 11:13:38

Job time: 814 sec
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Zheng C., Xie P., Chen Y.;
Molecular cloning and expression of circumsporozoite protein gene
"Molecular cloning and expression of circumsporozoite protein gene
"From Plasmodium falciparum FCC-1/HN strain in mycobacterium.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF315469; AAG37074.1;
InterPro: IPR0000884; TSP.
InterPro: IPR0000884; TSP.
Pfam; PF00090; tsp_1;
Pfam; PF00090; tsp_1;
PRINTS; PR01303; CRCMSPRZOITE.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
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Q9BPK7
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Q25212
       Query Match 100.
Best Local Similarity 100.
Matches 13; Conservative
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SEQUENCE
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Q25829
ID Q2
AC Q2
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Q76637 human immun
Q74231 human immun
Q88042 chimpanzee
Q88059 chimpanzee
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human immun
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                              version 4.5
- 2000 Compugen Ltd.
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                                                                                                                                                                        January 29, 2002, 11:12:09
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Maximum Match 100%
Listing first 45 summaries
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Q27325
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sp_bacteria:*
sp_fung1:*
sp_fung1:*
sp_human:*
sp_invertebrate:*
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Copyright (c) 1993
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sp_vertebrate:*
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sp_phage:*
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seq length: 200000000
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Perfect score:
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Maximum DB
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Query Match
Best Local Similarity 100.
Matches 13; Conservative
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Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                                                                                                                                         109 KHKKLKQPGDGNP 121
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      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=5833;
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                    STRAIN=K1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=K1;
MEDLINE=84250215; PubMed=6204383;
Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A.,
Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D.,
Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.;
"Structure of the gene encoding the immunodominant surface antigen on
the sporozolic of the human malaria parasite Plasmodium falciparum.";
Science 225:593-599(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                           Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum (isolate Kl / Thailand).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 75; DB 5; Length 416; 100.0%; Pred. No. 4.8e-05;
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                                                                                                                                                                                                                                              la Cruz V.F.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                       D3EF560B2D368DE9 CRC64;
01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            420 AA.
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                                                                                                                                                                                                                                                                                                      Jongwutiwes S., Tanabe K., Kanbara H.;
Mol. Biochem. Parasitol. 0:0-0(0).
EMBL; M83172; AAA29550.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000884; TSP1.
InterPro; IPR003067; Crcmsprzoite.
                                                                                                            STRAIN=MAD20;
MEDLINE=84250215; PubMed=6204383;
                                                                                                                                                                                                                                                                                                                                                                                                     44829 MW;
                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
           01-JUN-2001 (TrEMBLrel. 1 CIRCUMSPOROZOITE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 KHKKLKQPGDGNP 121
                                                 Plasmodium falciparum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KHKKLKQPGDGNP 13
                                                                                                                                                                                                                                                                                                                                                                                                     416 AA;
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                                                                                              SEQUENCE FROM N.A.
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                                                            Eukaryota; Alveo
NCBI_TaxID=5833;
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                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                  Length 420;
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                                                                                                                                                                                                                                    F7F70F1C4939DEA7 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                     100.0%; Score 75; DB 5; L
100.0%; Pred. No. 4.8e-05;
Micmatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        420 AA.
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Jongwutiwes S., Tanabe K., Kanbara H.; Mol. Biochem. Parasitol. 0:0-0(0). BMBL; M83174; AAA29552.1; -. InterPro; IPR000884; TSP1. InterPro; IPR003067; Crcmsprzoite. Pfam; PF00090; tsp_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jongwutiwes S., Tanabe K., Kanbara H. Mol. Biochem. Parasitol. 0:0-0(0). EMBL; M63161; AAA29574.1; -InterPro: IPR000884; TSP1. InterPro: IPR000884; TSP1. InterPro: IPR000806; TSP1. IPRINTS; PR01303; CRCMSPEZOITE. SMART; SM00209; TSP1: 1
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                                                                                                                                                     PRINTS; PR01303; ČRCMSPRZOITE.
PROSITE; PSS0092; TSP1; 1.
SMART; SM00209; TSP1; 1.
SEQUENCE 420 AA; 45318 MW;
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01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2001 (TrEMBLrel. 17,
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Gaps

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MEDLINE-84250215; PubMed-6204383;
Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A.,
Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D.,
Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.;
"Structure of the gene encoding the immunodominant surface antigen on
the sporozoite of the human malaria parasite Plasmodium falciparum.";
                 ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
: - MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
                       WOULD BE THE SURE...

R InterPro; IPR000884; TSP1.

R InterPro; IPR030867; Cromsprzoite.

R Pfam; PF00090; Lsp_1; 1.

DR PRINTS; PR01303; CRCMSPRZOITE.

DR SMART; SM0209; TSP1; 1.

KW Malaria; Repeat; Sporozoite; Signal.

- A74 CIRCUMSPOROZOITE PROPEIN.
                                                                                                                                                                                                                                                                                                                   Length 424;
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Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
EMBL; M83155; AAA29568.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                         45609 MW; BF6D0F906C664B8F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                               Score 75; DB 5; Pred. No. 4.9e-05;
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Interpro; IPR003067; Crcmsprzoite.
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3: CRCMSPRZOITE.
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Best Local Similarity 100.0%;
Matches 13; Conservative 0
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EMBL; M83152; AAA29565.1; -
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SMART; SM00209; TSP1;
SEQUENCE 432 AA; 46
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424 AA;
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SEQUENCE
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Mol. Blochem. Parasitol. 45:179-182(1991).
-!- FUNCTION: THE CIRCUMSPOROZOTTE PROTEIN IS THE IMMUNODOMINANT
SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
VERTEBRATE HOST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lockyer M.J.; "Clonal variation in the Plasmodium falciparum circumsporozoite
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01-NOV-1996 (TERBLrel. 01, Created)
01-NOV-1996 (TERBLrel. 01, Last sequence update)
01-NOV-1996 (TERBLrel. 17, Last annotation update)
01-JUN-2001 (TERBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (CS) PRECURSOR, VARIANT 2 (FRAGMENT).
                                                                                                                                                             Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
EMBL: M83169; AAA29567.1; -.
EMBL; M83149; AAA29562.1; -.
InterPro; IPR00884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
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                            Q27425 PRELIMINARY; PRT; 424 AA. 027425; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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MEDLINE-84250215; PubMed-6204383;
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MEDLINE-91270295; PubMed-2052038;
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PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
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                                                                                                                           CIRCUMSPOROZOITE PROTEIN
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Matches 13; Conserv
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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MEDLINE=84250215; PubMed=6204383;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                             Eukaryota: Alveolata; Apicomplexa: Haemosporida; Plasmodium.
NCB1_TaxID=5833;
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          Indels
                                                                                                                                                                                                                                                                                                                    Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                2CE8D9A68E11945F CRC64;
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                                                                                                                      Last sequence update)
Last annotation update)
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Pred. No. 4.9e-05;
Mismatches 0;
                                                                                           432 AA.
          Mismatches
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Mal. M83165; AAA.29543.1.;
InterPro; IPR000884; TSP1.
InterPro; IPR003067; Cremsprzoite.
Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
                                                                                                              Created)
                                                                                           PRT;
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MEDLINE-84250215; Pubmed=6204383;
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SMART; SM00209; TSP1; 1.
100.08;
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                                                                                                                                                                                                                                                                      Science 225:593-599(1984).
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                                                                                                                                       CIRCUMSPOROZÒITE PROTEIN.
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 Best Local Similarity 100.
Matches 13; Conservative
                                                                                           PRELIMINARY;
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                                       109 KHKKLKQPGDGNP 121
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                                                                                                                                                           Plasmodium falciparum
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Best Local Similarity
Matches 13; Conserv
                             KHKKLKQPGDGNP
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SEQUENCE FROM N.A.
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MEDLINE-84250215; PubMed=6204383;
Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A.,
Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D.,
Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.;
"Structure of the gene encoding the immunodominant surface antigen on
the sporozoite of the human malaria parasite Plasmodium falciparum.";
Science 225:593-599(1984).
Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A., Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D., Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.; "Structure of the gene encoding the immunodominant surface antigen on the sporozoite of the human malaria parasite Plasmodium falciparum."; Science 225:593-599(1984).
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NCBL_TaxID-5833;
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Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; M83164; AAA295421; -.
EMBL; M83163; AAA295531; -.
EMBL; M83163; AAA29576.1; -.
                                                                                                                                                                                                                                                       la Cruz V.F.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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100.0%; Pred. No. 5e-05;
iive 0; Mismatches 0;
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Jongwuliwes S., Tanabe K., Kanbara H.;
Mol. Biochem. Parasitol. 0.0-0(0).
EMBL; M83167; AAA29545.1; -
InterPro; IPR000884; TSP1.
InterPro; IPR003067; Cromsprzoite.
Pfam; PF00090; tsp_1; 1.
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InterPro; IPR000884; TSP1.
InterPro; IPR000806; Crcmsprzoite.
PRMINS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
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Best Local Similarity
Matches 13; Conserv
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Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A., Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D., Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.; "Structure of the gene encoding the immunodominant surface antigen on the sporozoite of the human malaria parasite Plasmodium falciparum."; Science 225:593-599(1984).
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EMBL; M57498, AAA63421.1; -
InterPro; IPR000884; TSP1.
InterPro; IPR0003067; Crcmsprzoite.
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Mol. Biochem. Parasitol. 45:179-182(1991).
-!- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT
SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Clonal variation in the Plasmodium falciparum circumsporozoite
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (CS) PRECURSOR, VARIANT 1 (FRAGMENT).
                                                  Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
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100.0%; Pred. No. 5.2e-05;
tive 0; Mismatches 0;
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Mol. Biochem. Parasitol. 0:0-0(0).
EMBL; M83156; AAA29569.1;
InterPro; IPR000884; TSP1.
InterPro; IPR03067; Crcmsprzoite.
PRAM: PR00090; ESP1: 1.
PRINTS; PR01303; CRCMSPRZOITE.
PROSITE; PS50092; TSP1: 1.
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                                                                                                                                                                                            MEDLINE-84250215; PubMed-6204383;
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SEQUENCE 452 AA; 48431 MW;
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PRINTS; PR01303; CRCMSPRZOITE.
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Best Local Similarity 100.
Matches 13; Conservative
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                          Plasmodium falciparum.
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Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A.,
Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D.,
Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.;
"Structure of the gene encoding the immunodominant surface antigen on
the sporozoite of the human malaria parasite Plasmodium falciparum.";
Science 225:593-599(1984).
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                               100.0%; Score 75; DB 5; Length 436; 100.0%; Pred. No. 5e-05; tive 0; Mismatches 0; Indels
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                                                                               46875 MW; F102683C5C1DC85A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               025834 PRELIMINARY; PRT; 452 AA. 025834; ILNOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) CIRCUMSPOROZOITE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 442 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-TQ/94;
Jongwutiwes S., Tanabe K., Kanbara H.;
Mol. Blochen. Parasitol. 0:0-0(0).
EMBL; M8373; AAA29551.1;
Interpro; IPR000884; TSP1.
Interpro; IPR003067; Crcmsprzoite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00090; tsp.1; 1. PRINTS; PR01303; CRCMSPRZOITE. SMART; SM00209; TSP1; 1. SEQUENCE 442 A.
PRINTS; PR01303; CRCMSPRZOITE
                          PROSITE; PS50092; TSP1; 1.
                                                                                                                                                      Ouery Match
Best Local Similarity 100.
Matches 13, Conservative
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Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                            109 KHKKLKQPGDGNP 121
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                                                     SMART; SM00209; TSP1; SEQUENCE 436 AA; 46
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01-NOV-1996
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Novembre F.J., Hirsch V.M., McClure H.M., Fultz P.N., Johnson P.R.;
"SIV from stump-tailed macaques: molecular characterization of a
highly transmissible primate lentivirus.";
Virology 186:783-787(1992).
EMBL; M83293; AAA91943.1; -.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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SUBMILLED A.B.
SUBMILLED (FEB-1995) to the EMBL/GenBank/DDBJ databases.
REMBL: U20969; AAA63153.1; ---
Interpro; IPR000884; TSP1. ---
R Interpro; IPR003087; Cramsprzoite.
R Pfam: PF00090; tsp_1; 1.
R PRNINTS; PR01303; GRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
SEQUENCE 408 AA: 43871 MW; A545BE517822515C CRC64;
                                                                                                                                                                                                                                                                                                                                  92.0%; Score 69; DB 5; Length 393; 92.3%; Pred. No. 0.0005; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 69; DB 5; Length 408;
Pred. No. 0.00052;
0; Mismatches 1; Indels
SMART; SM00209; TSP1; 1.
Malaria; Repeat: Sporozoite; Signal.

1 16 POTENTIAL.

1 7 > 393 CIRCUMSPOROZOITE PROTEIN.
4-RESIDUE TANDEM REPEATS.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNV-2001 (TrEMBLrel. 17, Last annotation update)
VPR PROTEIN.
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Best Local Similarity 92.3%;
Matches 12; Conservative
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Best Local Similarity
Matches 12; Conserv
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Q88146
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Pred. No. 0.62;
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InterPro; IPR000012; HIV_ORFXR.
Pfam; PF00522; VPR; I.
PRINTS; PR0044; HIVVPRPX.
PRINTS; PR0444; HIVVPRPX.
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53.8%;
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Best Local Similarity 53.8
Matches 7; Conservative
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1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/USOG_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/USOG_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
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10: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
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18: /cgn2_6/ptodata/2/paa/USOB_COMB.pep:*
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US-08-912-951-325
US-08-97-549-613
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US-09-376-330-4
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1 MKFLVNVALVFMVVYISYIYAD 22
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Sequence 25, Application US/09763397A

Sequence 25, Application US/09763397A

GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Corrcol and Prevention
APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A.
APPLICANT: Passain, Ya
APPLICANT: Passain, Ya
APPLICANT: Passain, NA
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APPLICANT: Lal, Altaf A.
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Sequence 316, Appli
Sequence 586, Appli
Sequence 215, Appli
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21 US-09-766-378-36
22 US-09-766-378-36
23 US-09-847-208-26
24 US-09-847-208-26
25 US-09-890-806-5
26 US-09-890-806-5
27 US-09-890-806-5
28 US-09-890-806-5
29 US-09-905-167-43
24 US-09-005-318A-43
24 US-09-005-318A-43
24 US-09-005-318A-43
25 US-09-176-741-43
26 US-09-176-741-43
27 US-09-176-741-43
28 US-09-37-827-24
29 US-09-337-827-24
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US-08-561-465A-755
US-08-933-002A-953
US-09-134-001C-3647
US-60-294-411-11
US-09-136-1364-215
US-09-227-357-215
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US-09-763-397A-25
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        SEQ ID NO 25
LENGTH: 22
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Gaps

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Length 22; Indels

100.0%; Score 108; DB 21; 100.0%; Pred. No. 4.8e-07; ive 0; Mismatches 0;

1 MKFLVNVALVFMVVYISYIYAD 22

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Gaps
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                                                                                                                                APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William
TITLE OF INVENTION: Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 108; DB 13;
100.0%; Pred. No. 1.1e-05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUBER: US/08/911,312 FILING DATE: 14 AUG-1997 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 015389-002500US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
FILING DATE: 01-0CT-1996
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION PARE:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 14-AUG-1997
PRIOR APPLICATION PARE: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
ATTORNEY AGENT INFORMATION:
AND ATTORNEY AGENT INFORMATION:
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AND ATTORNEY AGENT OF A ATTORNEY ATTORNEY AGENT OF A ATTORNEY AT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKFLVNVALVFMVVYISYIYAD 22
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TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 34:
                  Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
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Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                      APPLICANT:
                                                                 APPLICANT:
                                    APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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Sequence 2, Application US/09763397A

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the Department of Health and Human Services, Centers for Dis APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A.
APPLICANT: Hasnain, Seyed E.
APPLICANT: Hasnain, Seyed E.
TILE REFERENCE: 6395-5704
FILE REFERENCE: 6395-5704
CURRENT FILING DATE: 1090-016
FILE REPLATION NUMBER: US/09/763,397A
CURRENT FILING DATE: 1998-08-19
FRIOR APPLICATION NUMBER: PCT / US99/18869
FRIOR FILING DATE: 1999-08-19
FRIOR PELING DATE: 1999-08-19
FRIOR FILING DATE: 1999-08-19
FRIOR FELING DATE: 1999-08-19
FRIOR PELING DATE: 1999-08-19
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GENERAL INFORMATION:
APPLICART: MOSSEY, Mohamad A.
TITLE OF INVENTION: Non-anaphylactogenic IgE vaccines
CURRENT APPLICATION NUMBER: US/60/292,638
CURRENT FILIAG DATE: 2001-05-22
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 129
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Best Local Similarity 100.0%; Pred. No. 4.1e-06;
Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 108; DB 24;
100.0%; Pred. No. 1.9e-06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT : TYPE: PRT : ORGANISM: Baculovirus expressed human CH3 domain US-60-292-638-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; CTHER INFORMATION: Recombinant DNA/Protein US-09-763-397A-2
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; Sequence 34, Application US/08911312
; GENERAL INFORMATION:
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              1 MKFLVNVALVFMVVYISYIYAD 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.C
Best Local Similarity 100.C
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-763-397A-2
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US-08-911-312A-34

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Sequence 325, Application US/08912951
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Andrews, Milliam H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
TITLE OF INVENTION: THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/912,951

FILING DATE: 14-AuG-1997

CLASSIFICATION NUMBER: US/08/912,951

FILING DATE: 09-MAY-1997

CLASSIFICATION NUMBER: US 08/851,843

FILING DATE: 09-MAY-1997

CLASSIFICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

CLASSIFICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

CLASSIFICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

CLASSIFICATION NUMBER: US 08/846,017

FILING DATE: 18-APR-1997

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

CLASSIFICATION ADATA:

APPLICATION NUMBER: US 08/724,643

FILING DATE: 18-APR-1997

CLASSIFICATION NUMBER: US 08/724,643

FILING DATE: 18-APR-1997

CLASSIFICATION NUMBER: US 08/724,643

FILING DATE: 315-APR-1997

CLASSIFICATION NUMBER: US 08/724,643

FILING DATE: 315-APR-1997

CLASSIFICATION NUMBER: US 08/724,643

FILING DATE: 315-APR-1997

CLASSIFICATION NUMBER: US 08/724,643

FILING DATE: 18-APR-1997

ATORNEY ADDRIVENTOR NUMBER: US 08/724,643

FILING DATE: 18-APR-1997

ATORNEY ADDRIVENTOR NUMBER: US 08/724,643

FILING DATE: 18-APR-1997

ATORNEY ADDRIVENTOR NUMBER: US 08/724,643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 325:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Two Embarcad
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid STRANDEDNESS:
                                                         RESULT 6
US-08-912-951-325
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Sequence 34, Application US/08911312A
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Marany, Calvin B.
APPLICANT: Marley, Calvin B.
APPLICANT: Andrews, William
TITLE OF INVENTION: Telomerase Reverse Transcriptase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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ZIP: 94111-3834

COMPUTER STADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,312A
FILING DATE: 14-AUG-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 05-MAY-1997
PRIOR APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION NUMBER: US 08/854,050
FILING DATE: US-MAY-1997
PRIOR APPLICATION NUMBER: US-MAY-1997
PRIOR APPLICATION DATA: US-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 015389-002500US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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Length 1189; Indels

Query Match 100.0%; Score 108; DB 13; Best Local Similarity 100.0%; Pred. No. 1.1e-05; Matches 22; Conservative 0; Mismatches 0;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NOTE: 05/08/974,549 FILING DATE: 19-NOV-1997 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: WO PCT/US97/17885 FILING DATE: 01-OCT-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION: 300
PRIOR APPLICATION DATA
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-007-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
AND AT ANTANA NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
AND AT ANTANA NUMBER: US 08/912,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                 Sequence 613, Application US/08974549 GENERAL INFORMATION:
                       1 MKFLVNVALVFMVVISYIYAD 22
                                                                                                                                                                                                                                  APPLICANT: Gech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chagman, Karen B.
APPLICANT: Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (415) 576-0200
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                         US-08-974-549-613
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melittin signal sequence and full length
hTRT protein"
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MEDIUM TYPE: FIDAPY disk

COMPUTER: IBM PC compatible

COMPUTER: TBM PC COMPATIBLE

COMPUTER: PAGENIEN PC-DOS/MS-DOS

SOFTWARE: PAGENIEN PC-DOS/MS-DOS

CORTWARE: PAGENIEN PC-DOS/MS-DOS

CLASSIFICATION NUMBER: US/09/432,503 ·

FILING DATE: O2-Nov-1999

CLASSIFICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 05-APR-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 05-APR-1997

APPLICATION NUMBER: US 08/851,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/912,553

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Andrews, William H. TITLE OF INVENTION: Human Telomerase Catalytic Subunit NUMBER OF SEQUENCES: 727
                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                         100.0%; Score 108; DB 13;
nilarity 100.0%; Pred. No. 1.1e-05;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: WO PCT/US97/17618 FILLING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 613, Application US/09432503
GENERAL INFORMATION:
GENE, Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKFLVNVALVFMVVYISYIYAD 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKFLVNVALVFMVVISYIYAD 22
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Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
LENGTH: 1189 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                               FEATURE:
NAME/KEY: Protein
LOCATION: 1.1189
OTHER INFORMATION:
OTHER INFORMATION:
COTHER INFORMATION:
COTHER INFORMATION:
COTHER INFORMATION:
                      amino acid
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 22; Conserv
                           TYPE: amino STRANDEDNESS
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/960,190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: CORless, Peter F
REGISTRATION NUMBER: 33,860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 48C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-440
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKFLVNVALVEMVVXISXIYA 21
                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-766-378-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid . STRANDEDNESS: single
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                  ZIP: 02109
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                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                  STATE:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tessier, Daniel C.
APPLICANT: Bergeron, John J.M.
APPLICANT: Bergeron, John J.M.
APPLICANT: Thomas, David Y or
TITLE OF INVENTION: UDF-91ucose:91ycoprotein glucosyltransferase (UGGT) activity
TITLE OF INVENTION: und nucleic acid encoding for UGGT
TITLE OF INVENTION: UBP-91ucose:93ycoprotein glucosyltransferase (UGGT) activity
TITLE OF INVENTION: UBP-91ucose:93ycoprotein glucosyltransferase (UGGT) activity
TITLE OF INVENTION: UBP-91ucose:33ycoprotein glucosyltransferase (UGGT) activity
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NAME: APPLE, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFRAT (415) 576-0300
INFORMATION FOR SEQ ID NO: 613:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 108; DB 18;
100.0%; Pred. No. 1.1e-05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.4%; Score 102; DB 17;
100.0%; Pred. No. 2.8e-06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Melittin Signal Peptide sequence
US-09-376-330-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 36, Application US/09766378
GENERAL INFORMATION:
APPLICANT: Rhode, Peter R.
APPLICANT: Acevedo, Jorge
APPLICANT: Burkhardt, Martin
APPLICANT: Jiao, Jin-an
                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKFLVNVALVFMVVXISYIYAD 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKFLVNVALVFMVVYISYIYAD 22
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                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                Protein
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Best Local Similarity 100.0
Matches 22; Conservative
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Best Local Similarity 100.
Matches 21; Conservative
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US-09-766-378-36
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LENGTH: 21
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ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
APPLICANT: Wong, Hing C.

TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 38
CORRESPONDENCES: 38
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
CITT: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.4%; Score 102; DB 21; 100.0%; Pred. No. 2.8e-06;
                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastsEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SOLUBLE MHC METHODS OF (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 36, Application US/09766378A
GENERAL INFORMATION:
APPLICANT: Rhode, Peter R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acevedo, Jorge
Burkhardt, Martin
Jiao, Jin-an
Wong, Hing C.
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ORGANISM: Artificial Sequence
                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1999-02-02
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 21; Conservative
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Best Local Similarity
Matches 21; Conserv
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US-08-782-481-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 177
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STATE:
                                                                                                                            SEQ ID NO 5
LENGTH: 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2-908-068-60-SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                 TYPE: PRT
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APPLICART: JOHNSON et al.
TITLE OF INVENTION: INHIBITION OF THE MHC CLASS II ANTIGEN PRESENTATION
TITLE OF INVENTION: PATHWAY AND PRESENTATION TO CD4+ CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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US-09-847-208-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 70;
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APPLICANT: Zhu, Daoccheng
TITLE OF INVENTION: EVSION MOLECULES AND TREATMENT OF
TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
FILE REPERENCE: UG67.002A
CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.4%; Score 102; DB 22;
100.0%; Pred. No. 7.2e-06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.4%; Score 102; DB 21;
100.0%; Pred. No. 2.8e-06;
live 0; Mismatches 0;
           CURRENT APPLICATION DATA.

APPLICATION NUMBER: US/09/766,378A
FILING DATE: 19-Jan-2001
CLASSIFICATION: Jan-2001
CLASSIFICATION NUMBER: 08/960,190
FILING DATE: 29-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: COTLESS, PECET F
REGISTRATION NUMBER: 33,860
REFERENCE/COCKET NUMBER: 34,860
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-766-378A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 26, Application US/09847208
GENERAL INFORMATION:
APPLICANT: Saxon, Andrew
                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKFLVNVALVEMVVYISYIYA 21
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Matches 21; Conservative
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Best Local Similarity
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LENGTH: 70
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TITLE OF INVENTION: INHIBITION OF THE MHC CLASS II ANTIGEN PRESENTATION
TITLE OF INVENTION: PATHWAY AND PRESENTATION TO CD4+ CELLS
TITLE OF INVENTION: PATHWAY AND PRESENTATION TO CD4+ CELLS
FILE REFERENCE: 0899-59399
CURRENT APPLICATION NUMBER: US/09/890,806
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: US/09/02740
PRIOR FILING DATE: 2000-02-02
PRIOR APPLICATION NUMBER: 60/118,287
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GENERAL INFORMATION:
APPLICAMT: Hein, Mich B.
APPLICAMT: Hiat, Andrew C.
APPLICANT: Fitchen, John H.
TITLE OF INVENTION: NOVEL EPITHELIAL TISSUE TARGETING AGENT NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence:chimera US-09-890-806-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 177;
                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: chimera PCT-US00-02740-5
                                                                                                                                                                                                                                                                                                                                                                             Score 102; DB 1; Length 177;
Pred. No. 1.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 102; DB 22;
Pred. No. 1.5e-05;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
FILE REFERENCE: 0899-54203 Johnson
CURRENT APPLICATION NUMBER: PCT/US00/02740
CURRENT FILING DATE: 2000-02-02
EARLIER APPLICATION NUMBER: 60/118,287
EARLIER FILING DATE: 1999-02-02
SALLIER FILING DATE: 1999-02-02
NUMBER OF SEO ID NOS: 7
SOFTWARE: PATENTIN Ver. 2.1
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                94.4%; So
ilarity 100.0%; P
Conservative 0;
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COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
FILING DATE: 10-0An-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REFERENCE/DOCKET NUMBER: 310098.401
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFHONE: (206) 682-6031
INFORMATION POR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acids
TOPPLOST: 11near
MOLECULE TYPE: protein
US-08-782-481-43

QUERY MATCh
BEST LOCAL SIMILATITY 95.5%; Pred. NO. 4.3e-05;
MATCHES 21: CONSERVATIVE O; Mismatches 0; Indels 1; Gaps 1;
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Search completed: January 29, 2002, 11:06:41 Job time: 623 sec

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1, Appli 1, Appli 5313, Ap 18, Appl

Sequence Sequence Sequence

Sequence

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

108, App 2, Appli

Sequence Sequence Sequence

Sequence

Sequence Sequence

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Sequence 613, Application US/09402181A
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor STREET: San Francisco STATE: California
           US-09-966-262-328

US-09-886-055-349

US-09-894-221-349

US-09-997-516-5313

US-09-966-521-18

US-09-966-521-18

US-09-966-521-18

US-09-966-521-18

US-09-966-521-18

US-09-830-123-15

US-09-830-123-15

US-09-889-442-108

US-09-989-442-108

US-09-989-442-108

US-09-986-433-14

US-09-968-433-14

US-09-968-433-14
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FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRICE DATE: 29-Sep-197
CLASSIFICATION NUMBER: US/09/402,181A
FILING DATE: 29-Sep-1997
CLASSIFICATION: CUBKNOWN>
PRIOR APPLICATION NUMBER: US 08/724,643
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: US 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: US 09-MAY-1997
APPLICATION NUMBER: US 08/951,312
FILING DATE: US 09-MAY-1997
                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
               177
1177
1298
2298
2298
401
401
401
502
550
553
621
337.0
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 Sequence 2, Appli
Sequence 128, App
Sequence 367, App
Sequence 367, App
Sequence 12, Appli
Sequence 12, Appl
Sequence 186, App
Sequence 19299, A
Sequence 3624, Ap
Sequence 3624, Ap
Sequence 3624, Ap
Sequence 17563, A
Sequence 227, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 613, App
Sequence 10432, A
Sequence 211, App
Sequence 2, Appli
                                                                                                         (without alignments)
26.919 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                         Search time 29.91 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                       Pending_Patents_AA_New:*

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'cgn2_6/ptodata/2/paa_VUS06_NEW_COMB.pep:*

'cgn2_6/ptodata/2/paa_VUS08_NEW_COMB.pep:*

'cgn2_6/ptodata/2/paa_VUS08_NEW_COMB.pep:*

'cgn2_6/ptodata/2/paa_VUS09_NEW_COMB.pep:*

'cgn2_6/ptodata/2/paa_VUS09_NEW_COMB.pep:*

'cgn2_6/ptodata/2/paa_VUS0]_NEW_COMB.pep:*
            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-402-181A-613
US-09-721-477-613
US-09-811-247-10432
US-09-973-278-211
US-10-002-854-2
US-10-002-854-2
US-09-804-055-367
US-09-804-730-128
US-09-918-779-12
US-09-918-779-12
US-09-918-779-12
US-09-918-779-136-1
US-09-708-427-19299
US-09-708-427-1562
US-09-708-427-17562
US-09-708-427-17561
US-09-708-427-12941
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US-09-708-427-12941
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                                                                                                                                                                                                                                        173191 seqs, 36597120 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                           108
1 MKFLVNVALVFMVVYISYIYAD 22
                                                                                         January 29, 2002, 11:07:15
                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                 protein search, using sw model
                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                              US-09-763-397A-25
                                                                                                                                                                                                                                                                                            seq length: 0
seq length: 200000000
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Match Length
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Maximum DB s
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OTHER INFORMATION: /note= "fusion protein composed of melittin signal sequence and full length hTRT protein"
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TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: TORKARYOTES
FILE REPRENCE: ELITAA.01A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/245,578
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                           NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 108; DB 5;
100.0%; Pred. No. 5.3e-08;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; SEQUENCE DESCRIPTION: SEQ ID NO: 613: US-09-721-477-613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10432, Application US/09815242
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/269,308
FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 613:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKFLVNVALVFWVVYISYIYAD 22
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
1..1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-09-815-242-10432
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR
PRIOR
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                                                                                                                                                                                                                                                                                                 NAME/KEY: Protein

LOCATION: 1..1189

COTHER INFORMATION: /note= "fusion protein composed of melittin signal sequence and full length hirt protein"

SEQUENCE DESCRIPTION: SEQ ID NO: 613:
US-09-402-181A-613
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Best Local Similarity 100.0%; Pred. No. 5.3e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 22-Nov-2000
CLASSIFICATION: -UNknown>
PRIOR APPLICATION AUMER: 08/974,549
FILING DATE: -UNknown>
APPLICATION NUMBER: 08/974,419
FILING DATE: -UNKnown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
  NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ. 10 NO: 613:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/911,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence bls, crr-
GENERAL INFORMATION:
GENERAL LINGORAL CECh, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 613, Application US/09721477
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKFLVNVALVFMVVYISYIYAD 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKFLVNVALVFMVVYISYIYAD 22
                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
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Gaps

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APPLICANT: Scadden, David T.
APPLICANT: Scadden, David T.
APPLICANT: Olszak, Twona T.
APPLICANT: Olszak, Twona T.
APPLICANT: Brown, Edward M.
TITLE OF INVENTION: THE CAR RECEPTOR AS A MEDIATOR OF
TITLE OF INVENTION: MIGRATORY CELL CHEMOTAXIS AND/OR CHEMOKINESIS
FILE REFERENCE: W0765/7038/ERG/KA
CURRENT APPLICATION NUMBER: US/10/002,854
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: PCT/US00/15440
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
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60;
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2;
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Pred. No. 2;
4; Mismatches
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Pred. No. 60;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COCATION: (1)...(1078)
COTHER INFORMATION: Ca-sensing Receptor US-10-002-854-2
                                                   PRIOR APPLICATION NUMBER: 60/055,950
PRIOR FILING DATE: 1997-08-18
PRIOR PILING DATE: 1997-08-18
PRIOR PILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: 60/055,964
PRIOR APPLICATION NUMBER: 60/055,964
PRIOR APPLICATION NUMBER: 60/056,360
PRIOR FILING DATE: 1997-08-18
                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/055, 684
PRIOR PELING DATE: 1997-08-18
PRIOR PELING DATE: 1997-08-18
PRIOR FILING DATE: 1997-08-18
PRIOR PELING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: 60/055, 954
PRIOR FILING DATE: 1997-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 60/058,661
PRIOR FILING DATE: 1997-09-12
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-002-854-2; Sequence 2, Application US/10002854; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41.78;
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 41.7
Best Local Similarity 50.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 41.7
Best Local Similarity 45.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-973-278-211
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LENGTH: 1078
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                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                       Length 127;
                                                                                                                                                                                                                                                                                              Indels
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TITLE OF INVERTION: 123 Human Secreted Proteins
FILE REFERENCE: P01002
CURRENT APPLICATION NUMBER: US/09/973,278
CURRENT APPLICATION NUMBER: US/09/973,278
CURRENT APPLICATION NUMBER: US/09/973,278
PRIOR PILING DATE: 1000-10-13
PRIOR PLILNG DATE: 1990-01-08
PRIOR FILING DATE: 1990-01-08
PRIOR PLILNG DATE: 1990-01-08
PRIOR PLILNG DATE: 1997-07-08
PRIOR PLILNG DATE: 1997-08-18
                                                                                                                                                                                                                                       Score 47; DB 5;
Pred. No. 3.5;
                                                                                                                                                                                                                                                                                           7; Mismatches
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10432
LENGTH: 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 211, Application US/09973278 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                         1 MKFLVNVALVFMVVYISYIYAD 22
                                                                                                                                                                                                                                                                                                                                                                             43.5%;
                                                                                                                                                                                                               Query Match
Best Local Similarity 40.9%
Local Similarity 40.9%
Local Similarity
Conservative
                                                                                                          ; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-815-242-10432
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US-09-973-278-211
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Gaps ö ö

Gaps

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; NAME/KEY: peptide; LOCATION: (1)..(542); LOCATION: (1)..(542); OTHER INFORMATION: Amino acid sequence of protein regulating the pH of vacuoles US-09-830-123-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2. Application US/09830123

Sequence 2. Application US/09830123

Sequence 2. Application US/09830123

Sequence 3. Application US/09830123

APPLICANT: Inda, Shigaru

APPLICANT: Inda, Shishide

ITILE OF INVENTION: Genes Encoding Proteins Regulating the pH of Vacuoles

FILE REFERENCE: 101500-397

CURRENT FILING DATE: 2001-04-24

CURRENT FILING DATE: 2001-04-24

PRIOR FILING DATE: 2000-08-24

PRIOR FILING DATE: 1999-08-24

PRIOR FILING DATE: 1999-08-24

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn Version 3.1

SEQ ID NO 2

LENGTH. 542
Sequence 367, Application US/09804291

Sequence 367, Application US/09804291

Sequence 367, Application US/09804291

Sequence 367, Application SERGEX

TILE OF INFORMATION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME

FILE REFERENCE: P 0278005

CURRENT FILING DATE: 2001-03-13

PRIOR PELLOR INON NUMBER: 60/188,914

PRIOR PELLOR APPLICATION NUMBER: 60/198,474

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-04-24

PRIOR FILING DATE: 2000-06-23

PRIOR FILING DATE: 2000-06-23

PRIOR FILING DATE: 2000-06-23

PRIOR PILING DATE: 2000-09-26

PRIOR FILING DATE: 2000-09-07

PRIOR PRILING DATE: 2000-09-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43; DB
Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 39.8
Best Local Similarity 40.0
Matches 6; Conservative
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204 NIFFVLLVIFISYLF 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens US-09-804-291-367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Ipomea nil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS
  US-09-804-291-367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-830-123-2
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APPLICANT: Recipon, Herve
APPLICANT: Cafferkey, Robert
APPLICANT: Cafferkey, Robert
APPLICANT: All, Shujath
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
FILE REFERENCE: DEX-0281
CURRENT APPLICATION NUMBER: US/10/001,879
CURRENT FILING DATE: 2001-11-20
PRIOR PILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 201
SOFTWARE: Patentin version 3.1
SEQ ID NO 128
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Sequence 1NFORMATION:
APPLICANT: STRYER, LUBERT
APPLICANT: SOZULYA, SERGEY
TITLE OF INVENTION: BECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS
FILE REFERENCE: 078003-0277150
CURRENT APPLICATION NUMBER: US/09/886,055
CURRENT FILING DATE: 2001-06-22
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 522
NUMBER OF SEQ ID NOS: 522
SOFTWARE: Patentin Ver. 2.1
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Pred. No. 33;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43;
                                                                                                                                                                                               Sequence 128, Application US/10001879 GENERAL INFORMATION:
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                                                          805 KEITESMLIFFIVWISFIPA 824
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                              2 KFLVNVALVFMVVYISYIYA 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 FLVLVSLIYMYEYIIFF 21
                                                                                                                                                                                                                                                  APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
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Best Local Similarity 44.4
Matches 8; Conservative
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204 NIFFVLLVIFISYLF 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-09-886-055-367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapien
US-10-001-879-128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                US-10-001-879-128
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LENGTH: 309
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APPLICANT: Ruben et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REFERENCE: P2013P2
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CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 09/774,639
PRIOR FILING DATE: 2001-02-01
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 1909-02-04
PRIOR PLILNG DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/244,112
PRIOR APPLICATION NUMBER: 09/244,112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/056,371
PRIOR APPLICATION NUMBER: 60/056,367
PRIOR PILING DATE: 1997-08-19
PRIOR PILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR PILING DATE: 1997-08-19
PRIOR PELICATION NUMBER: 60/056,367
PRIOR PELICATION NUMBER: 60/056,571
PRIOR PELICATION NUMBER: 60/056,571
PRIOR PELICATION NUMBER: 60/056,531
PRIOR PELICATION NUMBER: 60/056,531
PRIOR PELICATION NUMBER: 60/055,916
PRIOR PELICATION NUMBER: 60/055,311
PRIOR PELICATION NUMBER: 60/054,803
PRIOR PELICATION NUMBER: 60/054,803
PRIOR PELING DATE: 1997-08-05
          293 RFTQNISAIEPLIVFMFSYLSYLAAE 318
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                                                                                                                                                                                                 Sequence 147, Application US/09969730 GENERAL INFORMATION:
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SEQ ID NO 147
LENGTH: 61
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APPLICANT: Stone, David
APPLICANT: Stone, David
APPLICANT: Southson, Glenda
APPLICANT: Smithson, Glenda
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-074 US/09/918,779
CURRENT APPLICATION NUMBER: US/09/918,779
CURRENT APPLICATION NUMBER: US/09/918,779
FRIOR APPLICATION NUMBER: 60/221,409
FRIOR APPLICATION NUMBER: 60/222,840
FRIOR APPLICATION NUMBER: 60/223,752
FRIOR APPLICATION NUMBER: 60/223,752
FRIOR APPLICATION NUMBER: 60/223,769
FRIOR APPLICATION NUMBER: 60/223,769
FRIOR FILING DATE: 2000-08-08
FRIOR PROPLICATION NUMBER: 60/225,146
FRIOR APPLICATION NUMBER: 60/225,146
FRIOR PELING DATE: 2000-08-18
FRIOR APPLICATION NUMBER: 60/225,146
FRIOR FILING DATE: 2000-08-15
FRIOR PELING DATE: 2000-08-16
                                           Gaps
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                                        Indels
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34.6%; Pred. No. 91;
tive 7; Mismatches
                                        5; Mismatches
          Pred. No.
                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/09918779
GENERAL INFORMATION:
APPLICANT: Taupier, Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                Padigaru, Muralidhara
Rastelli, Luca
Spaderna, Steven
Shimkets, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gusev, Vladimir
Grosse, William
Alsobrook, John
Lepley, Denise
Burgess, Catherine
Best Local Similarity 50.0%;
Matches 8; Conservative
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Shenoy, Suresh
Li, Li
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MacDougall, John
Stone, David
                                                                                                                                        253 VALMMLMSYLSYIMAE 268
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Best Local Similarity 34.6
Matches 9; Conservative
                                                                                                7 VALVFMVVYISYIYAD 22
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SOFTWARE: PatentIn Ver.
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US-09-918-779-12
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APPLICANT:
APPLICANT:
APPLICANT:
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Sequence 3623, Application US/09708427

GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
TITLE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: US/09-11-09
NUMBER OF SEQ ID NOS: 85364
SEQ ID NO 3623
SEQ ID NO 3623
                                                                                                                                                                                                     Sequence 3624, Application US/09708427

GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILLE REPERBENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SSEQ ID NO 3624
LENGTH: 347
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Length 217;
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                                        Indels
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Score 42; DB 5;
Pred. No. 32;
9; Mismatches
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Pred. No. 61;
6; Mismatches
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Pred. No. 51;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1..347
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..347
OTHER INFORMATION: Ceres Seq. ID 1810723
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; OTHER INFORMATION: Ceres Seq. ID 1810722
US-09-708-427-3623
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OTHER INFORMATION: Xaa is any
NAME/KEY: misc_feature
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43.8%;
    38.9%;
29.4%;
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43.8%;
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Best Local Similarity 43.8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 VALMMIMAYLSYMLAE 176
                                                                                                      | : ::: ::|:| | 34 VSFSIIIIIVFVYYLYA 50
                                                                              5 VNVALVEMVVXISYIYA 21
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                                            Conservative
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Best Local Similarity
Matches 7; Conserv
                    Best Local Similarity
Matches 5; Conserv
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US-09-708-427-3623
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US-09-708-427-3624
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        Query Match
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
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TITLE OF INVENTION: 90 Human Secreted Proteins
FITLE OF INVENTION: 90 Human Secreted Proteins
FILLE REFERENCE: P201391
CURRENT APPLICATION NUMBER: US/09/774,639
CURRENT FILING DATE: 2001-07-09
PRIOR RILING DATE: EARLIER FILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 371
SOFTWARE: PATCHIN VET. 2.0
SEC ID NO 186
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                                                                                                    Length 61;
                                                                                                                                         Indels
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Pred. No. 8.9;
7; Mismatches 4
                                                                                                  Score 42; DB 5;
Pred. No. 8.7;
7; Mismatches 4
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; OTHER INFORMATION: Xaa equals stop translation
US-09-774-639-186
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LOCATION: 1..217
OTHER INFORMATION: Xaa is any amino acid
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                                                                                                                                                                                                                                                                                                                Sequence 186, Application US/09774639 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Arabidopsis thaliana
                                                                                                  Query Match 38.9%;
Best Local Similarity 35.3%;
Matches 6; Conservative 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.9%;
35.3%;
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8 FILNIIVIECIVIDSYL 24
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8 FILNIIVIFCIVIDSYL 24
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Best Local Similarity 35.3
Matches 6; Conservative
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LOCATION: 1..217
          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-969-730-147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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LENGTH: 217
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US-09-774-639-186
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Search completed: January 29, 2002, 11:07:16 Job time: 534 sec

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Sequence 71, Sequence 13,

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sequence 34, Appl Sequence 12, Appl Sequence 6, Appl Sequence 6, Appl Sequence 49, Appl Sequence 49, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 25, Appl Sequence 55, Appl Sequence 1, Appli
Sequence 4, Appli Sequence 32, Appl Sequence 63, Appl Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 12, Appli Sequence 12, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli

equence 4, Appli Sequence 7, Appli Sequence 7, Appli

Seguence 4

Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Sequence 7, Application PC/TUS0025239
GENERAL INFORMATION:
APPLICANT: Schenk, Dale B.
APPLICANT: Schenk, Dale B.
APPLICANT: Schenk, Dale B.
TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease FILE REFERENCE: 152701-005900PC
CURRENT FPLICATION NUMBER: PCT/US00/25239
CURRENT FILING DATE: 1090-06-01
PRIOR APPLICATION NUMBER: US 60/137,010
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence:tetanus toxoid; OTHER INFORMATION: TT 830-844 universal T-cell epitope PCT-US00-25239-7
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Pred. No. 1.2e-06;
Mismatches 0;
US-09-148-711-7

US-09-148-711A-7

US-09-362-731-13

US-09-362-731-13

US-09-36-731-13

US-09-36-731-13

US-09-405-986-12

US-09-580-13-186-12

US-09-580-015-49

US-09-580-015-49

US-09-580-019-49

US-09-780-019-49

US-09-780-019-49

US-09-785-215-4

US-09-785-215-4

US-09-785-215-4

US-09-785-215-4

US-09-785-215-4

US-09-785-215-4

US-09-1395-215-4

US-09-1395-39

US-09-1395-39

US-09-1395-63

US-08-057-166-4

US-08-091-466-4

US-09-1395-63

US-08-091-466-4

US-08-091-466-4

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US-08-091-466-4

US-08-091-466-4

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US-08-08-275-4

US-08-275-4

US-08-275-16-4

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ilarity 100.0%;
Conservative 0;
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    Query Match
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Matches 15; Conserv
    PCT-US00-25239-7
   SEQ ID NO 7
LENGTH: 15
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Sequence 2, Appli
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Sequence 69, Appl
                                                                                                        Search time 353.23 Seconds (without alignments) 11.791 Million cell updates/sec
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1: /cgn2_6/ptodata/2/paa/VSOG_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/VSOG_COMB.pep:*

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10: /cgn2_6/ptodata/2/paa/VSOB_COMB.pep:*

11: /cgn2_6/ptodata/2/paa/VSOB_COMB.pep:*

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13: /cgn2_6/ptodata/2/paa/VSOB_COMB.pep:*

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PCT-US99-06325-2
US-08-161-889-69
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Copyright (c) 1993 - 2000
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VACCINES AND ANTIGENIC CONJUGATES
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                                                                                                                                                                                                                                                                        RESULT 4
US-08-161-889A-69
US-08-161-889A-69
Sequence 69, Application US/08161889A
GENERAL INFORMATION:
APPLICANT: Geysen, H. Mario
APPLICANT: Redda, Stuart J.
TITLE OF INVENTION: T-Cell Epitopes
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08406916B
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Grant D. Green
STREET: 4560 Horton St.
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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              ; MOLECULE TYPE: peptide US-08-161-889-69
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MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 15; Conserv
TOPOLOGY: linear
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US-08-406-916B-2
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                                                 Sequence 2, Application PC/TUS9906325
Sequence 2. Application PC/TUS9906325
GENERAL INFORMATION:
APPLICANT: Sudhir Paul
APPLICANT: Larry J. Smith
APPLICANT: Gennady Golobbov
TITLE OF INVENTION: Methods for Identifying Inducers and
TITLE OF INVENTION: Inhibitors of Catalytic Antibodies, Compositions and Their
TITLE OF INVENTION: Use
TITLE OF INVENTION: UNMBER: PCT/US99/06325
CURRENT APPLICATION NUMBER: PCT/US99/06325
CURRENT FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA: US/08/161,889
FILING DATE: 02-DEC-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 74; DB 1;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 69, Application US/08161889
GENERAL INFORMATION:
APPLICANT: Geysen, H. Mario
APPLICANT: Rodda, Stuart J.
TITLE OF INVENTION: T-Cell Epitopes
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/984,852
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0222.002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 510-601-2706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Grant D. Green
STREET: 4560 Horton St.
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Clostridium tetani
PCT-US99-06325-2
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LENGTH: 15 amino acids
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ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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LENGTH: 15
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Sequence 1, Application US/09049847
Sequence 1, Application:
APPLICANT: Cantacuzene, Daniele
APPLICANT: Lo-Han, Richard
TITLE OF INVENTION: Comprising the same and use thereof
FILE REFERENCE: 102.166A
CURRENT FILING DATE: 1998-03-27
CURRENT FILING DATE: 1998-03-27
SEARLIER APPLICATION NUMBER: 60/041,726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 74; DB 11;
Pred. No. 1.2e-06;
                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/00292
FILING DATE: 13-MAR-1995
ATTORNEY/ACENT INFORMATION:
NAME: Calvetti, Frederick F.
REGISTRATION NUMBER: 28,557
RECISTRATION NUMBER: GROFO 7001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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GENERAL INFORMATION:
APPLICANT: Bay, Sylvie
APPLICANT: Cantacuzene, Daniele
APPLICANT: Leclerc, Claude
APPLICANT: Lo-Man, Richard
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100.0%;
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; ORGANISM: Clostridium tetani
US-09-049-847-1
                                                                                                                                                                                                                                    TELEFAX: (202)414-4040
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 15
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                    amino acid
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Best Local Similarity
Matches 15; Conserv
  FILING DATE:
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GENERAL INFORMATION:
APPLICANT: Gulchard, Gilles
APPLICANT: Muller, Sylviane
APPLICANT: Briand, Jean-Paul
APPLICANT: Regenmortel, Marc
TITLE OF INVENTION: Retropeptides, Antibodies Thereto, and
TITLE OF INVENTION: Uses Thereof for Vaccination and In Vitro Diagnosis
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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100.0%; Pred. No. 1.2e-06;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL: NO FRAGMENT TYPE: 830-844 fragment of tetanus toxoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/O8/716,249
                                                                                                                         COMPTRY: USA

ZIP: 43068
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
COMPUTER: IBM PS/2 COMPATIBLE 486 DX 33
OPERATING SYSTEM: MS DOS 6.2
SOFTWARE: WORDPERECT FOR MS DOS 5.1
SOFTWARE: WORDPERECT FOR MS DOS 5.1
CURRENT APPLICATION DATA: US/08/406,916B
FILING DATE: 27 MAR 1995
PRIOR APPLICATION DATA: PCT/US92/08370
FILING DATE: 30 SEP 1992
ATTORNEY/AGENT INFORMATION:
NAME: KREMBLAS, FRANCIS T., JR.
REGISTATION NUMBER: 22,773
REGISTATION NUMBER: 22,773
REGISTATION NUMBER: 22,773
REGISTATION NUMBER: URF 2 056 3 3 3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Spencer & Frank
STREET: 1100 New York Avenue, Suite 300E
CITY: Washington, D.C.
                                      ADDRESSEE: MILLARD, SIDNEY W.
STREET: 7612 SLATE RIDGE BOULEVARD
CITY: REYNOLDSBURG
STATE: OHIO
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: T cell epitope
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TELEFAX: (614) 575 2149
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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                      CORRESPONDENCE ADDRESS:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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MOLECULE TYPE:
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Gaps

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Indels

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GENERAL INFORMATION:
APPLICANT: Bakaletz, Lauren O.
APPLICANT: Kaumaya, Parvin T.
TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides
NUMBER OF SEGUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/09148711A

; GENERAL INFORMATION:

; APPLICART: The Ohio State University

; TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides

; FILE REFERENCE: 18525-04010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version #1.25
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Best Local Similarity 100.0%; Score 74; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 15; Conservative 0; Mismatches 0;
              Pred. No. 1.2e-06;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Calfee, Halter and Griswold STREET: 800 Superior Avenue CITY: Cleveland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 18525-04010
CURRENT APPLICATION NUMBER: US/09/148,711A
CURRENT FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: 08/460,502
NUMBER FILING DATE: 1955-06-02
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY MEENT INFORMATION:
NAME: GOLTICK, Mary E.
REGISTATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00120
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/460,502
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/148,711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
100.08; PI
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IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (216) 622-8458
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 7:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: peptide US-09-148-711-7
                                                                                  1 QYIKANSKFIGITEL 15
                                                                                                               1 QYIKANSKFIGITEL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sin
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         Best Local Similarity
Matches 15; Conserv
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44114-2688
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              TITLE OF INVENTION: Mutiple antigen glycopeptide carbohydrate, vaccine TITLE OF INVENTION: comprising the same and use thereof FILE REFERENCE: 102.166A
CURRENT APPLICATION NUMBER: US/09/049,847A
CURRENT FILING DATE: 1998-03.27
PRIOR APPLICATION NUMBER: 60/041,726
PRIOR FILING DATE: 1997-03.27
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,716
FILING DATE: 22-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/661,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
OF ANTI-FC RECEPTOR ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 74; DB 15;
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illarity 100.0%; Pred. No. 1.2e-06;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-102-716-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/09102716 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: <Unknown>
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Joel Goldstein
Robert Graziano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                               ; ORGANISM: Clostridium tetani
US-09-049-847A-1
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ZIP: 02109-1875
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Best Local Similarity
Matches 15; Conserv
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Query Match

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Sequence 34, Application US/09396937
GENERAL INFORMATION:
APPLICANT: M&E Biotech A/S
APPLICANT: HALKIER, Torben
APPLICANT: HANNING, Jesper
TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
TITLE OF INVENTION: Activity
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       Length 15;
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                                                                                                                                                                                                                                                       Sequence 6, Application US/09364088
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo, et al.
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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100.0%; Pred. No. 1.2e-06;
iive 0; Mismatches 0;
    100.0%; Score 74; DB 17; 100.0%; Pred. No. 1.2e-06;
                                                  0; Mismatches
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APPLICATION NUMBER: US 09/188,082
APPLICATION NUMBER: US 09/188,082
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
APPLICATION NUMBER: US 08/484,172
ATTORNEY AGENT INFORMATION:
NAME: Remillard, Jane E:
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: AMI-043CP2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: LAHIVE & COCKFIELD, LLP STREET: 28 State Street, 24th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/364,088 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (617)227-7400
TELEFAX: (617)742-7414
INFORMATION FON EGG ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100
Best Local Similarity 100
Matches 15; Conservative
                                                  Conservative
                                                                                                                       1 QYIKANSKFIGITEL 15
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COUNTRY: USA
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                       Best_Local Similarity
Matches 15; Conserv
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FRAGMENT TYPE:
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US-09-364-088-6
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       Query Match
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GENERAL INFORMATION:
APPLICANTY U.C.B. S.A.
TITLE CANTY U.C.B. CAPOUND AND METHOD FOR THE PREVENTION AND/OR THE
TITLE OF INVENTION: COMPOUND AND METHOD FOR THE PREVENTION AND/OR THE
TITLE OF INVENTION: TREATMENT OF ALLERGY
FILE REPERENCE: P.UGB.09/WO
CURRENT APPLICATION NUMBER: US/09/362,731
CURRENT FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 15
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US-09-362-731-13
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APPLICANT: Heggard, Peter Mikael Helweg
TITLE OF INVENTION: Non-Dendritic Backbone Peptide Carrier
FILE REFERENCE: 2316.1009-000
CURRENT APPLICATION NUMBER: US/09/165,878B
CURRENT FILING DATE: 1998-10-02
EARLIER APPLICATION NUMBER: PCT/DK97/00146
EARLIER APPLICATION NUMBER: DK 0398/96
EARLIER FILING DATE: 1996-04-03
EARLIER FILING DATE: 1996-04-03
SALIER FILING DATE: 1996-04-03
SALIER FILING DATE: 1906-04-03
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                        Length 15;
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                                                                                                                                                                                   Query Match 100.0%; Score 74; DB 15; Best Local Similarity 100.0%; Pred. No. 1.2e-06; Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                US-09-165-878-71; Sequence 71, Application US/09165878B; GENERAL INFORMATION:
    PatentIn version 3.0
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ORGANISM: Artificial Sequence
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                                                                                           ; ORGANISM: clostridium tetani
US-09-148-711A-7
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LENGTH: 15
SOFTWARE:
SEQ ID NO 7
LENGTH: 15
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; FILE REFERENCE: 22021 PC 1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Clostridium tetani
US-09-396-937-34

Query Match
Best Local Similarity 100.0%; Score 74; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 1 QYIKANSKFIGITEL 15
| Db 1 QYIKANSKFIGITEL 15
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TYPE: PRT
                                                         Search time 29.91 Seconds (without alignments)
18.354 Million cell updates/sec
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1: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO7_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*
GenCore version 4.5
(c) 1993 - 2000 Compugen Ltd.
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US-09-9806-916-14

US-09-980-916-32

US-09-980-916-35

US-09-980-916-36

US-09-980-916-16

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Maximum Match 100%
Listing first 45 summaries
                                       OM protein - protein search, using sw model
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sequence 42, Appl
Sequence 4901, Ap
Sequence 10491, Ap
Sequence 6808, Ap
Sequence 5943, Ap
Sequence 5603, Ap
Sequence 2, Appl1
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                  US-09-980-916-44
US-09-787-1126-18
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US-09-806-703A-39
US-09-908-460-41
US-09-908-460-42
US-09-915-242-4901
US-09-815-242-10491
US-09-897-516-6808
US-09-946-290-3
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US-09-978-756-2
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Sequence 34, Application US/09787126
GEMERAL INFORMATION:
APPLICANT: MAE Biotech A/S
APPLICANT: HALKIER, Torben
APPLICANT: HAANING, Jesper
TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
TITLE OF INVENTION: Activity
FILE REFERENCE: 3631-0108P
CURRENT APPLICANTION NUMBER: US/09/787,126
CURRENT FILING DATE: 2001-10-09
NUMBER OF SEQ ID NOS: 36
SEQ ID NO 34
LENGTH: 15
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Pred. No. 1e-07;
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Best Local Similarity 100.0%;
Matches 15; Conservative 0;
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US-09-787-126-34
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US-09-677-374-19

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Sequence 19, Application US/09677374

Sequence 19, Application US/09677374

GENERAL INFORMATION:

APPLICANT: Burian, Jahan

APPLICANT: Ruzyk, Michael

APPLICANT: Thornton, Julian

APPLICANT: Thornton, Julian

TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY AGAINST

TITLE OF INVENTION: NACCINES AND ASSOCIATED PREVENTATIVE THERAPY

TITLE OF INVENTION: NACCINES AND ASSOCIATED PREVENTATIVE THERAPY

TITLE OF INVENTION NUMBER: US/09/677,374

CURRENT APPLICATION NUMBER: US 60/154,437

PRIOR PLING DATE: 1999-09-17

PRIOR APPLICATION NUMBER: IE 2000/0752

PRIOR FILING DATE: 2000-09-15

PRIOR FILING DATE: 2000-09-18

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: RALESON, Gunilla
APPLICANT: Raribsson, Gunilla
APPLICANT: Rasmussen, Peter
TITLE OF INVENTION: Novel Methods for Therapeutic Vaccination
TITLE OF INVENTION: Novel Methods for Therapeutic Vaccination
FILE REFERENCE: 3631-0109P
CURRENT APPLICATION NUMBER: US/09/806,703A
CURRENT APPLICATION NUMBER: PCT/DK99/00525
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 60/105,011
PRIOR FILING DATE: 1998-10-05
PRIOR FILING DATE: 1998-10-05
PRIOR FILING DATE: 1998-10-05
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                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-09-806-703A-15
Sequence 15, Application US/09806703A
; GENERAL INFORMATION:
; APPLICANT: Steinaa, Lucilla
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Clostridium tetani
US-09-980-916-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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Leach, Dana
Nielsen, Klaus
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SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 15
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Leach, Dana
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Best Local Similarity
Matches 15; Conserva
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US-09-806-703A-16
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APPLICANT:
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APPLICANT:
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APPLICANT: Leach, Dana
APPLICANT: Leach, Dana
APPLICANT: Railson, Klaus
APPLICANT: Railson, Gunilla
CURRENT: RAILSON NOVEL Methods for Therapeutic Vaccination
FILE REFERENCE: 3631-0109P
CURRENT PELLING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: DCT/DK99/00525
PRIOR APPLICATION NUMBER: DCT/DK99/00525
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1998-10-05
PRIOR PILING DATE: 1998-10-05
PRIOR PILING DATE: 1998-10-20
NUMBER OF SED IN 083: 41
SOFTWARE: Patentin Ver: 3.0
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Sequence 23, Application US/09980916
GENERAL INFORMATION:
APPLICANT: MAE Biotech A/S
APPLICANT: Klysner, Steen
TITLE OF INVENTION: Method For Down-Regulating IL5 Activity
FILE REFERENCE: 33631-0112P
CURRENT APPLICATION NUMBER: US/09/980,916
CURRENT FILING DATE: 2001-10-23
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           PRIOR APPLICATION NUMBER: GB 0022825.4 PRIOR FILING DATE: 2000-09-18 PRIOR APPLICATION NUMBER: CL 2544-2000 PRIOR FILING DATE: 2000-09-15 NUMBER OF SEQ ID NOS: 20 SOFTWARE: Patentin version 3.0 SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-806-703A-12; Sequence 12, Application US/09806703A; GENERAL INFORMATION:
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US-09-806-703A-12
                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Clostridium tetani
US-09-677-374-19
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APPLICANT: Mouritsen, Soren
APPLICANT: Gautam, Anand
APPLICANT: Dalum, Iben
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity
Matches 15; Conserv
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US-09-980-916-23
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OTHER INFORMATION: Description of Artificial Sequence:Murine IL5 OTHER INFORMATION: modified by substitution with tetanus toxoid P2
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LOCATION: (30)...(44)

OTHER INFORMATION: Tetanus toxoid P2 epitope (SEQ ID NO: 23)

OTHER INFORMATION: Tetanus toxoid P2 epitope (SEQ ID NO: 23)

NAME/KEY: SIMILAR

LOCATION: (1)...(29)

OTHER INFORMATION: Identical to residues 1-29 in SEQ ID NO: 12

NAME/KEY: SIMILAR

LOCATION: (45)...(116)

OTHER INFORMATION: Identical to residues 42-113 in SEQ ID NO: 12

US-09-980-916-14
                                                                                                                                                                                                                 APPLICANT: Klysner, Steen
TITLE OF INVENTION: Method For Down-Regulating IL5 Activity
FILE REFERENCE: 3631-0112P
CURRENT APPLICATION NUMBER: US/09/980,916
CURRENT FILING DATE: 2001-10-23
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PATEULIN Ver. 2.1
SEQ ID NO 14
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                                                                                                                               US-09-980-916-14; Sequence 14, Application US/09980916; GENERAL INFORMATION:
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Matches 15; Conservative
                                                                                                                                                                                                  APPLICANT: M&E Biotech A/S APPLICANT: Klysner. Steen
               6 QYIKANSKFIGITEL 20
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US-09-980-916-52
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APPLICANT: Karlsson, Gunilla
APPLICANT: Rasmussen, Peter
TITLE OF INVENTYON: Novel Methods for Therapeutic Vaccination
FILE REFERENCE: 3631-0109P
CURRENT APPLICATION NUMBER: US/09/806,703A
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: DY/D899/00525
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1998-10-05
PRIOR FILING DATE: 1998-10-05
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 16
FEASTOR FILING DATE: 3.0
SEQ ID NO 16
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FEATURE:
CHER INFORMATION: Description of Artificial Sequence: Fusion of
JOHER INFORMATION: tetanus toxoid epitope and PSM
US-09-806-703A-16
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APPLICANT: Balum, Iben
APPLICANT: Hanning, Jesper
APPLICANT: Hanning, Jesper
APPLICANT: Nelsen, Klaus
APPLICANT: Rarisson, Gunilla
APPLICANT: Rarisson, Gunilla
APPLICANT: Rasmussen, Peter
TILE OF INVENTION: Novel Methods for Therapeutic Vaccination
FILE REFERENCE: 3631-01099
CURRENT APPLICATION NUMBER: US/09/806,703A
CURRENT APPLICATION NUMBER: US/09/806,703A
PRIOR FILING DATE: 2001-04-04
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US (10-05)
PRIOR APPLICATION NUMBER: US (60/105,011)
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Gautam, Anand
Dalum, Iben
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SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 17
LENGTH: 25
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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  Length 116;
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GENERAL INFORMATION:
APPLICANT: M&E Biotech A/S
APPLICANT: M&E Biotech A/S
TITLE OF INVENTION: Method For Down-Regulating IL5 Activity
FILE REFERENCE: 3631-0112P
CURRENT APPLICATION NUMBER: US/09/980,916
CURRENT FILING DATE: 2001-10-23
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PATENTIN Ver. 2.1
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100.0%; Score 74; DB 5; 1 100.0%; Pred. No. 1.2e-06;
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Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 15; Conservative 0; Mismatches 0;
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32 QYIKANSKFIGITEL 46

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30 QYIKANSKFIGITEL 44

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OTHER INFORMATION: Description of Artificial Sequence:Murine IL5 OTHER INFORMATION: modified by substitution with tetanus toxoid P2 OTHER INFORMATION: epitope
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LOCATION: (72)..(122)
COTHER INFORMATION: Identical to residues 63-113 in SEQ ID NO: 12
US-09-980-916-15
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OTHER INFORMATION: Identical to residues 1-83 in SEQ ID NO: 12
NAME/KEY: SHMLAR
LOCATION: (99)..(122)
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Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels
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OTHER INFORMATION: Tetanus toxoid P2 epitope (SEQ ID NO: 23)
NAMES/REY: SIMILAR
LOCATION: (1)...(56)
OTHER INFORMATION: Identical to residues 1-56 in SEQ ID NO:
                         Sequence 15, Application US/09980916

Sequence 15, Application US/09980916

GENERAL INFORMATION:
APPLICANT: MEE Biotech A/S
APPLICANT: Klysner, Steen
TITLE OF INVENTION: Method For Down-Regulating IL5 Activity
TITLE OF INVENTION: Method For Down-Regulating IL5 Activity
CURRENT FILING DATE: 2001-10-23

NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15.
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TITLE OF INVENTION: Method For Down-Regulating IL5 Activity
FILE REFERENCE: 3631-0112P
CURRENT APPLICATION NUMBER: US/09/980,916
CURRENT FILING DATE: 2001-10-23
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 122
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OTHER INFORMATION: Tetanus toxoid P2 epitope (SEQ ID NAME/KEY: SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/09980916; GENERAL INFORMATION:
APPLICANT: M&E Biotech A/S
APPLICANT: Klysner, Steen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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RESULT 12
US-09-980-916-15
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OTHER INFORMATION: modified by substitution with tetanus toxoid
OTHER INFORMATION: epitope
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CTHER INFORMATION: Identical to residues 44-115 in SEQ ID NO: US-09-980-916-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: SIMILAR
LOCATION: (1)..(31)
OTHER INFORMATION: Identical to residues 1-31 in SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: MUTAGEN
LOCATION: (32)..(46)
OTHER INFORMATION: Tetanus toxoid P2 epitope (SEQ ID NO: 23)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Klysner, Steen
TITLE OF INVENTION: Method For Down-Regulating IL5 Activity
FILE REFERENCE: 3631-0112P
CURRENT APPLICATION NUMBER: US/09/980,916
CURRENT FILING DATE: 2001-10-23
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 2.1
                                                                                                                             APPLICANT: Klysner, Steen
TITLE OF INVENTION: Method For Down-Regulating IL5 Activity
FILE REFERENCE: 3631-0112P
CURRENT APPLICATION NUMBER: US/09/980,916
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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11arity 100.0%; Pred. No. 1.2e-06;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 74; DB 5; L
100.0%; Pred. No. 1.2e-06;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-980-916-36; Sequence 36, Application US/09980916; GENERAL INFORMATION:
       RESULT 10
US-09-980-980-916-3
US-09-980-916-3
Sequence 3, Application US/09980916
GENERAL INFORMATION:
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTHER INFORMATION: modified to THER INFORMATION: epitope US-09-980-916-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: M&E Biotech A/S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 OYIKANSKFIGITEL 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 QYIKANSKFIGITEL 46
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Best Local Similarity
Matches 15; Conserv
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                            SEO ID NO 3
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OTHER INFORMATION: modified by substitution with tetanus toxoid P2
OTHER INFORMATION: epitope
NAME/KEY: MUTAGEN
LOCATION: (59)..(73)
OTHER INFORMATION: Tetanus toxoid P2 epitope (SEQ ID NO:23)
NAME/KEY: SIMILAR
LOCATION: (1)..(58)
OTHER INFORMATION: Identical to residues 1-58 in SEQ ID NO: 1
NAME/KEY: SIMILAR
LOCATION: (74)..(124)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Murine I1-5; OTHER INFORMATION: modified by substitution with tetanus toxoid OTHER INFORMATION: epitope US-09-980-916-54
. OTHER INFORMATION: Identical to residues 90-113 in SEQ ID NO: 12 US-09-980-916-16
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                                                                                                                                                                                                                                                                                                                                  Sequence 54, Application US/09980916
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MEE Biotech A/S
APPLICANT: MLysner. Steen
TITLE OF INVENTION: Method For Down-Regulating IL5 Activity
FILE REFERENCE: 3631-0112P
CURRENT FAPLICATION NUMBER: US/09/980,916
CURRENT FILIG DATE: 2001-10-23
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 54
LENGTH: 122
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                                                                                                 Length 122
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GENERAL INFORMATION:
APPLICANT: M&E Biotech A/S
APPLICANT: Klysner, Steen
TITLE OF INNENTION: Method For Down-Regulating IL5 Activity
FILE REFERENCE: 3631-0112P
                                                                                               Query Match 100.0%; Score 74; DB 5; Length 12 Best Local Similarity 100.0%; Pred. No. 1.3e-06; Matches 15; Conservative 0; Mismatches 0; Indels
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CURRENT FILING DATE: 2001-10-23
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 15; Conserv
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US-09-980-916-54
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; OTHER INFORMATION: Identical to residues 65-115 in SEQ ID NO: 1
US-09-980-916-4
Query Match
Query Match
Best Local Similarity 100.0%; Score 74; DB 5; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 1 QYIKANSKFIGITEL 15
Db 59 QYIKANSKFIGITEL 73
Search completed: January 29, 2002, 11:07:15
Job time: 533 sec
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(without alignments)
13.363 Million cell updates/sec
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                                                                                                                January 29, 2002, 11:06:39; Search time 353.23 Seconds
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/cgn2_6/ptodata/2/paa/USO92_COMB.pep:*
/cgn2_6/ptodata/2/paa/USO93_COMB.pep:*
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/cgn2_6/ptodata/2/paa/VS098_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US095_COMB.pep:*
/cgn2_6/ptodata/2/paa/US096_COMB.pep:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                3148936 seqs, 277657034 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                             US-09-763-397A-23
84
                                                                                                                                                                                                                                                                                                                                                                                                             seq length: 0 seq length: 2000000000
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Sequence:
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Maximum DB s
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Result Query No. Score Match DB ID Description

No. Score Match Length DB ID Description

1 84 100.0 17 21 US-09-763-397A-2 Sequence 23, Appl 3 45 53.6 743 16 US-09-58-11817 Sequence 2, Appl 5 44 52.4 169 19 US-09-583-110-4656 Sequence 4556, Ap 5 44 52.4 174 15 US-09-107-433-3442 Sequence 3442, Ap 5 44 52.4 225 24 US-06-269-308-4746 Sequence 4576, Ap 6 44 52.4 225 24 US-06-269-308-4746 Sequence 25566, Ap 7 3 51.2 86 1 PCT-US00-07726-121 Sequence 121, App 9 43 51.2 86 1 PCT-US00-07726-122 Sequence 122, App
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Sequence 1711, Ap	1642,	1793,	3012,	221, A	27800	Sequence 36112, A	Sequence 28258, A	426,	86' 1	3853	Sequence 3852, Ap	3851,	Sequence 882, App	Sequence 10, Appl	10,	~	Sequence 6, Appli	Sequence 108, App	Sequence 14, Appl		Sequence 36939, A	Sequence 17910, A	u,	Sequence 2, Appli	Sequence 17012, A		15,	•	577	1829	10,	16,	Sequence 11, Appl	Sequence 11, Appl
1 PCT-US00-05988-1711	US-60-146-394-	US-09-760-475-	US-09-760-475	US-60-245-201	US-60-173-464-2780	US-60-191-637	US-60-191-681-	US-60-212-664-	US-60-216-770-	US-09-391-631-	0S-09	US-09-391-631-	⊃	US-08-697-826-1	US-08-697-826A	ö	Ö		US-60-172-959-	PCT-US01-08631-	PCT-US01-08631-3	24 US-60-324-109-17910	US-09-573-655A-	Δ,	US-60-324-109-170	US-09-252-991A	us-08	ns-08-	US-09-270-767-577	US-09-270-849B-	US-09-147-729-1	US-09-284-327	-09-632-426	0 US-09-632-570-11
98 1													203	325		325	325																	
51.2																															46.4	46.4	46.4	46.4
43	43	43	43	43	43	43	43	42	42	42	42	42	42	41	41	41	41	40	40	40	40	40	40	40	40	40	40	40	39	39	39	39	39	39
10	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	36	40	41	42	43	44	45

ALIGNMENTS

Sequence 23, Application US/09763397A GENERAL INFORMATION:

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APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the Department of Health and Human Services, Centers for APPLICANT: Control and prevention
APPLICANT: Lal, Altaf A.
APPLICANT: Lal, Altaf A.
APPLICANT: Lal, Altaf A.
APPLICANT: Ping Shi, Ya
APPLICANT: Ping Shi, Ya
APPLICANT: Day Shi, Ya
APPLICANT: Ping Shi, Ya
APPLICANT: Now Shi Shi, Ya
APPLICANT: Ping Shi, Ya
CURRENT FILING DATE: 1980-08-21
PRIOR APPLICATION NUMBER: PCT / US99/18869
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 23
LENGTH: 17
LENGTH: 17
CORGANISM: Plasmodium falciparum
US-09-763-397A-23
Query Match
Matches 17: Conservative 0: Mismatches 0: Indels 0; Gaps 0;
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US-09-107-433-3442
US-09-107-433-3442,
Sequence 3442, Application US/09107433
Sequence 3442, Application US/09107433
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCCCCUS PNEUMONIAE
THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/05153
FILING DATE: JULy 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: CURROWN>
OPERATING SYSTEM: CURROWN>
SOFTWARRE: CURROWN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Streptococcus pneumoniae US-09-583-110-4656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 3442:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.4%;
50.0%;
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 50.0.
Trace 7; Conservative
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57 SRFLKKYKHELQDF 70
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                                                                                                                                       APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the Department of Health and Human Services, Centers for Dis APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A.
APPLICANT: Hashaih, Seyed E.
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falci TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falci CURRENT APPLICANTON NUMBER: US/09/763,397A
CURRENT APPLICANTON NUMBER: US 60/097,703
PRIOR FILING DATE: 1998-08-21
PRIOR PILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17817, Application US/09248796
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE OF INVENTION:
FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.13
CURRENT APPLICATION UNMBER: US/09/248,796
CURRENT FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 28206
SEQ ID NO 17817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknd
US-09-248-796-17817
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Pred. No. 2e+02;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 84; DB 21;
hilarity 100.0%; Pred. No. 2.5e-05;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Recombinant DNA/Protein
US-09-763-397A-2
                                                                                                                    Sequence 2, Application US/09763397A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 53.6%;
Best Local Similarity 64.3%;
Matches 9; Conservative
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            Query Match
Best Local Similarity
Matches 17; Conservat
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                                                                                          RESULT 2
US-09-763-397A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 2
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                           Indels
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                                                                                                                                          RESULT 8
PCT-USO0-07726-121
Sequence 121, Application PC/TUSO007726
Sequence 121, Application PC/TUSO007726
GENERAL INFORMATION:
TITLE OF INVENTION: 50 Human Secreted Proteins
FILE REFERENCE: PS538PCT
CURRENT APPLICATION NUMBER: PCT/USO0/07726
CURRENT FILING DATE: 2000-03-23
EARLIER APPLICATION NUMBER: 60/126,597
EARLIER FILING DATE: 1999-03-26
EARLIER FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 128
SOFTWARE PLEING VET: 2000-11-07
WHOMER OF SEQ ID NOS: 128
SOFTWARE: PLEING VET: 2.0
SEQ ID NO 121
LENGTH: 86
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Sequence 122, Application PC/TUSO007726
GENERAL INFORMATION:
TITLE OF INVENTION: 50 Human Secreted Proteins
FILE REFERENCE: PS538PCT
CURRENT FILING DATE: 2000-03-23
EARLIER PELING DATE: 1999-03-26
EARLIER PILING DATE: 1999-03-26
EARLIER PILING DATE: 1999-03-26
EARLIER FILING DATE: 1999-03-26
EARLIER FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 128
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33;
      Pred. No. 22;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
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Pred. No.
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      72.78;
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SEQ ID NO 122
LENGTH: 86
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Best Local Similarity 53.3
Matches 8; Conservative
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Best Local Similarity 53.3
Matches 8; Conservative
                       8; Conservative
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PCT-US00-07726-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
PCT-US00-07726-122
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34 TRMMKEFKGEI 44
                                                                  3 TRLMKKFKAEI 13
      Best Local Similarity
Matches 8; Conserv
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PCT-US00-05988-1711
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ORGANISM:
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Sequence 4746, Application US/60269308

Sequence 4746, Application US/60269308

SERENAL INFORMATION:
APPLICANT: Haselbeck, RW
APPLICANT: Chisen, KL
APPLICANT: Zyskind, JW
APPLICANT: Trawick, JD
APPLICANT: Trawick, JD
APPLICANT: Parawick, JD
APPLICANT: Correction of Essential Genes in Staphylococcus aureus, Pseuch TILLE OF INVENTION: Aecralia
TITLE OF INVENTION: Aecralia
FILLE REFERENCE: ELITRA.017PRS
CURRENT APPLICATION NUMBER: US/60/269,308
CURRENT APPLICATION NUMBER: US/60/269,308
CURRENT FILING DATE: 2001-02-16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4746
LENGTH: 225
APPLICANT: APPLICATION APPLICATION APPLICATION 4.0
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KEITH G. WEINSTOCK ET AL.
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS
TITLE OF INVENTION: PUNICATUS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATH99-10
CURRENT APPLICATION NUMBER: US/09/417,507
CURRENT FILING DATE: 1999-10-14
NUMBER OF SEQ ID NOS: 44312
SEQ ID NO 25566
LENGTH: 62
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Pred. No. 52;
5; Mismatches 2; Indels
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                                                                                ORGANISM: Streptococcus pneumoniae
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LOCATION: (B) LOCATION 1...174
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SEQUENCE DESCRIPTION: SEQ ID NO: 3442:
US-09-107-433-3442
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50.0%;
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60.0%;
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
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Best Local Similarity 50.0
Matches 7; Conservative
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92 TNTMRDFEAEIRDEF 106
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62 SRFLKKYKHELQDF 75
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ORGANISM: A.fumigatus
US-09-417-507-25566
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Best Local Similarity
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US-09-417-507-25566
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Sequence 1793, Application US/09760475

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
TITLE OF INVENTION: NUMBER: US/09/760,475

CURRENT APPLICATION NUMBER: US/09/760,475

CURRENT APPLICATION OF 201-01-16

Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 4122

SEQ ID NO 1793

LENGTH: 301
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Pred. No. 1.6e+02;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT249
CURRENT APPLICATION NUMBER: US/09/760,475
CURRENT FILING DATE: 2001-01-16
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 4122
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3012
LENGTH: 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 21; Length 301;
Pred. No. 1.5e+02;
                                                                  DB 24; Length 155;
67;
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                                                                                                                                   1; Mismatches
                                                                                            Score 43;
Pred. No. 6
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US-60-245-201-221
; Sequence 221, Application US/60245201
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53.3%;
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53.3%;
                                                                                                51.2%;
81.8%;
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Best Local Similarity 53.3
Matches 8; Conservative
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Best Local Similarity 53.3
Matches 8; Conservative
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282 LATRFLKSFKANLEN 296
                                                                                                Query Match 51.2
Best Local Similarity 81.8
Matches 9; Conservative
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CORGANISM: Homo sapiens
US-09-760-475-3012
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| S3 LALRVMKKFKA 63
; TYPE: PRT
; ORGANISM: Drosophila
US-60-146-394-1642
                                                                                                                                                                               1 LATRLMKKFKA 11
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                                                          TITLE OF INVENTION: "Human Prostate Cancer Associated Gene Sequences and Polypeptides FILE REFERENCE: PA101PCT
CURRENT APPLICATION NUMBER: PCT/USO0/05988
CURRENT FILING DATE: 2000-03-08
EARLIER APPLICATION NUMBER: 60/124,270
EARLIER FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1111
LENGTH: 98
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US-60-146-394-1642
US-60-146-394-1642
Sequence 1642, Application US/60146394
SEQUENCE 1642, Application US/60146394
GENERAL INFORMATION:
TATURE OF INVENTION: ACID MOLECULES ENCODING DROSOPHILA PROTEINS, AND USES THERE
TITLE OF INVENTION: ACID MOLECULES ENCODING DROSOPHILA PROTEINS, AND USES THERE
TITLE OF INVENTION: ACID MOLECULES ENCODING DROSOPHILA PROTEINS, AND USES THERE
CURRENT APPLICATION NUMBER: US/60/146,394
CURRENT FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 1866
SOFTWARE: FASLEG for Windows Version 3.0
SOFTWARE: FASLEG for Windows Version 3.0
SOFTWARE: 155
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APPLICANT: Steve Ruben
TITLE CART: Steve Ruben
TITLE CART: Steve Ruben
TITLE CART: Steve Ruben
TITLE CART: Steve Ruben
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT APPLICATION NUMBER: PCT/US00/05988
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SEQ ID NOS: 1890
SEQ ID NO 1711
LENGTH: 98
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                                                                                                                                                                                                                                                                                                                                                                       Length 98;
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                                                                                                                                                                                                                                                                                                                                                                     Score 43; DB 1;
Pred. No. 38;
3; Mismatches 4
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Pred. No.
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53.3%;
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79 LATRFLKSFKANLEN 93
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US-09-925-300-1711
                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
PCT-US00-05988-1711
                                     APPLICANT: Craig Rosen, APPLICANT: Steve Ruben
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Matches 8; Conserv
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Best Local Similarity
Matches 8; Conserv
                    GENERAL INFORMATION:
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LENGTH: 155

GENERAL INFORMATION:

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TITLE OF INVENTION: DRUG-METABOLIZING PHASE II
TITLE OF INVENTION: DRUG-METABOLIZING PROFEINS, NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: HUMAN DRUG-METABOLIZING PHASE II PROTEINS, AND USES THEREOF
TITLE OF INVENTION: HUMAN DRUG-METABOLIZING PHASE II PROTEINS, AND USES THEREOF
CURRENT APPLICATION NUMBER: US/60/245,201
CURRENT FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 221
LENGTH: 509
LENGTH: 509
TYPE: PRT
ORGANISM: Human
US-60-245-201-221
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                                                                                                                                                                                                                                                                                                                                                                                           Score 43; DB 24; Length 509;
Pred. No. 2.8e+02;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: January 29, 2002, 11:06:40 Job time: 622 sec
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LATRIMKKFKAEIRD 15
|||| :| ||| :
490 LATRELKSFKANLEN 504
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; ORGANISM: Enterococcus faecalis
US-09-815-242-5021
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Best Local Similarity 60.0
Matches 9; Conservative
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92 TNTMRDFEAEIRDEF 106
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                                                                                                                                           (without alignments)
20.801 Million cell updates/sec
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                                                                                                                    Search time 29.91 Seconds
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/cgn2_6/ptodata/2/paa/NG6_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US03_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US03_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US03_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-815-242-5021
US-09-108-427-10555
US-09-708-427-10555
US-09-708-427-30719
US-09-708-427-30719
US-09-708-427-30719
US-09-708-427-30719
US-09-708-427-29819
US-09-708-427-29818
US-09-708-427-29818
US-09-708-427-19349
US-09-708-427-19349
US-09-708-427-19349
US-09-708-427-19349
US-09-708-427-58150
US-09-708-427-58169
US-09-708-427-57580
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                                                                                                                                                                                                                                                                                                                                            173191 segs, 36597120 residues
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                                                                                                                  January 29, 2002, 11:07:15
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pending_Patents_AA_New:*
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                          1 LATRLMKKFKAEIRDFF 17
                                                                                                                                                                                      US-09-763-397A-23
84
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Maximum DB seq length: 2000000000
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Match
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Sequence:
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                                                                              OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                    Run on:
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Sequence 32986, A Sequence 32985, A Sequence 15113, A Sequence 15112, A Sequence 15111, A Sequence 7669, Ap Sequence 7669, Ap Sequence 25459, A Sequence 25459, A Sequence 63471, A Sequence 63471, A Sequence 63471, A Sequence 63469, A Sequence 63471, A Sequence 63471, A Sequence 63469, A Sequence 63471, A Sequence 63471, A Sequence 63471, A Sequence 63469, A Sequence 7949, Ap Sequence 7949, Ap Sequence 1213, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: HASELDECK, KOUELL
APPLICANT: Oblisen, Kari L.
APPLICANT: Oblisen, Kari L.
APPLICANT: Oblisen, Wall, Daniel
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Vanmamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVEWION: Identification of Essential Genes in
TITLE OF INVEWION: Identification of Essential Genes in
TITLE OF INVEWION: Prokaryotes
FILE REFREENCE: ELITRAN.011A
CURRENT APPLICATION NUMBER: 06/191,078
PRIOR APPLICATION NUMBER: 60/201,177
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-28
PRIOR APPLICATION NUMBER: 60/207,777
PRIOR APPLICATION NUMBER: 60/207,777
PRIOR APPLICATION NUMBER: 60/207,777
PRIOR APPLICATION NUMBER: 60/207,931
PRIOR APPLICATION NUMBER: 60/203,938
PRIOR APPLICATION NUMBER: 60/203,938
PRIOR APPLICATION NUMBER: 60/203,938
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/209,308
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/209,308
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/209,308
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/209,308
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-20-10
SOOTWARE: FastSED for Windows Version 4.0
SOOTWARE: FastSED for Windows Version 4.0
LEWATH: 225
               US-09-708-427-32985
US-09-708-427-32984
US-09-708-427-15113
US-09-708-427-15113
US-09-708-427-15111
US-09-620-394B-7669
US-09-620-394B-7667
US-09-708-427-25458
US-09-708-427-25458
US-10-708-427-25458
US-10-708-427-25458
                                                                                                                                                                                                                                                             US-09-708-427-63470
US-09-708-427-63469
US-09-708-446A-1237
US-09-897-516-7949
US-09-760-446A-1213
                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5021, Application US/09815242
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
 1073
11122
1206
1810
191
191
207
337
483
330
330
1715
1715
155
155
167
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Gaps

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Length 225 Indels

DB 5;

Score 44; DB 5 Pred. No. 5.4; 2; Mismatches

52.4%; 60.0%;

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Sequence 10553, Application US/09708427

GENERAL INFORMATION:
APPLICANT: N. ALEXANDROW et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOGTWARE: Patentin version 3.1
SEQ ID NO 10553
LENGTH: 353
                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: THEREBY
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SEQ ID NO 10554
LENGTH: 335
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           Length 297;
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                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43; DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43; DB 5;
Pred. No. 12;
4; Mismatches
             Score 43; DB 5;
Pred. No. 11;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1..353
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ID 1821588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
CATTON: 1..335
COTHER INFORMATION: Ceres Seq. ID 1821589
08-09-708-427-10554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Arabidopsis thaliana
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LOCATION: 1..353
CTHER INFORMATION: Ceres Seq.
US-09-708-427-10553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1..335
OTHER INFORMATION: Xaa is any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.2%;
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                  51.2%;
58.3%;
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Matches 7; Conservative
                                                            Conservative
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36 LDKFKSDIQDFF 47
Query Match
Best Local Similarity
7; Conserve
                                                                                                     6 MKKFKAEIRDFF 17
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US-09-708-427-10553
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Sequence 10555, Application US/09708427

Sequence 10555, Application US/09708427

Sequence 10555, Application US/09708427

GENERAL INFORMATION:

APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: THEREBY

TITLE OF INVENTION: THEREBY

TITLE OF INVENTION: THEREBY

CURRENT APPLICATION NUMBER: US/09/708, 427

CURRENT APPLICATION NUMBER: US/09/708, 427

SOFTWARE: PATENTING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SEQ ID NO 10555

LENGTH: 297
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                                                                                                                                                                                                                     APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-12-22
PRIOR PELING DATE: 2000-12-22
PRIOR PELING DATE: 2010-12-22
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LOCATION: 1..297
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..297
OTHER INFORMATION: Ceres Seq. ID 1821590
US_09-708-427-10555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FastSEQ for Windows Version 4.0
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Pred. No.
                        Sequence 10689, Application US/09815242 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Enterococcus faecalis
US-09-815-242-10689
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                                                                                                                                                    Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.4%;
                                                                                          Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 52.4
Best Local Similarity 60.0
Matches 9; Conservative
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92 TNTMRDFEAEIRDEF 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 10689
                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH
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APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 29820
LENGTH: 593
                                                                                                                                                                APPLICATE: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REPERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 5;
34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 42; DB 5;
Pred. No. 22;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
1.593
1.0CATION: 1.593
2.0CHION: INFORMATION: Xaa is any amino acid
3.NAME/KEY: misc_feature
1.593
1.0CATION: 1..593
US-09-708-427-29820
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..398
. CTHER INFORMATION: Ceres Seq. ID 1830097
US-09-708-427-30717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42;
Pred. No.
                                                                                                                                    Sequence 30717, Application US/09708427 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 29820, Application US/09708427 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Arabidopsis thaliana
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61.5%;
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60.0%;
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Best Local Similarity 60.0.
See 9; Conservative
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Best Local Similarity 61.5
Matches 8; Conservative
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165 ATRLFKKLRVEIEMF 179
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    2 ATRLMKKFKAEIRDF 16
                                        85 ATRLFKKLRVEIEMF 99
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LOCATION: 1..398
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LENGTH: 398
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Sequence 30718, Application US/09708427
Sequence 30718, Application US/09708427
GENERAL INFORMATION:
TITLE OF INVERTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVERTION: THEREBY
TITLE OF INVERTION: THEREBY
TITLE OF INVERTION: THEREBY
TITLE OF INVERTION: THEREBY
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 30718
                                                                                                                                                                                                                            APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
LENGTH: 313
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                      Indels
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17;
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Pred. No. 17;
1; Mismatches
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Pred. No. 13;
4; Mismatches
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LOCATION: 1..313
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: misc_feature
; LCCATION: 1..313
; CTHER INFORMATION: Ceres Seq. ID 1830099
US-09-708-427-30719
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NAME/KEY: misc_feature
LOCATION: 1..318
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US-09-708-427-30719
; Sequence 30719, Application US/09708427
; GENERAL INFORMATION:
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60.0%;
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  58.3%;
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Best Local Similarity 60.0
Matches 9; Conservative
Best Local Similarity 58.3
Matches 7; Conservative
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Matches 9; Conservative
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92 LDKFKSDIQDFF 103
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LOCATION: 1..318
                                                        6 MKKFKAEIRDFF 17
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US-09-708-427-19349

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APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 19348
Sequence 19349, Application US/09708427
Sequence 19349, Application US/09708427
Sequence ID SEQUENCE ALLEXANDROW et al.
APPLICANT: N. ALEXANDROW et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID FILLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: US/09/708,427
SUFFRENT APPLICATION NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 19349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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ced. No. 24;
Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5;
23;
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NAME/KEY: misc_feature
CATATON: 1.314
US-09-708-427-19348
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Pred. No.
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LOCATION: 1..303
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Ceres Seq. ID 1835886 US-09-708-427-19349
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US-09-708-427-19347
; Sequence 19347, Application US/09708427
; GENERAL INFORMATION:
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity 66.7
Matches 8; Conservative
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LOCATION: 1..314
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| 139 RVMKKVQAEIRE 150
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128 RVMKKVQAEIRE 139
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Matches 8; Conserv
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 29818
LENGTH: 743
                                                                                                APPLICANT: N. ALEXANDROV et al.
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REPERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 29819
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Pred. No. 40;
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Pred. No. 44;
1; Mismatches
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LOCATION: 1..743
OTHER INFORMATION: Xaa is any amino acid
MAME/KEY: misc_feature
LOCATION: 1..743
OTHER INFORMATION: Ceres Seq. ID 1827156
                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
CCATION: 1..686
CTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
CCATION: 1..686
CTHER INFORMATION: Ceres Seq. ID 1827157
US-09-708-427-29819
                                                                               ; Sequence 29819, Application US/09708427; GENERAL INFORMATION:
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61.5%;
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61.5%;
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Best Local Similarity 61.5
Matches 8; Conservative
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285 LMKKFQTSTRDLF 297
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Best Local Similarity
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US-09-708-427-29818
                                                                   US-09-708-427-29819
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US-09-708-427-58150
Sequence 58150, Application US/09708427
GENERAL INFORMATION:
TERRETE INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOGTWARE: PATENTIN VENTION 3.1
SEQ ID NO 58150
LENGTH: 302
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
FILE REFERENCE: 2750-1243P
CURRENT PILLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 19347
LENGTH: 503
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Pred. No. 41;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: 1..503
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..503
COTHER INFORMATION: Ceres Seq. ID 1835884
US-09-708-427-19347
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NAME/KEY: misc_feature
LOCATION: 1..302
O'THER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..302
COTHER INFORMATION: Ceres Seq. ID 1941286
US-09-708-427-58150
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ORGANISM: 2ea mays subsp. mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 66.7%;
Matches 8; Conservative
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119 RVMKKLQAEVRAY 131
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328 RVMKKVQAEIRE 339
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                                                                                                                                                                                                                                             TYPE: PRT
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Search completed: January 29, 2002, 11:07:15 Job time: 533 sec

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us-09-763-397a-22.rapm

Sequence 1817, A Sequence 3322, Ap Sequence 3322, Ap Sequence 219, App Sequence 11, App Sequence 12, App Sequence 12, App Sequence 60, App Sequence 60, App Sequence 60, App Sequence 110, App Sequence 2703, Ap Sequence 2703, Ap Sequence 2703, Ap Sequence 33984, A Sequence 180, App Sequence 18, App Sequence 18, App Sequence 18, App Sequence 18, App Sequence 118, App Sequence 118, App Sequence 117792, A Sequence 21, App Seq

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Sequence 22, Application US/09763397A

APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Control and Prevention

APPLICANT: Lal, Altaf A.

APPLICANT: Lal, Altaf A.

TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Fa FILE REPRENEUE. 6395-57049

TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Fa CURRENT APPLICATION NUMBER: US/09/763,397A

CURRENT APPLICATION NUMBER: US 60/097,703

PRIOR FILING DATE: 1998-08-21

PRIOR FILING DATE: 1999-08-19

PRIOR FILING DATE: 1999-08-19

SEQ ID NOS: 26

SEQ ID NOS: 26

SEQ ID NOS: 26

SEQ ID NOS: 26
         14 US-60-324-109-18117

15 US-60-169-840-5493

16 US-60-173-469-1145

17 US-09-768-459-219

18 US-09-396-149-14

19 US-09-396-149-14

19 US-09-396-149-16

19 US-09-396-149-16

19 US-09-396-149-16

19 US-09-396-149-16

19 US-09-396-149-16

19 US-09-396-149-16

19 US-09-396-149-18

19 US-09-50-083-3186

19 US-09-50-083-4481

19 US-09-396-149-18

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tive 0;
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 Query Match
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Sequence 15071, A
Sequence 11903, A
Sequence 409, Appl
Sequence 26094, A
Sequence 10, Appli
Sequence 2, Appli
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Sequence 15071, A
Sequence 11903, A
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13.363 Million cell updates/sec
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-763-397A-2
US-60-191-637-15071
US-60-191-681-11903
US-60-324-109-26094
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Gaps

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Length 17; Indels

Score 79; DB 21; Pred. No. 0.00015; Mismatches 0;

States of America, as represented by the of Health and Human Services, Centers for

Sequence Sequence Sequence

ALIGNMENTS

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GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE O
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-758-443-408
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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US-09-758-443-408
Sequence 408, Application US/09758443
Sequence 408, Application US/09758443
Sequence 408, Application US/09758443
FILE REPERBERE: PM039
CURRENT PILLE DESTRERENCE: PM039
CURRENT FILING DATE: 2001-01-11
PRIOR PPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR PPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 432
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 408
LENGTH: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Pred. No. 7.9e+02;
1; Mismatches 2; Indels
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pred. No. 21; 
4; Mismatches 3; Indels
Sequence 11903, Application US/60191681
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Matches 10; Conservative
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Best Local Similarity 76.9
Matches 10; Conservative
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645 PSSTDNSPSNAKS 657
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ORGANISM: Homo sapiens
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US-60-191-681-11903
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US-60-324-109-26094
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Sequence 2, Application US/09763397A

Sequence 2, Application US/09763397A

GENERAL INFORMATION:

APPLICANT: The Government of the United States of America, as represented by the papplicant: Secretary of the Department of Health and Human Services, Centers for Dis APPLICANT: Cootrol and Prevention

APPLICANT: Lal, Altaf A.

APPLICANT: Lal, Altaf A.

APPLICANT: Ping Shi, Ya.

APPLICANT: Ping Shi, Ya.
                                                                                                                                                                                                                                                                                                                                                                                                                           PAPLICANT: Hasnain, Seyed E.
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falci
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falci
CURRENT PAPLICATION NUMBER: US/09/763,397A
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR PILING DATE: 1998-08-21
PRIOR FILING DATE: 1998-08-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
SEQ ID NO S: 26
LENGTH: 350
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TITLE OF INVENTION: UNCLEIC ACID DETECTION KITS COMPRISING
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000392
CURRENT APPLICATION UNMBER: US/60/191,637
CURRENT FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 42660
SOFTWARRE: FastSEQ for Windows Version 4.0
SEQ ID NO 15071
LENGTH: 2559
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Pred. No. 0.16;
0; Mismatches 0; Indels 1
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94.48;
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Matches 10; Conservative
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Best Local Similarity 94.4
Matches 17; Conservative
                        1 SSPSSTKSSPSNVKSAS 17
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645 PSSTDNSPSNAKS 657
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US-60-191-637-15071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-60-191-637-15071
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US-60-191-681-11903

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1 SSPSSTKSSPSNVKSAS 17
       SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 64.7
Matches 11; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (1)...(106)
                                                                                                     TYPE: PRT CORGANISM: Arabidopsis PCT-US99-08954-2
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US01-08631-37162
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US-09-715-774-10
                                   SEQ ID NO 2
LENGTH: 328
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PCT-US99-08954-2
; Sequence 2, Application PC/TUS9908954
; General J. Application PC/TUS9908954
; General Linchard State St
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                                                    APPLICANT: Cao, Yongwei
APPLICANT: Edgerton, Michael D
APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REPERENCE: 38-10(52726)B
CURRENT APPLICATION NUMBER: US/60/324,109
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 33196
SEQ ID NO 26094
LENGTH: 179
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Pred. No. 74;
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Pred. No. 1.5e+02;
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Sequence 10, Application PC/TUSO031739
GENERAL INFORMATION:
TITLE OF INVENTION: Modulation of Abscisic Acid
FILE REFERENCE: 35718/205302
CURRENT PFLIATON NUMBER: PCT/USO0/31739
CURRENT FLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: US 60/166,080
PRIOR FILING DATE: 1999-11-17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
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Sequence 26094, Application US/60324109 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60.8%;
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64.7%;
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Matches 11; Conservative
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Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Glycine max
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| EBROTH | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 197 | 1
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; Sequence 1145, Application US/60173469
; GENERAL INFORMATION:
APPLICANT: BONAZZI, VIVIEN
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: UGCENCE ACID MOLECULES ENCODING HUMAN SECRETED PROTIENS AND
; TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                        TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REPERENCE: CL000121
CURRENT APPLICATION NUMBER: US/60/17,571
CURRENT FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 5082
SOFTWARE: FRALSEQ for Windows Version 4.0
SEQ ID NO 3322
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERCECE: PMO29
CURRENT APPLICATION NUMBER: US/09/758,459
CURRENT PILING DATE: 2001-01-11
FRIOR FILING DATE: 2000-01-01-11
FRIOR FILING DATE: 2000-01-01-11
FRIOR FILING DATE: 2000-01-04
NUMBER OF SEQ ID NOS: 406
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 176;
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Pred. No. 1.6e+02;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 46; DB 24;
Pred. No. 1.4e+02;
1; Mismatches 5
                                                                                                                                      Sequence 3322, Application US/60177571 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-758-459-219; Sequence 219, Application US/09758459; GENERAL INFORMATION:
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64.7%;
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64.7%;
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                       145 SSPSSLSTSPPEVFSAS 161
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Best Local Similarity 64.7
Matches 11; Conservative
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Best Local Similarity 64.7%
Matches 11; Conservative
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1 SSPSSTKSSPSNVKSAS 17
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CORGANISM: Homo sapiens
US-09-758-459-219
                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: HUMAN
US-60-177-571-3322
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US-60-173-469-1145
                                                                                                     RESULT 13
US-60-177-571-3322
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                                          QQ
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TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
FITLE OF INVENTION: USES THEREOF
FITLE REFERENCE: CLOOO164
CURRENT APPLICATION NUMBER: US/60/169,840
NUMBER OF SEQ ID NOS: 9628
SOFTWARE: FASTESO for Windows Version 4.0
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APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)B
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 33196
SEQ ID NO 18117
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                                                                                  Length 106;
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                                                                                                                            4; Indels
; OTHER INFORMATION: Xaa - X or * as defined in Table PCT-US01-08631-37162
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Pred. No. 1.4e+02;
1; Mismatches 5;
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Pred. No. 1.2e+02;
                                                                                  Score 46; DB 1;
Pred. No. 79;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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; LOCATION: (1)...(174)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-60-169-840-5493
                                                                                                                                                                                                                                                                                                           Sequence 18117, Application US/60324109 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5493, Application US/60169840; GENERAL INFORMATION: APPLICANT: Bonazzi, Vivien
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Best Local Similarity 64.7%;
Matches 11; Conservative
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Best Local Similarity 58.8%;
Matches 10; Conservative
                                                                                      58.2%;
58.8%;
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                                                                                                                                                                                               41 SSPSSSSPSPSSSSSS 57
                                                                                                                                Conservative
                                                                                      Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Zea mays
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ORGANISM: Human
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LENGTH: 174
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US-09-801-368-384
   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16088, A Sequence 384, App Sequence 120, App Sequence 119, App Sequence 119, App Sequence 1118, App Sequence 1119, App Sequence 3136, App Sequence 3136, App Sequence 3869, App Sequence 3689, App Sequence 3589, App Sequence 3596, App Sequence 3596, App Sequence 3596, App Sequence 5596, App Sequence 5596, App Sequence 5596, App Sequence 76259, App
                                                                                                                                                                                                                            (without alignments)
20.801 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                 Search time 29.91 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pending_Patents_AA_New:*

!: /cgn1_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

!: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

!: /cgn2_6/ptodata/2/paa/USO7_NEW_COMB.pep:*

!: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*

!: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*

!: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*

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                        4.5
Compugen Ltd
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US-09-801-368-384

US-09-637-780B-120

US-09-708-427-82455

US-09-708-427-82455

US-09-708-427-82455

US-09-708-427-82455

US-09-708-427-82453

US-09-708-427-8137

US-09-708-427-3136

US-09-708-427-3136

US-09-708-427-3136

US-09-708-427-3136

US-09-708-427-3168

US-09-708-427-31008

US-09-708-427-3108-427-5596

US-09-708-427-5596

US-09-708-427-5596

US-09-708-427-5596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173191 seqs, 36597120 residues
                                                                                                                                                                                           January 29, 2002, 10:58:22;
                        GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                          1 SSPSSTKSSPSNVKSAS 17
                                                                                                                                           protein search, using
                                                                                                                                                                                                                                                                                            US-09-763-397A-22
79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq length: 0 seq length: 2000000000
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Match Length
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Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB
Maximum DB
                                                                                                                                        OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                                                                                                                 Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Result
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Sequence 16088, Application US/09708427
GENERAL INFORMATION:
APPLICAMT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REPERENCE: 2750-1143P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Partentin version 3.1
SEQ ID NO 16088
LENGTH: 328
                                                                                                                                                                                                                                                                                                                                                                                                                                471, Ab.
26 47193, A
26 4151, Ap
20, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
       4982, Ap
4981, Ap
3568, Ap
17129, A
17127, A
3567, Ap
                                                                                                                                                                                                                                                                                                           424, App
2, Appli
4152, Ap
47194, A
761, App
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7376, Ap
61, Appl
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                                          Sequence Seq
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64.7%; Pred. No. 2.7;
iive 2; Mismatches 4; Indels
US-09-620-111B-4982

US-09-620-11B-4981

US-09-708-427-3568

US-09-708-427-17129

US-09-708-427-17129

US-09-708-427-17127

US-09-708-427-3567

US-09-801-368-424

US-09-964-238-2

US-09-964-238-2

US-09-964-238-2

US-09-964-238-2

US-09-620-111B-4152

US-09-620-111B-761

US-09-620-111B-761

US-09-620-111B-761

US-09-620-111B-761

US-09-620-111B-761

US-09-620-111B-761

US-09-620-111B-760

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 1..328
CUTER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..328
OTHER INFORMATION: Ceres Seq. ID 1830172
US-09-708-427-16088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 384, Application US/09801368
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Mathne, Todd
APPLICANT: Mary
APPLICANT: Mary
APPLICANT: Mary
APPLICANT: Solie
Salama, Solie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 SSPSSVSSSSSSVSAAS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SSPSSTKSSPSNVKSAS 17
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Matches 11; Conservative
```

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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid;
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
CURRENT APPLICATION NUMBER: US/09/637,780B
CURRENT FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 1401
SEQ ID NO 119
LENGTH: 200
                                                                                                                           APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
TITLE OF INVENTION: Thereby
FILE REPERENCE: 2750-1036P
CURRENT APPLICATION NUMBER: US/09/637,780B
CURRENT RILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 1401
SEQ ID NO 120
LENGTH: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 46; DB 5;
Pred. No. 3.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 46; DB 5;
Pred. No. 3.3;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature

: LOCATION: 1..208

: CHER INFORMATION: Ceres Seq. ID 1481702

US-09-637-780B-119
                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 1..200
CHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..200
OTHER INFORMATION: Ceres Seq. ID 1481703
US-09-637-7808-120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Xaa is any amino acid
                                                             Sequence 120, Application US/09637780B GENERAL INFORMATION: APPLICANT: ALEXANDROV, Nickolai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                              ORGANISM: Arabidopsis thaliana
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58.8%;
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 10; Conserv
                                  RESULT 4
JS-09-637-780B-120
                                                                                                                                                                                                                                                                                                              TYPE: PRT
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APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Sulmars, Eaff
APPLICANT: Summers, Eaff
APPLICANT: Summers, Eaff
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT PEPLICATION NUMBER: US/09/801,368
CURRENT PELLING DATE: 2000-03-07
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SEQ ID NOS: 440
SEQ ID NO 384
LENGTH: 515
                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production
TITLE OF INVENTION: an Fungi
FILE REFERENCE: 109272.147
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                              DB 5; Length 515;
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Pred. No. 6.3;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 6.3;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/487,558
CURRENT FILING DATE: 2000-01-19
                                                                                                                                                                                                                                                                                                                                                                                                  Score 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION UNMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US/09/801,368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 384, Application US/09487558
GENERAL INFORMATION:
APPLICANT: Busby, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Saccharomyces cerevisiae US-09-487-558-384
                                                                                                                                                                                                                                                                                                                      ORGANISM: Saccharomyces cerevisiae US-09-801-368-384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 440, SOFTWARE: PatentIn version 3.0
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56.2%;
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Hecht, Peter
Holtzman, Doug
Madden, Kevin
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 59.5
Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 SPSSTKSSPSNVKSAS 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Royer, John
Salama, Sofie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sherman, Amir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maxon, Mary
Milne, Todd
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APPLICANT:
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                                                                                                                                                                                                                                                                                                        TYPE: PRT
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Gaps

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SIPTSLKSSPAPVTSGS 141

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Gaps

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RESULT

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Gaps

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4; Indels

130 SPSSTNSTPSTIQGLS 145

2 SPSSTKSSPSNVKSAS 17

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TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding Polypeptid TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding Polypeptid TITLE OF INVENTION: Thereby FILE OF INVENTION: Thereby CURRENT APPLICATION NUMBER: US/09/637,780B CURRENT FILING DATE: 2000-08-11 NUMBER OF SEQ ID NOS: 1401 SEQ ID NOS: 1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT PAPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
LENGTH: 297
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; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID;
; TITLE OF INVENTION: THEREBY
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5;
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Pred. No. 5
                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
1.0297
1.020710N: 1.0397
2.07HER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
1.0CATION: 1..297
3.07HER INFORMATION: Ceres Seq. ID 1481701
US-09-637-7809-118
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Pred. No. 5
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; LCCATION: 1..297
US-09-708-427-82453
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                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Arabidopsis thaliana
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58.8%;
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58.8%;
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ORGANISM: Zea mays subsp.
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Matches 10; Conservative
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LOCATION: 1..297
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US-09-708-427-11927
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SEOFWARE: Patentin version 3.1
SEO ID NO 84454
LENGTH: 273
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Pred. No. 4.5;
3; Mismatches
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Pred. No. 4.6;
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US-09-708-427-82455
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: LOCATION: 1..273

: OTHER INFORMATION: Ceres Seq. ID 1960818

US-09-708-427-82454
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                                                                                 Sequence 82455, Application US/09708427 GENERAL INFORMATION:
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58.8%;
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58.8%;
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Best Local Similarity 58.8
Matches 10; Conservative
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Best Local Similarity 58.8
Matches 10; Conservative
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LOCATION: 1..272
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LOCATION: 1..272
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LOCATION: 1..273
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Sequence 3870, Application US/09620394B

Sequence 3870, Application US/09620394B

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-1067P
CURRENT APPLICATION NUMBER: US/09/620,394B

CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9131
SEQ ID NO 3870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1249
FILE REFERENCE: 2750-1249
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 3135
LENGTH: 1194
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Pred. No. 45;
4; Mismatches
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46;
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                                                              TYPE: PT.

TYPE: PT.

TYPE: PT.

OKGANISM: Arabidopsis thaliana

FEATURE:

NAME/KEY: misc_feature

COCATION: 1..1170

OTHER INFORMATION: Xaa is any amino acid

NAME/KEY: misc_feature

'OCATION: 1..1170

'OTHER INFORMATION: Araba Seq. ID 1810131
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LOCATION: 1..1194
OTHER INFORMATION: Xaa is any amino acid
OTHER INFORMATION: LOCATION: 1..1194
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; OTHER INFORMATION: Ceres Seq. ID 1810130
US-09-708-427-3135
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Pred. No.
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US-09-708-427-3136
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52.9%;
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Best Local Similarity 52.5.
Conservative 9;
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Best Local Similarity 52.9
Matches 9; Conservative
                SOFTWARE: PatentIn version
SEQ ID NO 3136
LENGTH: 1170
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NUMBER OF SEQ ID
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
FILE REPRENCE: 1750-11249
FILE REPRENCE: 2750-11249
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PALENTIN VETSION 3.1
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44;
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Pred. No. 7.7;
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Pred. No. 4
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CCATION: 1..229

OTHER INFORMATION: Xaa is any amino acid
NAME/REY: misc_feature

LOCATION: 1..229

COTHER INFORMATION: Ceres Seq. ID 1824027

US-09-708-427-11927
      FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SEQ ID NO 11927
LENGTH: 229
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CATTON: 1...1157
CTHER INFORMATION: Xaa is any am;
NAME/KEY: misc_feature
CATTON: 1...1157
CTHER INFORMATION: Ceres Seq. ID
US-09-708-427-3137
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                                                                                                                                                                ORGANISM: Arabidopsis thaliana
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58.8%;
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Matches 10; Conservative
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Best Local Similarity
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US-09-708-427-3136
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US-09-708-427-3137
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RESULT 15
US-09-620-394B-3869
US-09-620-394B-3869
Sequence 3869, Application US/09620394B
Sequence 3869, Application US/09620394B
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
CURRENT APPLICATION NUMBER: US/09/620,334B
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9131
SEQ ID NOS: 9131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 54.4%; Score 43; DB 5; Length 231; Best Local Similarity 58.8%; Pred. No. 11; Matches 10; Conservative 3; Mismatches 4; Indels
             TYPE: PRT
ORCANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
COCATION: 1..215
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
1..215
COTHER INFORMATION: Ceres Seq. ID 1387751
US-09-620-3948-3870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
| LOCATION: 1..231
| COTHER INFORMATION: Xaa is any amino acid
| NAME/KEY: misc_feature
| LOCATION: 1..231
| COCATION: 1..231
| COCATION: Ceres Seq. ID 1387750
US-09-620-394B-3869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Arabidopsis thaliana
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Best Local Similarity 58.88
Matches 10; Conservative
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LENGTH: 215
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Sequence 7160, Ap Sequence 849, App Sequence 849, App Sequence 60152, A Sequence 7042, A Sequence 7042, A Sequence 6776, App Sequence 6776, App Sequence 568, App Sequence 5749, App Sequence 5749, App Sequence 5749, App Sequence 6011, App Sequence 6011, App Sequence 2749, App Sequence 2749, App Sequence 6011, App Sequence 2041, App Sequence 2230, App Sequence 2230, App Sequence 2230, App Sequence 2230, App Sequence 2241, App Sequence 24612, App Seque

Sequence 9961, Ap Sequence 964, App Sequence 4681, Ap Sequence 7145, Ap Sequence 2730, Ap Sequence 6302, Ap Sequence 11, App1 Sequence 11, App1 Sequence 11, App1

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Gaps

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Length 8; Indels

Score 41; DB 21; Pred. No. 2.9e+06; Mismatches 0;

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Sequence 21, Application US/09763397A

GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Cascretary of the Department of Health and Human Services, Centers for APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A.
APPLICANT: Hasnain, Seyed E.
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Fa FILE REFERENCE: 6395-57049
CURRENT FLING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US/09/763,397A
CURRENT FLING DATE: 1998-08-21
PRIOR APPLICATION NUMBER: PCT / US99/18869
PRIOR APPLICATION NUMBER: PCT / US99/18869
US-09-328-352-7160

US-00-146-055-775

US-00-147-055-775

US-09-270-469B-189381

US-09-270-767-4698

US-09-270-767-4698

US-00-173-464-7042

US-00-191-637-8177

US-00-191-637-8177

US-00-191-637-8177

US-09-270-767-4564

US-09-270-767-4564

US-09-270-767-4564

US-09-270-767-4564

US-09-107-532-5749

US-00-101-507-316-1993

US-00-101-700-2169

US-00-101-700-2169

US-00-101-700-2169

US-00-101-700-2169

US-00-101-700-2169

US-00-101-700-2169

US-00-101-700-2169

US-00-314-050-7145

US-00-314-050-7145

US-00-314-050-7145

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US-00-314-050-7145

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US-00-259-128-468
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Best Local Similarity 100.0%; Pr
Matches 8; Conservative 0;
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SOFTWARE: Patentin version 3.1
SEQ ID NO 21
    1 LTPLEELY
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  ORGANISM:
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Sequence 2, Appli
Sequence 2603, Ap
Sequence 113, App
Sequence 35531, A
Sequence 440, Ap
Sequence 440, Ap
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Sequence 60, Appl
Sequence 2, Appli
                                                                                             Search time 1760.55 Seconds (without alignments) 1.262 Million cell updates/sec
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1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/DSO6_COMB.pep:*
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4: /cgn2_6/ptodata/2/paa/USO8_COMB.pep:*
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23: /cgn2_6/ptodata/2/paa/USO9_COMB.pep:*
23: /cgn2_6/ptodata/2/paa/USO9_COMB.pep:*
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                version 4.5
- 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                       protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                GenCore
Copyright (c) 1993
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                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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ALIGNMENTS

us-09-763-397a-21.rapm

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Sequence 35531. Application US/09417507
Sequence 35531. Application US/09417507
SERBRAL INFORMATION:
APPLICANT: KETTH G. WEINSTOCK ET AL.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS
TITLE OF INVENTION: FUMICATUS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATH99-10
CURRENT APPLICATION NUMBER: US/09/417,507
CURRENT FILING DATE: 1999-10-14
NUMBER OF SEQ ID NOS: 44312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADPLICANT: VENTER: J. Craig et al.
ADPLICANT: VENTER: J. Craig et al.
TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
TITLE OF INVENTION: USES THEREOF
FILE REPERENCE: CLOO786
CURRENT APPLICATION NUMBER: US/09/948,947
PRIOR APPLICATION NUMBER: 60/231,397
PRIOR FILING DATE: 2000-09-08
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                                                                                             Sequence 2603, Application US/09760475
; Sequence 2603, Application US/09760475
; GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
TITLE OF INVENTION: NUMBER: US/09/760,475
; CURRENT APPLICATION NUMBER: US/09/760,475
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION GATE: 2001-01-16
; SOFTWARE: PALCHIN VET. 2.0
; SOFTWARE: PALCHIN VET. 2.0
; SEQIID NO 2603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB 21; Length 242; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 2172
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 113
LENCTH: 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.1%; Score 39;
87.5%; Pred. No. 5
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; GENERAL INFORMATION:
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Best Local Similarity 87.5,
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 7; Conserv
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92 ITPLEELY 99
176 LTPLEELY 183
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92 ITPLEELY 99
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ORGANISM: Human
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US-09-417-507-35531
                                                                         RESULT 4
US-09-760-475-2603
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Sequence 2, Application US/09763397A

Sequence 2, Application US/09763397A

SERVERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis APPLICANT: Control and Prevention
APPLICANT: Lal, Allaf A.
APPLICANT: Ping Shi, Ya
APPLICANT: Hasnain, Seyed E.
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falci
FILE REFERENCE: 6395-57049
FILE REFERENCE: 6395-57049

CURRENT FILING DATE: 1001-02-16

PRIOR FILING DATE: 1998-08-21

PRIOR FILING DATE: 1998-08-19

NUMBER OF SEQ ID NOS: 26

SSOFTWARE: PatentIn Version 3.1
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                                                                                                                                                                                              APPLICANT: Jakobsen, Peter Mikael Helweg
APPLICANT: Jakobsen, Palle Hoy
TITLE OF INVENTION: Non-Dendritic Backbone Peptide Carrier
FILE REFERENCE: 216 1009-000
CURRENT APPLICATION NUMBER: US/09/165,878B
CURRENT FILING DATE: 1998-10-02
EARLIER APPLICATION NUMBER: PCT/DK97/00146
EARLIER PILING DATE: 1997-04-03
EARLIER PILING DATE: 1996-04-03
SARLIER FILING DATE: 1996-04-03
SARLIER FILING DATE: 1996-04-03
SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 41; DB 15; 100.0%; Pred. No. 2.9e+06;
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                                                                                                                                                   Sequence 60, Application US/09165878B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GOTHER INFORMATION: Unknown US-09-165-878-60
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Best Local Similarity 100.
Matches 8; Conservative
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RESULT 9
PCT-USO0-26524B-4656
Sequence 4656, Application PC/TUSO026524B
Sequence 4656, Application PC/TUSO026524B
GENERAL INFORMATION:
APPLICANT: Birse et. al.
FILLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
FILLE OF INVENTION NUMBER: PCT/USO0/26524B
CURRENT FILLING DATE: 2000-09-28
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR PILING DATE: 1999-11-03
PRIOR PLING DATE: 1999-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTE
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7160
LENGTH: 806
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GENERAL INFORMATION:
APPLICANT: BODAZZI, VIVIAN:
TITLE OF INVENTION: MOLECULES ENCODING SECRETED PROTEINS, AND USES THEREOF;
FILLE REFERENCE: CLO00067
CURRENT APPLICATION NUMBER: US/60/146,055
CURRENT FILING DATE: 1999-07-28
CURRENT FILING DATE: 1999-07-28
NUMBER OF SEQ ID NOS: 938
SOFTWARE: FASTSEQ for Windows Version 3.0
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Pred. No. 4.5e+02;
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75.0%; Pred. No. 4...
2; Mismatches
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US-09-328-352-7160
                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 75.0
Matches 6; Conservative
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ORGANISM: Homo sapiens
PCT-US00-26524B-4656
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    272 TPLEELY 278
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US-09-328-352-7160
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LENGTH: 284
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GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
TITLE OF INVENTION: Identification of Essential Genes of Aspergillus fumigatus and Me
TITLE OF INVENTION: USe
TITLE OF INVENTION: USe
CURRENT APPLICATION NUMBER: US/60/316,362
CURRENT FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 4037
SOFTWARE: Patentin version 3.1
SEQ ID NO 3517
LENGTH: 310
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US-09-543-681A-4430

US-09-543.681A-4430

Sequence 4430, Application US/09543681A

SEQUENCE 4430, Application US/09543681A

SEQUENCE INFORMATION:

APPLICANT: GARY BRETON

TITLE OF INVENTION: DIAGROSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT APPLICATION NUMBER: US 60/128,706

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1990-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 4430

LENGTH: 338
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                                                                                                                                       90.2%; Score 37; DB 18; Length 88; 100.0%; Pred. No. 18; ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 86;
tive 0; Mismatches
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; ORGANISM: Proteus mirabilis
US-09-543-681A-4430
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Best Local Similarity luv...
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Best Local Similarity 100.
Matches 7; Conservative
                                                        ; ORGANISM: A.fumigatus
US-09-417-507-35531
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| 59 TPLEELY 65
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SEQ ID NO 35531
                    LENGTH: 88
                                       TYPE: PRT
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US-09-270-767-44698
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Sequence 849, Application US/60147189
GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: MOLECULES ENCODING SECRETED PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000072
CURRENT APPLICATION NUMBER: US/60/147,189
CURRENT FILING DATE: 1999-08-08
NUMBER OF SEQ ID NOS: 1115
SSCTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 849
LENGTH: 71
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster. FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 60152

LENGTH: 148
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Pred. No. 36;
2; Mismatches 0; Indels
                                                                                                                 Score 35; DB 24; Length 71;
Pred. No. 36;
2; Mismatches 0; Indels
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Pred. No.
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6.09-270-767-60152
Sequence 60152, Application US/09270767
GENERAL INFORMATION:
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ORGANISM: Drosophila melanogaster
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75.0%;
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                      Query Match 85.4
Best Local Similarity 75.0
Matches 6; Conservative
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; ORGANISM: Drosophila
US-60-147-189-849
                                TYPE: PRT
CORGANISM: Drosophila
US-60-146-055-775
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46 ITPLEELF 53
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46 ITPLEELF 53
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SEQ ID NO 775
LENGTH: 71
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Sequence 44698, Application US/09270767

General Information:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFUMARE: Patentin Ver. 2.0
SEQ ID NO 44698
LENGTH: 329
                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: at any location having Xaa, Xaa means any amino acid US-09-270-849B-189381
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Pred. No. 89;
1; Mismatches 0; ThAal
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Pred. No. 2.4e+02;
1; Mismatches 0; Indels
Sequence 189381, Application US/09270849B
GENERAL INFORMATION:
APPLICANT: Swimmer et al.
ITLE OF INVENTION: Insect genome survey devices
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/270,849B
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 195450
SOFTWARR: Patentin Ver. 2.0
SEQ ID NO 189381
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Best Local Similarity 85.7.
6; Conservative
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Matches 6; Conserv
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7798, Ap 7797, Ap 58997, A 7796, Ap 58996, A

5, Appli 9, Appli 7798, Ap

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Sequence:

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Sequence 3470, Application US/09620394B

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-1067P
CURRENT APPLICATION NUMBER: US/09/620,394B
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9131
SEQ ID NO 3470
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT PEPLICATION NUMBER: US/09/708,427
CURRENT PILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 40050
LENGTH: 106
                                            Sequence Seq
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          Sequence
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US-09-916-790-17

US-09-916-790-7

US-09-910-150-27

US-09-922-138-11

US-09-922-138-11

US-09-922-138-11

US-09-922-138-18

US-09-922-138-18

US-09-922-138-18

US-09-910-150-17

US-09-910-150-17

US-09-910-150-17

US-09-910-150-17

US-09-910-150-17

US-09-910-150-17

US-09-910-150-17

US-09-910-150-17

US-09-910-150-17

US-09-620-394B-7799

US-09-620-394B-7796

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; LOCATION: 1..89
; OTHER INFORMATION: Ceres Seq. ID 1386864
08-09-620-394B-3470
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NAME/KEY: misc_feature
LOCATION: 1..89
OTHER INFORMATION: Xaa is
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Matches 6; Conserv
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US-09-620-394B-3470
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US-09-708-427-40050
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      LENGTH: 89
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2.421 Million cell updates/sec
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1: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO7_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*
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Maximum Match 100%
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Perfect score:
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US-09-708-427-40049

US-09-708-427-40049

Sequence 40049, Application US/09708427

GENERAL INFORMATION:

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID

TITLE OF INVENTION: THEREBY

FILLE REFERENCE: 275-012438

CURRENT FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SEQ ID NO 40049

LENGTH: 134
                                                                                                                                                                                                                                                                                                                                                             Sequence 3468, Application US/09620394B
Sequence 3468, Application US/09620394B
SEGUENCE TO THE SEARCH ON SEQUENCE TO TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
TITLE REPERENCE: 2750-1067P
CURRENT APPLICATION NUMBER: US/09/620,394B
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9131
SEQ ID NO 3468
LENGTH: 122
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Pred. No. 15;
0; Mismatches
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14;
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LOCATION: 1..134
OTHER INFORMATION: Xaa is any amino acid
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LOCATION: 1..122
CTHER INFORMATION: Ceres Seq. ID 1386862
US-09-620-394B-3468
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OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: 1..117
; CTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; NAME/KEY: misc_feature
; COCATION: 1..117
; CTHER INFORMATION: Ceres Seq. ID 1386863
US-09-620-3948-3469
                                                                                                                                                                      78.0%; Score 32; 100.0%; Pred. No.
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100.0%; Pre
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LOCATION: 1..122
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Best Local Similarity
'...has 6; Conserve
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Best Local Similarity
Local 6; Conserva
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34 PLEELY 39
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Thereby
TITLE FEFERENCE: 2750-71067P
CURRENT APPLICATION NUMBER: US/09/620,394B
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9131
SEQ ID NO 3469
LENGTH: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 40054, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243F
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VETSION 3.1
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100.0%; Pred. No. 13;
iive 0; Mismatches
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; LOCATION: 1..106
; CTHER INFORMATION: Ceres Seq. ID 1842101
08-09-708-427-40054
                                                                   NAME/KEY: misc_feature
COCATION: 1..106
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
COCATION: 1..106
COCATION: 1..106
US-09-708-427-40050
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US-09-620-394B-3469
; Sequence 3469, Application US/09620394B
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, NICKOLai
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ORGANISM: Arabidopsis thaliana
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ORGANISM: Arabidopsis thaliana
                           ORGANISM: Arabidopsis thaliana FEATURE:
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LOCATION: 1..106
OTHER INFORMATION: Xaa is
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Best Local Similarity 100..
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Matches 6; Conserv
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6 PLEELY 11
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LENGTH: 106
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APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTMARE: PALENTIN VERSION 3.1
SEQ ID NO 40052
LENGTH: 139
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APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
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Pred. No. 18;
                                                     78.0%; Score 32; DB 5; 100.0%; Pred. No. 18; iive 0; Mismatches
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CURRENT FILING DATE: 2001.03.07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR PELICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
                                                                                                                                                                                                                                                        Sequence 40052, Application US/09708427 GENERAL INFORMATION:
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APPLICANT: Call, Brian
APPLICANT: Hecht, Peter
APPLICANT: Hottzman, Doug
APPLICANT: Madden, Kevin
                                       Query Match
Best Local Similarity 100.
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Best Local Similarity 100.
Matches 6; Conservative
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Royer, John
Salama, Sofie
Sherman, Amir
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39 PLEELY 44
 US-09-708-427-40048
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
CURRENCE: 2750-1243P
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SEQ TO NOS: 85364
SEQ TO NOS: 85364
SEQ ID NOS : 85364
SEQ ID NOS : 800-11-09
LENGTH: 134
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 40048
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                                                                                                          DB 5; Length 134;
17;
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17;
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                                                                                                          78.0%; Score 32; DB 100.0%; Pred. No. 17; Live 0; Mismatches
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CCATION: 1..134
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LCCATION: 1..134
COTHER INFORMATION: Ceres Seq. ID 1842100
US-09-708-427-40053
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LOCATION: 1..139
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..139
OTHER INFORMATION: Ceres Seq. ID 1842095
; NAME/KEY: misc_feature
; LOCATION: 1..134
: OTHER INFORMATION: Ceres Seq. ID 1842096
US-09-708-427-40049
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Best Local Similarity luv..
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Best Local Similarity 100.
Matches 6; Conservative
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34 PLEELY 39
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US-09-708-427-40053
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US-09-708-427-40048
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NAME/KEY: misc_feature
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APPLICANT: Summers, End
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production
CURRENT APPLICATION NUMBER: US/09/487,558
PRIOR FILING DATE: 2001-03-07
PRIOR PAPLICATION NUMBER: US 09/487,558
PRIOR PALICATION NUMBER: US 09/487,558
PRIOR PALICATION NUMBER: US 09/487,558
PRIOR PAPLICATION NUMBER: US 09/487,558
PRIOR PRIING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 09/487,558
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Sphingomonas elodea genome sequences and uses thereof FILE NEFERBNCE: 38-10(15806)B CURRENT APPLICATION NUMBER: US/10/015,127
                                                                                                                                                                                                          Gaps
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Pred. No. 70;
3; Mismatches 0; Indels
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Pred. No. 70;
3; Mismatches 0
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                                                                             ORGANISM: Saccharomyces cerevisiae US-09-801-368-150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.0 SEQ ID NO 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.0%;
62.5%;
SOFTWARE: PatentIn version 3.0
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ilarity 62.5%;
Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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Holtzman, Doug
Madden, Kevin
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Salama, Sofie
Sherman, Amir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Norman, Thea
                                                                                                                                                                  Query Match
Best Local Similarity
Matches 5; Conserv
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90 LSPLEDIY 97
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90 LSPLEDIY 97
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US-10-015-127-11693
                                          LENGTH: 435
                 SEQ ID NO 150
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Sequence 3777, Application US/09620394B
Sequence 3777, Application US/09620394B
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-1067P
CURRENT APPLICATION NUMBER: US/09/620,394B
CURRENT APPLICATION DOS: 9131
SEQ ID NOS: 9131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: N. ALEXANDROV et al.

ITILE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT PAPPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
ENGTH: 295
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Pred. No. 63;
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Pred. No. 50;
0; Mismatches
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PRIOR APPLICATION NUMBER: US 60/252,455
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 14357
SEQ ID NO 11693
LENGTH: 224
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S.09-708427-18806
Sequence 18806, Application US/09708427
GENDRAL INFORMATION:
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ORGANISM: Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.6%;
                                                                                                                        TYPE: PRT; ORGANISM: Sphingomonas elodea
US-10-015-127-11693
                                                                                                                                                                                                                          75.6%;
85.7%;
                                                                                                                                                                                                                        Query Match 75.6
Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
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LOCATION: 1..271
OTHER INFORMATION: Xaa
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69 ITTLEELY 76
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1 Sequence 12, Application US/09995542

5 Sequence 12, Application US/09995542

5 GENERAL INFORMATION:

APPLICANT: Shutter, John

APPLICANT: Shutter, John

TITLE OF INVENTION: APP-Binding Cassette Transporter-Like Molecules and

TITLE OF INVENTION: Uses Thereof

FILE REFERENCE: 00-658-A

CURRENT APPLICATION NUMBER: US/09/995,542

CURRENT FILING DATE: 2001-11-28

PRIOR FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 24

SOFTHARE: Patentin Ver. 2.0

SEQ ID NO 12

LENGTH: 2273

TTPE: DATA HOMO Sapiens

US-09-995-542-12
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                                                                                                                                                                          Query Match 75.6%; Score 31; DB 5; Length 295; Best Local Similarity 75.0%; Pred. No. 70; Matches 6; Conservative 1; Mismatches 1; Indels
; LOCATION: 1..295
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: 1..295
; OTHER INFORMATION: Ceres Seq. ID 1834879
US-09-708-427-18806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: January 29, 2002, 10:58:18 Job time: 2514 sec
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| 1267 TPLEEIF 1273
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Sequence 2, Appl1
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Sequence 3, Appl1
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Sequence 72, Appl
Sequence 72, Appl
Sequence 170, Ap
Sequence 170, Ap
Sequence 174, Ap
Sequence 174, Ap
Sequence 173, App
Sequence 174, App
Sequence 177, App
Sequence 177, Appl
Sequence 17, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sim. Betty K
APPLICANT: Sim. Betty K
APPLICANT: Haynes, David J
APPLICANT: Haynes, David J
APPLICANT: Calandi, Palmar A
APPLICANT: Carter, John M
APPLICANT: Carter, John M
APPLICANT: Canus, Daniel
APPLICANT: Canus, Canus, Canus
Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus, Canus,
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US-08-105-185-3

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US-09-165-878-39

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US-09-165-878-39

US-09-165-878-39

US-09-165-878-39

US-00-167-217-22207

US-00-173-464-18047

US-00-173-464-18047

US-09-228538-173

PCT-US99-228538-173

PCT-US99-228538-173

PCT-US99-228538-173

US-09-284-020-14

US-08-591-447-17

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US-60-236-359-14953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08295164 GENERAL INFORMATION:
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Sequence 3, App
Sequence 5, App
Sequence 2, App
Sequence 4, App
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| cgn2_6/ptodate/2/paa/USO6_COMB.pep:*
| cgn2_6/ptodate/2/paa/USO6_COMB.pep:*
| cgn2_6/ptodate/2/paa/USO8_COMB.pep:*
| cgn2_6/ptodate/2/paa/USO9_COMB.pep:*
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-295-164-3
US-08-295-164-4
US-09-763-397A-2
PCT-US94-1033-4
US-08-487-826-4
US-08-568-459-4
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                                                                                                                             January 29, 2002, 10:56:12
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Sequence:

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                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,164
FILING DATE: 24-AUG-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 96; DB 6; 100.0%; Pred. No. 6.5e-07; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/07606259
GENERAL INFORMATION:
APPLICANT: SIM, Betty Kim Lee
APPLICANT: ORLANDI, Palmer A.
APPLICANT: KLOTZ, Francis W.
APPLICANT: CARTER, John Mark
APPLICANT: CARTER, John Mark
APPLICANT: CARTER, John Mark
APPLICANT: ZEGHANS, Michael E.
APPLICANT: ZEGHANS, Michael E.
APPLICANT: TEGHANS, Michael E.
APPLICANT: TEGHANS, Michael E.
TITLE OF INVENTION: Malaria Vaccine
MUMBER OF SEQUENCES: 6
                                                                                                                                                                              STREET: John Morank
STREET: HQ. USAMRDC, FORT DETRICK
STREET: Frederick
STATE: ...
                                                                            APPLICANT: Zegans, Michael E
APPLICANT: Chuley, Jeffrey D
APPLICANT: Hadley, Terence J
TITLE OF INVENTION: Malaria Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Plasmodium falciparum
STRAIN: EBA-175
                                                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Hendricks, Glenna M
REGISTRATION NUMBER: 32,535
REFERENCE/CDCKET NUMBER: Sims
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-7807
Orlandi, Palmar A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NEREDERTLIKEYEDIVLK 19
                     Klotz, Francis W
Carter, John M
Camus, Daniel
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SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-terminal
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Best Local Similarity 100.
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE: NORIGINAL SOURCE:
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US-07-606-259-5
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                                            APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the Department of Health and Human Services, Centers for Dis APPLICANT: Control and Prevention APPLICANT: Control and Prevention APPLICANT: Lal, Altaf A. APPLICANT: Lal, Altaf A. APPLICANT: Hasnain, Seyed E. TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falci TITLE OF INVENTION: NUMBER: US/09/763,397A
CURRENT APPLICATION NUMBER: US/09/7763,397A
CURRENT FILING DATE: 1998-08-21
PRIOR FILING DATE: 1998-08-21
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 20
LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 96; DB 6; I
100.0%; Pred. No. 2.3e-07;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20, Application US/09763397A GENERAL INFORMATION:
          NAME: Hendricks, Glenna M
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: Sims
TELECOMMUNICATION INFORMATION:
TELEPRONE: (301) 619-7807
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08295164 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Plasmodium falciparum
US-09-763-397A-20
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APPLICANT: Haynes, David J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NEREDERTLIKEYEDIVLK 19
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                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.7
Matches 19; Conservative
                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                              STRAIN: EBA-175 US-08-295-164-5
                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
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; Sequence 4, Application PC/TUS9410230
   ATTORNEY/AGENT INFORMATION:
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Best Local Similarity
Matches 19; Conserv
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US-08-295-164-4
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FRAGMENT TYPE: N
ORIGINAL SOURCE:
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PCT-US94-10230-4
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ADDRESSEE: U.S. Army Medical Research and Development ADDRESSEE: Command
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                           ADDRESSEE: Command
STREET: Fort Detrick
CITY: Frederick
STATE: Maryland
COUNTR: USA
ZIP: 21702-5012
COMPUTER: USA
A ZIP: STATE: WASABLE FORM:
MEDIUM TYPE: FOLPOPY disk
COMPUTER: IBM PC COMPATIBLE
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PRESS #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/606,259
FILING DATE: 19901031
CLASSIFICATION NUMBER: US/07/606,259
FILING DATE: 27-SEP-1985
ATTORNEY/AGENT INFORMATION:
NAME: MORAN JOHN F.
REGISTATION NUMBER: 26,313
TELEPHONE: (301)619-2416
INFORMATION FOR SED 1D 00: 5:
INFORMATION FOR SED 1D 00: 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Haynes, David J
APPLICANT: Orlandi, Palmar A
APPLICANT: Collandi, Palmar A
APPLICANT: Carter, John M
APPLICANT: Camus, Daniel
APPLICANT: Zegans, Michael E
APPLICANT: Chuley, Jeffrey D
APPLICANT: Hadley, Terence J
TITLE OF INVENTION: Malaria Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: John Morank
STREET: HO. USAMRDC, FORT DETRICK
CITY: Frederick
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APPLICATION NUMBER: US/08/295,164
FILING DATE: 24-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08295164
GENERAL INFORMATION:
APPLICANT: Sim, Betty K
APPLICANT: Haynes, David J
APPLICANT: Orlandi, Palmar A
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 amino acids
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Best Local Similarity 100.
Matches 19; Conservative
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: John Mora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 24-AUG
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
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COUNTRY: L
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US-08-295-164-4
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APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the Department of Health and Human Services, Centers for APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A. APPLICANT: Lal, Altaf A. APPLICANT: Hasnain, Seyed E. APPLICANT: Ping Shi, Ya APPLICANT: Ping Shi, Ya APPLICANT: Ping Shi, Ya TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Fa FILE REFERENCE: 6395-57049
CURRENT APPLICATION NUMBER: US/09/763, 397A
CURRENT FILING DATE: 2001-02-16
PRIOR FILING DATE: 1998-08-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 96; DB 6;
Pred. No. 6.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PCT / US99/18869
PRIOR FILING DATE: 1999-08-19
                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09763397A GENERAL INFORMATION:
NAME: Hendricks, Glenna M
REGIZTRATION NUMBER: 32,535
REFRENCE/DOCKET NUMBER: Sims
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-7807
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acids
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100.0%;
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SOFTWARE: Patentin version 3.1
SEQ ID NO L
LENGTH: 350
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Best Local Similarity 100.
Matches 19; Conservative
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                                                                                                                                                                                                                                       STRANDEDNESS: single
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Gaps
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ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,459
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 96; DB 8; I
100.0%; Pred. No. 6.2e-05;
Live 0; Mismatches 0;
  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELEPHONE: (619) 235-0176
ITELEPHONE: (619) 235-0176
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/119,677
                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Plasmodium falciparum US-08-487-826-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1066 NEREDERTLIKEYEDIVLK 1084
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INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NEREDERTLIKEYEDIVLK 19
                                                                                                                                                                                                                 LENGTH: 1426 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0
Best Local Similarity 100.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Steuart Stre
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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US-08-568-459-4
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GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Put Wellems, Tin-zhaun
APPLICANT: Wellems, Tin-mas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE: ADDRESS:
ADDRESSEE: Knobbe Mattens Olson & Bear
                               BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826
                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10230
FILING DATE: 07-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                            APPLICATION NUMBER: PC11 10537/10537

CLASSIFICATION: 07-5EP-1994
CLASSIFICATION DATA: PC10 APPLICATION BAPE: 08/119,677

PTILING DATE: 10-5EP-1993
ATTONNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
RECISTRATION NUMBER: 34,774

RECISTRATION NUMBER: 34,774

TELECHONEINICATION INFORMATION:
TELECHONE: (415) 543-9600

TELEPAX: (415) 543-9600

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARRACPERISTICS:
LENGTH: 1426 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1066 NEREDERTLIKEYEDIVLK 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 19; Conservative C
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                      Floppy disk
                                   TITLE OF INVENTION: BIND
TITLE OF INVENTION: AND
NUMBER OF SEQUENCES: 12
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US94-10230-4
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US-08-487-826-4
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Gaps
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100.0%; Pred. No. 6.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                        APPLICANT: Zegans, Michael E
APPLICANT: Chuley, Jeffrey D
APPLICANT: Hadley, Terence J
TITLE OF INVENTION: Malaria Vaccine
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: John Morank
STREET: HQ. USAMRDC, FORT DETRICK
CITY: Frederick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/295,164
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US-08-487-826A-4
Sequence 4, Application US/08487826A;
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCOMNEY AGENT INFORMATION:
NAME: Hendricks, Glenna M
REGISTRATION NUMBER: 32,535
REFRENCE/DOCKET NUMBER: Sims
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-7807
TELEPHONE: (301) 619-7714
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1435 amino acids
                                                                                        RESULT 11
US-08-295-164-2
; Sequence 2, Application US/08295164
; GENERAL INFORMATION:
                                                                                                                                                                                Haynes, David J
Orlandi, Palmar A
Klotz, Francis W
Carter, John M
Camus, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 1069 NEREDERTLTKEYEDIVLK 1087
                   1069 NEREDERTLIKEYEDIVLK 1087
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FILING DATE: 24-AUG-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                  Sim, Betty K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: John Mora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 19; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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ZIP: 21702-5012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; STRAIN: EBA-175
US-08-295-164-2
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                Length 1426;
                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Malaria Vaccine
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: U.S. Army Medical Research and Development
ADDRESSEE: Command
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/606,259
FILING DATE: 19901031
                                                                                                                                                                                Query Match 100.0%; Score 96; DB 9; I
Best Local Similarity 100.0%; Pred. No. 6.2e-05;
Matches 19; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SIM, Betty Kim Lee
APPLICANT: ORLANDI, Palmer A.
APPLICANT: HAYNES, JR., John David
APPLICANT: KLOTZ, Francis W.
APPLICANT: CARTER, John Mark
APPLICANT: CAMUS, Daniel
APPLICANT: ZEGHANS, Michael E.
APPLICANT: CHULAY, Jeffrey David
APPLICANT: HADLEY, Terence J.
                                                                                      ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum
US-08-568-459-4
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/07606259 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                            1066 NEREDERTLIKEYEDIVLK 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1435 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                       1 NEREDERTLIKEYEDIVLK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100./
Matches 19; Conservative
         STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Fort Detrick
CITY: Frederick
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-07-606-259-2
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFWARE: PATENTIA RELEASE #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,185
PRIOR APPLICATION NUMBER: WO PCT/GB94/01900
APPLICATION NUMBER: GB 93 18350.7
FILING DATE: 03-8EP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 94 17021.4
FILING DATE: 23-80G-1994
INFORMATION FOR SEQ 1D NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 1604 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 96; DB 10;
100.0%; Pred. No. 7.2e-05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 96; DB 16;
100.0%; Pred. No. 6.3e-05;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION NUMBER OF SEQUENCES: 23 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: FULLEr, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-6156
TELEPHONE: (619) 235-0176
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Plasmodium falciparum US-09-210-288-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08605185 GENERAL INFORMATION: APPLICANT:
                                          IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1069 NEREDERTLIKEYEDIVLK 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NEREDERTLIKEYEDIVLK 19
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1435 amino acids
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Best Local Similarity 100.
Matches 19; Conservative
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Best Local Similarity 100.0
Matches 19; Conservative
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YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
COMPUTER READABLE FORM:
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, HYPOTHETICAL:
US-08-605-185-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE
                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
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US-08-605-185-3
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GENERAL INCPRARTION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louls H.
APPLICANT: Peterson, David S.
APPLICANT: Peterson, David S.
APPLICANT: Wellems, Thomas E.
APPLICANT: Wellems, Thomas E.
APPLICANT: Miller DE INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                               TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826A
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ. 105.656
INFORMATION FOR SEQ. 1D NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 96; DB 8; 100.0%; Pred. No. 6.3e-05; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Knobbe Martens Olson & Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach STATE: California
                                                                                                                                                                                                    ADDRESSEE: Knobbe Martens Olson & Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach Center Drive 16th Floor CATE: Catherina COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum
                                          Peterson, David S.
Su, Xin-zhaun
Wellems, Thomas E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1069 NEREDERTLIKEYEDIVLK 1087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1435 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.9
Matches 19, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Ma
                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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ORGANISM: Pla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-487-826A-4
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                                                                         APPLICANT:
APPLICANT:
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100.0%; Score 96; DB 7; Length 1786;
Best Local Similarity 100.0%; Pred. No. 8.3e-05;
Matches 19; Conservative 0; Mismatches 0; Indels
                                                                            RESULT 15

US-00-307-742-3

US-00-307-742-3

Sequence 3, Application US/08307742

SEQUENCE INFORMATION:

TILE OF INVENTION: ANTI-VIRAL FUSION PEPTIDES

NUMBER OF SEQUENCES: 6

COMBUTER READABLE FORM:

MEDIUN TYPE: Floppy disk

COMBUTER: Bub PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/307,742

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9205276.0

FILING DATE: 11 WAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9215829.4

FILING DATE: 09-3UL-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9219562.7

FILING DATE: 08-3UL-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9304311.5

FILING DATE: 08-304-311.5

FILING DATE: 103-MAR-1993

INPORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1786 amino acids

TYPE: amino acid

TYPE: amino acid

TYPE: HYPOTHALIAN: YES

US-08-307-742-3
DD 1238 NEREDERTLTKEYEDIVLK 1256
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Search completed: January 29, 2002, 10:56:13 Job time: 2409 sec

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
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length: 2000000000
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2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

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Sequence 32947, A
Sequence 32946, A
Sequence 24697, A
Sequence 24696, A
Sequence 24696, A
Sequence 24696, A
Sequence 13441, A
Sequence 13441, A
Sequence 13449, A
Sequence 14, Appl
Sequence 7/02, Ap
Sequence 298, Appl
Sequence 298, App
Sequence 3212, A
Sequence 3212, A
Sequence 3212, A
Sequence 3212, A
Sequence 38012, A
Sequence 38010, A
Sequence 38010, A
Sequence 28018, A
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RESULT 1 US-09-708-427-32947 US-09-708-427-32947 ; Sequence 32947, Application US/09708427 ; GENERAL INFORMATION: ; APPLICANT: N. ALEXANDROV et al. ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID ; TITLE OF INVENTION: THEREBY ; FILE REFERENCE: 2750-1243P ; CURRENT APPLICATION UNMBER: US/09/708,427 ; CURRENT FILING DATE: 2000-11-09 ; NUMBER OF SEQ ID NOS: 85364 ; GOFTMARE: DEFERTA VEGENCE 373 1		22 22 22 32 32 33 33 34 34 35 36 36 37 36 37 38 38 38 38 38 39 39 39 39 39 39 39 39 39 39 39 39 39
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		Sequence 24762, A Sequence 14543, A Sequence 15453, A Sequence 15453, A Sequence 15452, A Sequence 2194, Ap Sequence 7367, Ap Sequence 6244, App1 Sequence 6224, Ap Sequence 10293, A Sequence 2002, App Sequence 2002, App Sequence 2001, App Sequence 2001, App Sequence 2001, App Sequence 76308, A Sequence 901, App Sequence 76307, A

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RESULT 2
US-09-708-427-32946
US-09-708-427
Sequence 32946, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: US/09/708,427
UNDER OF SEQ ID NOS: 85364
SOFTWARE: PACENTIN VERSION 3.1
SEQ ID NO 32946
                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Arabidopsis thaliana; FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..256
OTHER INFORMATION: Xaa is any am; NAME/KEY: misc_feature; LOCATION: 1..256
COTHER INFORMATION: Ceres Seq. ID US-09-708-427-32947
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Best Local Similarity
Matches 9; Conserv
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56.2%;
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LOCATION: 1..362
OTHER INFORMATION: Ceres Seq. ID 1835390
US-09-708-427-32946
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LOCATION: 1..368
LOCATION: 1..368
OTHER INFORMATION: Ceres Seq.
US-09-708-427-32945
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Best Local S
Matches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY FILE REPERENCE: 2750-1243P CURRENT APPLICATION NUMBER: US/09/708,427 CURRENT FILING DATE: 2000-11-09 NUMBER OF SEQ ID NOS: 85364 SOFTWARE: Patentin version 3.1 SEQ ID NO 32945
                                                                                                                                                                                                           Sequence 24697, Application US/09708427 GENERAL INFORMATION: APPLICANT: N. ALEXANDROV et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 32945, Application US/09708427 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                     SEQ ID NO 24697
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                                                                              TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY FILE REPERENCE: 2750-1243P CURRENT APPLICATION NUMBER: US/09/708,427 CURRENT FILING DATE: 2000-11-09 NUMBER OF SEQ ID NOS: 85364 SOFTWARE: Patentin version 3.1
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LOCATION: 1..362
OTHER INFORMATION: Xaa is any
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LOCATION: 1..368
OTHER INFORMATION: Xaa is any amino acid
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                ORGANISM: Arabidopsis thaliana
FEATURE:
                                 TYPE: PRT
                                                ENGTH: 376
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56.2%;
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; NAME/KEY: misc_feature
; LOCATION: 1..376
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: 1..376
; OTHER INFORMATION: Ceres Seq. ID 1812577
US-09-708-427-24697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 1..377
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..377
OTHER INFORMATION: Ceres Seq. ID 1812576
US-09-708-427-24696
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Best Local Similarity 5/...
Best Conservative
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LENGTH: 377

TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
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                                                                                               TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS:
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-12439
CURRENT APPLICATION UNMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 24695
LEBOTH: 384
                                                                                                                                                                                                                                                              Sequence 24655, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: N. ALEXANDROV et al
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             NAME/KEY: misc_feature LOCATION: 1..384
                                                                 ORGANISM: Arabidopsis thaliana
                                                FEATURE:
OTHER INFORMATION: Xaa is any amino
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165 NRKEDQRSLTRETE 178
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Local Similarity 57.18;
hes 8; Conservat;
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Pred. No.
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                US-09-708-427-13441; Sequence 13441, Application US/09708427
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US-09-897-516-7722
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CURRENT FILING DATE: 2000-11-09.
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13441
LENGTH: 1035
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/897,516
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215, 161
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
SEQ ID NO 7722
LENGTH: 974
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Best Local Similarity
Matches 8; Conserv
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TITLE OF INVENTION: Xenorhabdus sp. Genome
FILE REFERENCE: 38-21(51847)B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Corbin, David R.
               NAME/KEY: misc_feature LOCATION: 1..1035
OTHER INFORMATION: Xaa is any amino acid NAME/KEY: misc_feature LOCATION: 1..1035
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                                                                                                ORGANISM: Arabidopsis thaliana FEATURE:
                                                                                                                                 TYPE: PRT
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OTHER INFORMATION: Ceres Seq. ID 1826362
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Hinkle, Gregory J.
Huesing, Joseph E.
Krasomil-Osterfeld, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Malvar, Thomas M. Slater, Steven C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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57.18;
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Pred. No.
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..1104
; OTHER INFORMATION: Xaa is ;
; NAME/KEY: misc_feature
; LOCATION: 1..1104
; OTHER INFORMATION: Ceres So
                                                                                                                                                                                                                                                                                                           US-09-708-427-13439, Application US/09708427; Sequence 13439, Application US/09708427; GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TYPLE OF INVENTION: THERREBY
FILE REFERENCE: 2750-1243P
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LOCATION: 1..1072
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..1072
OTHER INFORMATION: Ceres Seq. ID 1826361
US-09-708-427-13440
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                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 13439
LENGTH: 1104
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85384
SOFTWARE: Patentin version 3.1
SEQ ID NO 13440
LENGTH: 1072
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Best Local Similarity
Matches 10; Conserv
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Best Local Similarity 62.4
Matches 10; Conservative
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
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                                                                                                                                                                          TYPE: PRT
                                                                                                                                                    ORGANISM: Arabidopsis thaliana
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62.5%;
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                  Seq.
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                      ID 1826360
                                                                            amino acid
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Pred. No. 1.9e+02;
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Pred. No. 1.9e+02;
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В
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                                               Query Match
Best Local Similarity
Watches 8; Conserve
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                                                                                                                                          ; ORGANISM: Homo sapiens US-09-825-882-14
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TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
FILE REFERENCE: 38-21(51847)B
CURRENT APPLICATION UNMBER: US/99/897,516
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION UNMBER: US 60/215, 161
PRIOR PILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
SEQ ID NO 7022
LENGTH: 198
                                                                                                                                                                                                                                Sequence 14, Application US/09825882

GENERAL INFORMATION:
APPLICANT: ADLER, JON EILLOT
TITLE OF INVENTION: 72R TASTE RECEPTORS AND GENES ENCODING SAME
FILE REFERENCE: 078003/0279152/RXT
CURRENT TAPLICATION NUMBER: US/09/825,882
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/195,532
PRIOR APPLICATION NUMBER: 60/247,014
PRIOR FILING DATE: 2000-101-13
NUMBER: 05 ED, ID NOS: 31
NUMBER: 05 ED, ID NOS: 31
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Best Local
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GENERAL INFORMATION:
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Best Local Similarity
Matches 8; Conserv
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LENGTH: 299
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                                                                                                                                                                           TYPE: PRT
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150 DERVWTKEYE 159
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                             5 DERTLTKEYE 14
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Slater, Steven C.
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Hinkle, Gregory J.
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Krasomil-Osterfeld, Karina
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Pred. No.
                                                                             Score 41; DB Pred. No. 74;
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46;
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; ORGANISM: Homo sapiens US-10-000-823-7
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                                               Query Match
Best Local Similarity
"hes 8; Conserv
                                                                                                                                                                                                                                                  ; ORGANISM: Saccharomyces cerevisiae US-09-801-368-298
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LENGTH: 871
TYPE: PRT
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GENERAL INFORMATION:
GENERAL INFORMA
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Best Local Similarity
"hehes 8; Conserv
                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version
SEQ ID NO 298
LENGTH: 1770
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 298, Applic GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/250,587
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 31
SOFTMARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: APPLICANT:
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CURRENT FILING DATE: 2001-11-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
CURRENT FILING DATE: 2001-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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334 NTRENTKFVTKMYDLLLLK 352
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Milne, Todd
Norman, Thea
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Salama, Sofie
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Holtzman, Doug
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Pred. No. 2.6e+02;
                                                                           Score 41; DB 5; Length 1770;
Pred. No. 5.9e+02;
4; Mismatches 7; Indels
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RESULT 15

US-09-487-588-298

Sequence 298, Application US/09487558

GENERAL INFORMATION:

APPLICANT BUSBY, Robert
APPLICANT BUSBY, Robert
APPLICANT Hoth, Beter
APPLICANT MILL BEIGH
APPLICANT MILL BEIGH
APPLICANT MILL BOUGH
APPLICANT Sherman, Amir
APPLICANT STATE SHERM
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Mon Feb

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EFTYMINFGRGONYWEHPYOKS
 Query Match '
Best Local Similarity
 US-09-763-397A-19
 US-09-763-397A-19
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46.5
46.5
 Matches
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 Sequence 19, Appl
Sequence 2, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 9, Appli
 Sequence 871, App
Sequence 606, App
Sequence 859, App
 (without alignments)
3.470 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Search time 1760.55 Seconds
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
 US-09-763-397A-19
US-09-763-397A-2
PCT-US92-02207-8
US-07-672-183A-8
US-08-072-867-8
US-08-075-783-9
US-08-075-783-9
US-08-01-01307-606
PCT-US01-01307-605
 fotal number of hits satisfying chosen parameters:
 3148936 seqs, 277657034 residues
 January 29, 2002, 10:56:11
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 131
1 EFTYMINFGRGQNYWEHPYQKS
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 US-09-763-397A-19
 Minimum DB seq length: 0 Maximum DB seq length: 2000000000
 7777
 Length
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350
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 Perfect score:
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11315, A
87, Appl
3455, Ap
4477, Ap
28697, A
31024, A
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US-60-233-625-2627
US-60-233-625-2627
US-60-191-637-31024
US-60-191-637-31023
US-60-191-637-3103
US-60-191-637-3103
US-60-191-637-3103
US-60-191-637-3103
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## ALIGNMENTS

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SPECIAL INCOGRAPTION:
SECRETARY Of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for APPLICANT: Socretary of the Department of Health and Human Services, Centers for APPLICANT: Lal, Altaf A.
APPLICANT: Lal, Altaf A.
APPLICANT: Hasnain, Seyed E.
TILE REFERENCE: 6395-57049
TILLE REFERENCE: 6395-57049
FILE REFERENCE: 6395-57049
FILE REFERENCE: 1998-08-21
CURRENT FILING DATE: 1998-08-21
FRIOR APPLICATION NUMBER: US 60/097,703
FRIOR FILING DATE: 1999-08-19
FRIOR FILING DATE: 1999-08-19
FRIOR FILING DATE: 1999-08-19
FRIOR FILING DATE: 1999-08-19
SEQ ID NO 19
LENGTH: 22
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 Length
 Score 131; DB 21;
Pred. No. 6.4e-13;
Mismatches 0;
Sequence 19, Application US/09763397A GENERAL INFORMATION:
 ORGANISM: Plasmodium falciparum
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1 Similarity 100.0%;
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 Length 622;
 Score 126; DB 1; Length 622;
Pred. No. 1.3e-10;
 APPLICANT: Paoletti, Enzo
APPLICANT: de Taisne, Charles
APPLICANT: Tine, John A.
ATTLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/672,183A
FILING DATE: 19910320
 ADDRESSEE: William S. Frommer ADDRESSEE: c/o Curtis, Morris & Safford, P.C. STREET: 530 Fifth Avenue
 Score 126; DB 3;
Pred. No. 1.3e-10;
0; Mismatches 1;
 0; Mismatches
 NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2300
TELECOMMONICATION INFORMATION:
 Sequence 8, Application US/07672183A GENERAL INFORMATION:
 RESULT 5
US-08-072-867-8
; Sequence 8, Application US/08072867
; GENERAL INFORMATION:
 14 EFTYMINFGRGONYWEHPYONS 35
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
 1 EFTYMINFGRGONYWEHPYOKS 22
 14 EFTYMINFGRGONYWEHPYONS 35
 1 EFTYMINFGRGONYWEHPYOKS 22
 (212) 840-3333
 TELEFAX: (212) 840-0712 INFORMATION FOR SEQ ID NO: 8:
 ATTORNEY/AGENT INFORMATION:
 LENGTH: 622 amino acids
TYPE: AMINO ACID
STRANDEDNESS: Single
TOPOLOGY: linear
 : 622 amino acids
amino acid
 STATE: New York
COUNTRY: United States
ZIP: 10036
 SEQUENCE CHARACTERISTICS:
 Query Match 96.2
Best Local Similarity 95.5
Matches 21; Conservative
 Query Match 96.2
Best Local Similarity 95.5
Matches 21; Conservative
INFORMATION FOR SEQ ID NO:
 SEQUENCE CHARACTERISTICS LENGTH: 622 amino aci
 single
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 ; TOPOLOGY: linear PCT-US92-02207-8
 New York
 CLASSIFICATION:
 STRANDEDNESS:
 TELEPHONE:
 RESULT 4
US-07-672-183A-8
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 APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the Department of Health and Human Services, Centers for Dis APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A. APPLICANT: Lal, Altaf A. APPLICANT: Hasnain, Seyed E. TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium FalciFILE REPERENCE: 6395-57049
CURRENT APPLICATION NUMBER: US/09/763,397A
CURRENT PILING DATE: 1998-08-21
PRIOR PILING DATE: 1998-08-21
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
 0;
 Gaps
 ó
 Length 350;
 Sequence 8, Application PC/TUS9202207
GENERAL INFORMATION:
APPLICANT: VIROGENETICS, CORPORATION
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
 Indels
 SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
 Query Match 100.0%; Score 131; DB 21; Best Local Similarity 100.0%; Pred. No. 1.1e-11; Matches 22; Conservative 0; Mismatches 0;
 ADDRESSEE: Cuttis, Morris, and Safford ADDRESSEE: c/o William S. Frommer STREET: 530 Fifth Avenue CITY: New York COUNTRY: USA
 ; OTHER INFORMATION: Recombinant DNA/Protein US-09-763-397A-2
 NAME: Frommer, William S.
REGISTATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2411
TELECOMMUNICATION INFORMATION:
 омыЕR: PCT/US92/02207
19-MAR-1992
1
 STATE: New YOLA
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
 Sequence 2, Application US/09763397A GENERAL INFORMATION:
 1 EFTYMINFGRGQNYWEHPYQKS 22
1 EFTYMINFGRGONYWEHPYOKS 22
 TYPE: PRT ORGANISM: Artificial Sequence
 (212) 840-3333
(212) 840-0712
 ATTORNEY/AGENT INFORMATION:
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER:
 CLASSIFICATION:
 FILING DATE:
 RESULT 3
PCT-US92-02207-8
 SOFTWARE:
 SEQ ID'NO 2
LENGTH: 350
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Sequence 871, Application US/60207216
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLO00580
CURRENT APPLICATION NUMBER: US/60/207,216
CURRENT APPLICATION NUMBER: US/60/207,216
CURRENT FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 898
SSEQ ID NO 871
LENGTH: 89
 Gaps
 Gaps
 ö
 Sequence 606, Application PC/TUS0101307
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc., et al.
TILE OF INVENTION: NOLE OF ACIDS, Proteins, and Antibodies
FILE REFERENCE: PT218PCT
CURRENT APPLICATION NUMBER: PCT/US01/01307
CURRENT APPLICATION NUMBER: PCT/US01/01307
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1040
SCOTWARE: PatentIn Ver. 2.0
SEQ ID NO 606
LENGTH: 99
 ö
 Length 622;
 Score 57; DB 24; Length 89; Pred. No. 0.97;
 Indels
 Indels
 Score 126; DB 4;
Pred. No. 1.3e-10;
0; Mismatches 1
 3; Mismatches
 NAME/KEY: VARIANT
LOCATION: (1)...(89)
OTHER INFORMATION: Xaa = Any Amino Acid
 NAME: Frommer, William S.
REGISTRATION UNDBER: 25,506
REFERENCE/DOCKET NUMBER: 45431
TELECOMMUNICATION INPORMATION:
TELEPHONE: (212) 840-333
TELEFAX: (212) 840-0712
INPORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
 14 EFTYMINEGRGONYWEHPYONS 35
 1 EFTYMINFGRGONYWEHPYOKS 22
 96.2%;
 43.58;
 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
 LENGTH: 622 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
 65 YFFNFANRQSIWDHPHDK 82
 4 YMINFGRGQNYWEHPYQK 21
 Query Match
Best Local Similarity 44...
Best Local 8; Conservative
 Query Match 96.2
Best Local Similarity 95.5
Matches 21; Conservative
 ORGANISM: HUMAN
 PCT-US01-01307-606
 US-60-207-216-871
 US-60-207-216-871
 US-08-075-783-9
 TYPE: PRT
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 Gaps
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 Score 126; DB 4; Length 622;
Pred. No. 1.3e-10;
0; Mismatches 1; Indels
APPLICANT: Paoletti, et al
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris, and Safford
ADDRESSEE: C/O William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
 Sequence 9, Application US/08075783
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Tine, John A.
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUTLIS, MORTIS & Safford
ADDRESSEE: COV Milliam S. Frommer
STREET: 530 Fifth Avenue
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,783
FILING DATE: 11-JUN-1993
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: COMPACTION SOCIATION SOCIATION SYSTEM: PC-DOS/MS-DOS
SOCIATION DATA:
APPLICATION NUMBER: US/08/072,867
 NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
 COUNTRY: United States of America
ZIP: 10036
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/852,305
FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INFORMATION:
 14 EFTYMINFGRGONYWEHPYONS 35
 TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
TYPE: amino acid
 1 EFTYMINFGRGONYWEHPYOKS 22
 96.2%;
95.5%;
 Query Match
Best Local Similarity 95.55,
Thes 21; Conservative
 STRANDEDNESS: Single
;
TOPOLOGY: linear
US-08-072-867-8
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 STATE: New York
 New York
 USA
 FILING DATE:
 10036
 STATE: NA COUNTRY:
 US-08-075-783-9
 RESULT
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8; Conservative
 | || || || || 315 YYFNFANGQSMWDHP 329
 4 YMINFGRGONYWEHP 18
 ORGANISM: Glycine max
 Best_Local Similarity
Matches 8; Conserv
 US-60-324-109-31002
 US-60-324-109-31002
 SEQ ID NO 31002
LENGTH: 313
 Query Match
 FEATURE
 οp
 οy
 q
 δ
 NAME/KEY: DOMAIN
LOCATION: (315)...(330)
OTHER INFORMATION: WW DOMAIN SIGNATURE domain identified by eMATRIX, accession OTHER INFORMATION: number PR00403B, p-value=3.898e-09, raw score of 12.19
 ö
 0
 LOCATION: (12)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 : OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids PCT-US01-01307-859
 Gaps
 Gaps
 ;
0
 ;
 Sequence 859, Application PC/TUS0101307
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc., et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PT1218PCT
CURRENT APPLICATION NUMBER: PCT/US01/01307
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1040
 RESULT 10
PCT-USO1-08631-48408
; Sequence 48408, Application PC/TUSO108631
; GENERAL INFORMATION:
 APPLICANT: Hyseq, Inc
 TITLE OF INVENTION:
 TITLE OF INVENTION:
 CURRENT APPLICATION NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
 CURRENT APPLICATION NUMBER: PCT/USO1/08631
 CURRENT FILING DATE: 2001-03-30
 PRIOR FILING DATE: 2000-03-31
 PRIOR FILING DATE: 2000-03-31
 PRIOR FILING DATE: 2000-08-23
 NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: CUSTON
; SEQ ID NO 48408
 DB 1; Length 103; 1.1;
 Score 57; DB 1; Length 99;
Pred. No. 1.1;
2; Mismatches 5; Indels
 5; Indels
 Score 57; DB 1
Pred. No. 1.1;
2; Mismatches
 Query Match 43.5%;
Best Local Similarity 53.3%;
Matches 8; Conservative
 43.5%;
 Query Match 43.5
Best Local Similarity 53.3
Matches 8; Conservative
 4 YMINFGRGONYWEHP 18
 | || || ||: ||: || || 54 YYFNFANGQSMWDHP 68
 4 YMINFGRGONYWEHP 18
 | || || ||: ||:||
54 YYENFANGQSMWDHP 68
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-01307-606
 ORGANISM: Homo sapiens
 ORGANISM: Homo sapiens
 RESULT 9
PCT-US01-01307-859
 NAME/KEY: SITE
 NAME/KEY: SITE
 LENGTH: 103
TYPE: PRT
 SEQ ID NO 859
 LOCATION:
 TYPE: PRT
 LOCATION:
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, NAME/KEY: DOMAIN
; LOCATION: (82)..(149)
. OTHER INFORMATION: Subtilase family domain identified by PFam, accession name
; OTHER INFORMATION: Peptidase_S8, E-value=9e-19, PFam score of 71.1
PCT-US01-08631-48408
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 Gaps
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 US-GOUSTA-1109-51202

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDN A SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)B
CURRENT PAPLICATION NUMBER: US/60/324,109
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 33196
 18;
 ;
 DB 24; Length 313; 22;
 Score 57; DB 1; Length 374;
Pred. No. 4.3;
 ; Sequence 2, Application US/09672785; Sequence 2, Application US/09672785; GENERAL INFORMATION:
APPLICANT: Mizutani, Masako
APPLICANT: Rasumi, Takaaki
APPLICANT: Rasumi, Takaaki
TITLE OF INVENTION: Genes Coding for Flavone Synthases;
FILE REFERENCE: 001560-383
CURRENT FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-01-30
PRIOR FILING DATE: 1999-01-28
PRIOR FILING DATE: 1999-01-28
PRIOR FILING DATE: 1999-01-28
PRIOR FILING DATE: 1999-01-19
PRIOR FILING DATE: 1999-01-19
PRIOR FILING DATE: 1999-01-19
PRIOR FILING DATE: 1999-01-19
SRIOR APLICATION NUMBER: JP 11-22427
PRIOR FILING DATE: 1999-01-29
NUMBER OF SED ID NOS: 8
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 2
LENGTH: 506
 3; Indels
 Score 52; DB 2
Pred. No. 22;
0; Mismatches
 2; Mismatches
 75 IGIGRGQEYWEQENIREEMPACROMFNIFHPY 106
 39.78;
34.48;
 43.5%;
 6 INFGRGONYWE-----
 Query Match 39.77
Best Local Similarity 34.4
Matches 11; Conservative
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 Sequence 5435, Application US/60196710
GENERAL INFORMATION:
APPLICANT: BONDAZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
GURRENT APPLICATION NUMBER: US/60/196,710
CURRENT FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 7166
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 30
 Sequence 775, Application US/60173468
GRERAL INFORMATION:
GRERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTIENS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTIENS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000181
CURRENT APPLICATION NUMBER: US/60/173,468
CURRENT FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 1418
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 775
 ö
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; ORGANISM: Antirrhinum majus
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of a protein having an activity to
; OTHER INFORMATION: directly convert flavanone to flavone
US-09-672-785-2
 Gaps
 Gaps
 Gaps
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 Score 52; DB 20; Length 506;
Pred. No. 36;
 Score 50; DB 24; Length 30;
Pred. No. 3.9;
2; Mismatches 6; Indels
 Score 50; DB 24; Length 30;
Pred. No. 3.9;
 Indels
 39.7%; Scur.
42.1%; Pred. No. 30,
 2; Mismatches
 391 FVNLWSMGRNPNYWENPME 409
 38.2%;
illarity 46.7%;
Conservative
 2 FTYMINFGRGONYWEHPYQ 20
 Conservative
 Query Match 38.2
Best Local Similarity 46.7
Matches 7; Conservative
 4 YMINFGRGONYWEHP 18
 4 YMINFGRGQNYWEHP 18
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16 YFFNFANRQSIWDHP 30
 16 YFFNFANROSIWDHP 30
 Query Match
Best Local Similarity
Matches 8; Conserv
 Query Match
Best Local Similarity
Matches 7; Conserv
 ORGANISM: HUMAN
US-60-196-710-5435
 ORGANISM: HUMAN
 US-60-196-710-5435
 US-60-173-468-775
 US-60-173-468-775
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Sequence 4, Application US/09672785

Sequence 5, Application US/09672785

APPLICAMT: Akashi, Tomoyoshi

TITLE OF INVENTION UNMER: US/09/672,785

CURRENT PAPLICATION NUMBER: DCT/JP00/04379

PRIOR PELING DATE: 2000-01-30

PRIOR APPLICATION NUMBER: PCT/JP00/0490

PRIOR APPLICATION NUMBER: PCT/JP00/0490

PRIOR APPLICATION NUMBER: PCT/JP00/0490

PRIOR PELING DATE: 1999-01-29

PRIOR APPLICATION NUMBER: JP 11-20529

PRIOR PELING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 8

SOTTAMES: PRECENT OF SEQ ID NOS: 8

CONTANT: 512

TYPE: PRT

OCANALISM: Torenia hybrida

FEATURE:

OCHER INFORMATION: Amino acid sequence of a protein having an activity to convert March

CONTANTE: PROCENTION: Amino acid sequence of a protein having an activity to convert March

SEQ ID NO 4

SEQ ID NO 5

SEQ ID NO 6

SEQ ID NO 6

SEQ ID NO 7

SEQ ID NO 7

SEQ ID NO 8

SEQ ID NO 8

SEQ ID NO 9

SEQ I
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Page

10593, A 10592, A 10591, A 757, App 2, Appli

Sequence

1036, Ap 27392, A

Sequence

10, Appl

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Sequence 15235, Application US/09708427

GENERAL INFORMATION:
APPLICANT:
APPL
 APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: US/09/708,427
SURRENT FILING DATE: 2000-11-09
NUMBER OF EQ. ID NOS: 85364
SOFTWARE: PATENTIN VERSION 3.1
SEQ. ID NO 15234
LENGTH: 341
 Score 47; DB 5; Length 292;
Pred. No. 7.6;
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US-09-708-427-10593
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US-09-976-594-757
US-09-96-733-945-2
US-09-468-6468-31
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US-09-708-427-20343
US-09-708-427-20342
 US-09-953-499-10
US-09-620-394B-1036
US-09-708-427-27392
US-09-708-427-27391
US-09-708-427-27391
 US-09-897-516-7363
 2; Mismatches
 NAME/KEY: misc_feature
| LCCATION: 1..292
| OTHER INFORMATION: Xaa is any amino acid
| NAME/KEY: misc_feature
| LCCATION: 1..292
| OTHER INFORMATION: Ceres Seq. ID 1828911
| US-09-708-427-15235
 Sequence 15234, Application US/09708427 GENERAL INFORMATION:
 TYPE: PRT
ORGANISM: Arabidopsis thaliana
 35.9%;
70.0%;
 7; Conservative
 Query Match
Best Local Similarity
Matches 7; Conserv
 9 GRGQNYWEHP 18
 RESULT 1
US-09-708-427-15235
 RESULT 2
US-09-708-427-15234
FEATURE:
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 Sequence 15235, A Sequence 15234, A Sequence 15234, A Sequence 5126, Ap Sequence 21796, A Sequence 21795, A Sequence 17, Appl Sequence 90, Appl Sequence 91, Appl Sequence 91, Appl Sequence 91, Appl Sequence 93, Appl Sequence 94, Appl Sequence 96, Appl Sequence 87, Sequence 67425, A
Sequence 67425, A
Sequence 9458, Ap
Sequence 16, Appl
Sequence 9457, Ap
Sequence 1903, Ap
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25013, A
 15, Appl
15743, A
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6.657 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 ; Search time 120.95 Seconds
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Sequence 1
Sequence 1
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4: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*
 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-708-427-15233
US-09-708-427-21796
US-09-708-427-21796
US-09-708-427-21796
US-09-815-242-4997
US-09-88-73-15-12
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US-09-87-67426
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US-09-708-427-9457
US-09-708-427-9457
US-09-708-427-9457
US-09-708-427-9513
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 173191 seqs, 36597120 residues
 131
1 EFTYMINFGRGQNYWEHPYQKS 22
 January 29, 2002, 10:58:16
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

 protein search, using sw model

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Gapop 10.0 , Gapext 0.5
 US-09-763-397A-19
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 Length
 Query
Match 1
 35.9
335.9
335.9
335.9
335.9
335.9
335.9
335.9
335.9
335.9
335.9
335.9
 rotal number of
 Score
 41.5
 Perfect score:
 Scoring table:
 OM protein
 Minimum DB
Maximum DB
 Sequence:
 Searched:
 Database
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0
 Result
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Gaps

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; Sequence 21795. Application US/09708427; SENERAL INFORMATION: APPLICANT: N. ALEXANDROV et al. TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
 Sequence 21796, Application US/09708427

GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION:
FILE REPERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT APPLICATION DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SOFTWARE: Patentin version 3.1
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 Gaps
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0
 ;
0
 Length 1620;
 Length 133;
 Indels
 9; Indels
 35.1%; Score 46; DB 5;
46.2%; Pred. No. 4.8;
tive 4; Mismatches
 DB 5;
 PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-22
PRIOR FILING DATE: 2001-26
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
SOFTWARE: 1620
 Pred. No. 44;
3; Mismatches
 NAME/KEY: misc_feature
LOCATION: 1..133
OTHER INFORMATION: Xaa is any amino acid
 ID 1840051
FILING DATE: 2000-03-21 APPLICATION NUMBER: 60/206,848
 OKGANISM: Pseudomonas aeruginosa
US-09-815-242-5126
 ORGANISM: Arabidopsis thaliana
 NAME/KEY: misc_feature

...LocATION: 1...133

...COTER INFORMATION: Ceres Seq.

US-09-708-427-21796
 35.9%;
36.8%;
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Best Local Similarity 36.0.
Local Similarity 36.0.
Local Similarity 36.0.
 | |::||| ::|
13 GSGEAFWEHEWEK 25
 9 GRGQNYWEHPYQK 21
 Best_Local Similarity
Matches 6; Conserv
 RESULT 6
US-09-708-427-21795
 US-09-708-427-21796
 SEQ ID NO 21796
LENGTH: 133
 Query Match
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 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY CURRENCE: 2750-1243P CURRENT APPLICATION NUMBER: US/09/708,427 CURRENT FILING DATE: 2000-11-09 NUMBER OF SEQ ID NOS: 85364 SOFTWARE: PATENTIN VERSION 3.1
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 Length 452;
 Length 341;
 1; Indels
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 APPLICANT: 279kInd, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
ITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REPERANCE: BLITRA 011A
CURRENT FILLIATICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
 Score 47; DB 5;
Pred. No. 12;
2; Mismatches
 DB 5;
 Score 47; DB Pred. No. 8.9; 2; Mismatches
 CTHER INFORMATION: Ceres Seq. ID 1828909
US-09-708-427-15233
 LOCATION: 1..341
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..341
COTHION: 1..341
USAHATION: 1..341
USAHATION: 1..341
 OTHER INFORMATION: Xaa is any amino acid
 Sequence 15233, Application US/09708427 GENERAL INFORMATION:
 US-09-815-242-5126; Sequence 5126, Application US/09815242; GENERAL INFORMATION:
 APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
 ORGANISM: Arabidopsis thaliana
 35.9%;
70.0%;
 ORGANISM: Arabidopsis thaliana
 35.9%;
70.0%;
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Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
 NAME/KEY: misc_feature
LOCATION: 1..452
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 NAME/KEY: misc_feature
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 9 GRGQNYWEHP 18
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 US-09-708-427-15233
 SEQ ID NO 15233
 LENGTH: 452
 FEATURE:
 á
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Gaps
 Sequence 17, Application US/09689730
GENERAL INFORMATION:
APPLICANT: SETIKI, Motcharu
APPLICANT: STEIKI, Motcharu
APPLICANT: SHINACAWA, Akira
TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
FILE REFERENCE: 55-20P
CURRENT APPLICATION NUMBER: US/09/689,730
CURRENT FILING DATE: 2000-10-13
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTI VET. 2.0
 ö
 GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Tyskind, Judith W.
APPLICANT: Garr, Grant J.
APPLICANT: Wall Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 05/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
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PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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SEQ ID NO 4997
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 Score 46; DB 5; Length 467;
Pred. No. 17;
 Indels
 Mismatches
 Sequence 4997, Application US/09815242 GENERAL INFORMATION:
 ; ORGANISM: Enterococcus faecalis US-09-815-242-4997
 35.1%;
50.0%;
 Ouery Match
Best Local Similarity 50.0°
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28 GKGQNIWDFWYQEA 41
 9 GRGQNYWEHPYQKS 22
 9 GRGQNYWEHPYQKS 22
 31 GKGONIWDFWYQEA 44
 TYPE: PRT
ORGANISM: Unknown
 RESULT 9
US-09-689-730-17
 SEQ ID NO 17
LENGTH: 631
 q
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 APPLICANT: Varian, JOACIAN W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yammanco, Robert T.
APPLICANT: Yammanco, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVEWTION: Identification of Essential Genes in TITLE OF INVEWTION: Protestyotes
FILE REFERENCE: ELITRA.01A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/101,078
RIOR FILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/207,727
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PRIOR PLICATION NUMBER: 60/205,365
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PRIOR PLILING DATE: 2000-10-23
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PRIOR PLILING DATE: 2000-12-22
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PRIOR PLILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARRE: FREESE FOR WINDOWS VERSION 4.0
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 Score 46; DB 5; Length 230;
Pred. No. 8.4;
 3; Indels
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 4; Mismatches
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 FILE REFERENCE: 2750-1143P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21795
LENGTH: 230
 NAME/KEY: misc_feature
LOCATION: 1..230
CTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..230
CTHER INFORMATION: Ceres Seq. ID 1840050
US-09-708-427-21795
 Sequence 10647, Application US/09815242 GENERAL INFORMATION:
 Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
 ; ORGANISM: Enterococcus faecalis
US-09-815-242-10647
 TYPE: PRT
ORGANISM: Arabidopsis thaliana
 35.1%;
46.2%;
 THEREBY
 APPLICANT: Haselbeck, Robert
 Query Match
Best Local Similarity 46.2
Matches 6; Conservative
 Query Match 35.1
Best Local Similarity 50.0
Matches 7; Conservative
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110 GSGEAFWEHEWEK 122
 9 GRGQNYWEHPYQK 21
TITLE OF INVENTION:
 US-09-815-242-10647
 APPLICANT:
 FEATURE:
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APPLICANT: BADYON COLLege of Medicine
APPLICANT: Thompson, Timothy C.
APPLICANT: Thompson, Timothy C.
APPLICANT: Ren, Chengachen
TITLE OF INVENTION: RPP Based Compositions and Methods for the Treatment of Prost
FILE REFERENCE: 38594.0027
CURRENT APPLICATION NUMBER: US, 60/209, 989
PRIOR PAPLICATION NUMBER: US 60/209, 989
PRIOR FILING DATE: 2000-06-08
PRIOR FILING DATE: 2000-06-08
SPRIOR FILING DATE: 2000-06-08
SOFTWARE: Patentin version 3.1
SED ID NOS: 5
SOFTWARE: Patentin version 3.1
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 APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: Mishina
APPLICANT: Mases, Peter S
APPLICANT: Rastelli, Luca
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-697
CURRENT APPLICATION NUMBER: US/09/800,198
CURRENT FILING DATE: 2001-03-05
PRIOR FILING DATE: 2000-03-03
MINMARP OF SEC OF NO. 10 NO. 20
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 Length 266;
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 Length 219;
 Indels
 6; Indels
 DB 5;
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 Score 43; DB Pred. No. 23; 5; Mismatches
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Pred. No.
 Sequence 90, Application US/09800198 GENERAL INFORMATION:
 Sequence 3, Application US/09876225; GENERAL INFORMATION:
 APPLICANT: Vernet, Cornie AM
APPLICANT: Fernandes, Elma
APPLICANT: Shimkets, Richard A
APPLICANT: Herrmann, John L
 32.8%;
 32.8%;
38.9%;
 171 FICNYGPGGNYPTWPYKR 188
 161 FICNYGPGGNYPTWPYKR 178
 4 YMINFGRGONYWEHPYOK 21
 4 YMINFGRGQNYWEHPYQK 21
 NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 90
LENGTH: 266
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) ORGANISM: Homo sapiens
US-09-876-225-3
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US-09-800-198-90
; ORGANISM: Homo sapiens
US-09-800-198-91
 Query Match
Best Local Similarity
 US-09-800-198-90
 US-09-876-225-3
 APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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 Sequence 15512, Application US/09708427
Sequence 15512, Application US/09708427
Sequence 15512.
Sequence 15512.
Sequence 15512.
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRACMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILLE REPERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
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 0;
 1;
 APPLICANT: Vernetion:
APPLICANT: Vernet, Cornie AM
APPLICANT: Vernandes, Elma
APPLICANT: Shimkets, Richard A
APPLICANT: Herrann, John L
APPLICANT: Harmann, John L
APPLICANT: Majumder, Kumud
APPLICANT: Mishra, Vishna
APPLICANT: Mases, Peter S
APPLICANT: Rastelli, Luca
FILE REPERENCE: 15966-697
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
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PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
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 Length 228;
 Score 45; DB 5; Length 631;
Pred. No. 34;
0; Mismatches 3; Indels
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LOCATION: 1..228
OTHER INFORMATION: Xaa is any amino acid
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COATION: 1..228

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US-09-708-427-15512
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58.8%;
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Best Local Similarity 54.59
Matches 6; Conservative
 1 EFTYMINFGRGONYWEH 17
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Best Local Similarity 58.8'
Matches 10; Conservative
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 11 GONYWEHPYOK 21
 US-09-708-427-15512
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US-09-800-198-91
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LENGTH: 219
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Search completed: January 29, 2002, 10:58:17 Job time: 2513 sec
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 10 RGQNYWEHPY 19
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 Sequence 3.7.0.5.2.

Sequence 3.7.0.5.2.

GENERAL INFORMATION:

APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P

CURRENT FILLING DATE: 2750-1243P

CURRENT FILLING DATE: 2750-11-09

NUMBER OF SEQ ID NOS: 85364

SEQ ID NOS: 85364

SEQ ID NOS: 85364

SEQ ID NO SEQ ID NOS: 85364

SEQ ID NO SEQ ID NOS: 85364

SEQ ID NO
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 ö
 APPLICANT: Vernet, Cornie AM
APPLICANT: Fernandes, Elma
APPLICANT: Fernandes, Elma
APPLICANT: Richard A
APPLICANT: Majumder, Richard A
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Vishna
APPLICANT: Mastelli, Luca
APPLICANT: Rastelli, Luca
APPLICANT: Rastelli, Luca
APPLICANTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILER REFERENCE: 15966-697
CURRENT APPLICATION NUMBER: US/09/80,198
CURRENT APPLICATION NUMBER: 00/186,596
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-03
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 89
LENGHH: 415
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 Score 43; DB 5; Length 415;
Pred. No. 44;
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| USCAMATION: Ceres Seq. ID 1932516
| US-09-708-427-67426
 Sequence 89, Application US/09800198; GENERAL INFORMATION:
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 TYPE: PRT
ORGANISM: Zea mays subsp. mays
 ; ORGANISM: Halocynthia roretzi
US-09-800-198-89
 Ouery Match 32.8%;
Best Local Similarity 53.8%;
Matches 7; Conservative
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268 NYGPGGNYPTHPF 280
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 US-09-708-427-67426
 US-09-800-198-89
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 FEATURE:
Matches
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 3148936 segs, 277657034 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
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1 DQPKQYEQHLTDYEKIKEG 19
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 US-09-763-397A-18
 Minimum DB seq length: 0 Maximum DB seq length: 20000000000
 Perfect score:
 Scoring table:
 Database :
 Searched:
 Sequence:
 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| Result |       | Query |                    |    |                       |                   |
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| 7      | 105   | 100.0 | 350                | 21 | US-09-763-397A-2      | Sequence 2, Appli |
| ιή     | 105   | 100.0 | 622                | _  | PCT-US92-02207-8      | Sequence 8, Appli |
| 4      | 105   | 100.0 | 622                | m  | US-07-672-183A-8      | Sequence 8, Appli |
| S      | 105   | 100.0 | 622                | 4  | US-08-072-867-8       | Sequence 8, Appli |
| 9      | 105   | 100.0 | 622                | 4  | US-08-075-783-9       | Sequence 9, Appli |
| 7      | 53    | 50.5  | 149                | 24 | 24 US-60-192-737-1135 | Sequence 1135, Ap |
| œ      | 53    | 50.5  | 149                | 24 | US-60-194-106-704     | Sequence 704, App |
| σ      | 23    | 50.5  | 160                | 24 | US-60-192-737-1317    | Segmence 1317. Ap |

| 808<br>2,<br>117<br>4, A<br>8, A | Sequence 4, Appli<br>Sequence 8, Appli<br>Sequence 4, Appli<br>Sequence 6, Appli<br>Sequence 6, Appli<br>Sequence 1, Appli       | Sequence 5, Appli<br>Sequence 6, Appli<br>Sequence 2, Appli<br>Sequence 3, Appli<br>Sequence 2, Appli                 | m                                                | Sequence 24, Appl<br>Sequence 26, Appl<br>Sequence 25756, A<br>Sequence 26164, A<br>Sequence 26768, A<br>Sequence 20, Appl<br>Sequence 20, Appl                          | 34516<br>403,<br>2423<br>3086<br>2457                                                                                        |
|----------------------------------|----------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------|--------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------|
|                                  | 21 US-09-371-674-4<br>21 US-09-706-426-8<br>22 US-09-855-145-4<br>1 PCT-USO0-02544-2<br>1 PCT-USO0-30542-6<br>15 US-09-152-814-1 | 7 US-09-371-674-2<br>1 US-09-706-426-6<br>2 US-09-855-145-2<br>3 US-09-99-3<br>8 US-09-494-810-2<br>8 US-09-494-810-2 | Q.                                               | 22 US-09-898-554-24<br>24 US-60-324-109-25756<br>24 US-60-324-109-26164<br>24 US-60-312-544-5497<br>24 US-60-324-109-26768<br>22 US-09-898-554-20<br>24 US-60-173-466-55 | 1 PCT-USO1-08631-34518<br>21 US-09-758-475-403<br>24 US-60-173-464-24239<br>24 US-60-191-637-30862<br>24 US-60-191-681-24571 |
|                                  |                                                                                                                                  | 1488444                                                                                                               | 10110111                                         | 302 22 23 23 24 25 25 25 25 25 25 25 25 25 25 25 25 25                                                                                                                   |                                                                                                                              |
| 33 50.5<br>30.5<br>50.5<br>50.5  | ស់សំសំសំសំ <b>សំ</b>                                                                                                             | 500<br>500<br>500<br>500<br>500<br>500<br>500<br>500<br>500<br>500                                                    | 166 443.8<br>166 443.8<br>166 443.8<br>166 443.8 | ڡؙ؈ؘڡ؈؈ <u>؈</u>                                                                                                                                                         | 441.9<br>41.9<br>41.9<br>6.1.9                                                                                               |
| 10<br>11<br>13<br>13             | 15<br>16<br>18<br>19<br>20                                                                                                       | 222<br>222<br>223<br>243<br>263                                                                                       | 32<br>32<br>33<br>33<br>33<br>33<br>33<br>33     | # # # # # # # # # # # # # # # # # # #                                                                                                                                    | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4                                                                                        |

## ALIGNMENTS

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Sequence 18, Application US/09763397A

Sequence 18, Application US/09763397A

Sequence 18, Application US/09763397A

GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A.
APPLICANT: Hasnain, Seyed E.
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Fa FILE REFERENCE: 6395-57049

TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Fa FILE REFERENCE: 6395-57049

CURRENT FILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: US 60/097,703

PRIOR FILING DATE: 1998-08-21

PRIOR PILING DATE: 1998-08-19

PRIOR PILING DATE: 1999-08-19
 Length 19;
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100.0%; Pred. No. 4.8e-09;
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 Plasmodium falciparum
 NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
 Query Match 100.0
Best Local Similarity 100.0
Matches 19; Conservative
 ; ORGANISM: Plas
US-09-763-397A-18
US-09-763-397A-18
 LENGTH: 19
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Gaps

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Indels

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 Length 622;
 Length 622;
 US-07-672-183A-8
Sequence 8, Application US/07672183A
Sequence 8, Application US/07672183A
GENERAL INFORMATION:
APPLICANT: de Taisne, Charles
APPLICANT: Tine, John A.
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
 Indels
 COMPUTER REACABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/672,183A
FILING DATE: 19910320
CLASSIFICATION: PATA
 Score 105; DB 3;
Pred. No. 3.8e-07;
 ADDRESSEE: William S. Frommer ADDRESSEE: c/o Curtis, Morris & Safford, P.C. STREET: 530 Fifth Avenue
 Score 105; DB 1;
Pred. No. 3.8e-07;
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 RESULT 5
US-08-072-867-8
; Sequence 8, Application US/08072867
; GENERAL INFORMATION:
 REFERENCE/DOCKET NUMBER: 4543
TELECOMMUNICATION INFORMATION:
TELEFAN: (212) 840-333
TELEFAN: (212) 840-0712
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHREACTERISTICS:
 .;
o
 ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
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100.0%;
 100.0%;
100.0%;
 348 DOPKOYEQHLTDYEKIKEG 366
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amino acid
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 1 DQPKQYEQHLTDYEKIKEG
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LENGTH: 622 amino acid
 single
 Query Match
Best Local Similarity
Matches 19; Conserva
 Query Match
Best Local Similarity
Matches 19; Conserval
 linear
 TOPOLOGY: linear
 New York
 New York
 STRANDEDNESS:
 TYPE: amino a STRANDEDNESS:
 US-07-672-183A-8
 PCT-US92-02207-8
 QC
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 qq
 APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis APPLICANT: Control and Prevention
APPLICANT: Control and Prevention
APPLICANT: Plat, Altaf A. APPLICANT: Ping Shi, Ya APPLICANT: Ping Shi, Ya APPLICANT: Hasnain, Seyed E. TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falci TITLE OF INVENTION: 8095-57049
CURRENT APPLICATION NUMBER: US/09/763,397A
CURRENT FILING DATE: 1998-08-21
PRIOR FILING DATE: 1998-08-21
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 26
NUMBER OF SEQ ID NOS: 26
NUMBER OF SEQ ID NOS: 26
 ö
 Gaps
 ;
0
 Length 350;
 Sequence 8, Application PC/TUS920207
GENERAL INFORMATION:
APPLICANT: VIROSENETICS, CORPORATION
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
 Indels
 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/USG2 ////
 ; Score 105; DB 21;
; Pred. No. 1.8e-07;
0; Mismatches 0;
 ADDRESSEE: Curtis, Morris, and Safford ADDRESSEE: c/o William S. Frommer STREET: 530 Fifth Avenue CITY: New York SPATE: New York COUNTRY: USA
 ; OTHER INFORMATION: Recombinant DNA/Protein US-09-763-397A-2
 ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2411
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 840-3333
TELEFRAX: (212) 840-0712
 J9-MAR-1992
 Sequence 2, Application US/09763397A GENERAL INFORMATION:
 COMPUTER READABLE FORM:
MEDUM TYPE: FLOPPy disk
COMPUTER: IBM PC compatible.
OPERATING SYSTEM: PC-DOS/MS-
 100.0%;
100.0%;
 264 DQPKQYEQHLTDYEKIKEG 282
 ORGANISM: Artificial Sequence
 1 DQPKQYEQHLTDYEKIKEG 19
 1 DQPKQYEQHLTDYEKIKEG 19
 Query Match
Best Local Similarity 100.
Matches 19; Conservative
 FILING DATE: 1 CLASSIFICATION:
 10036
R PF
 RESULT 3
PCT-US92-02207-8
 US-09-763-397A-2
 SEQ ID NO 2
LENGTH: 350
 TYPE: PRT
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Sequence 1135, Application US/60192737

Sequence 1135, Application US/60192737

GENERAL INFORMATION:

APPLICANT: Bonazzi, Vivien

TITLE OF INVENTION: ISCLATED HUMAN KINASE PROTEINS OF THE

TITLE OF INVENTION: SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES

TITLE OF INVENTION: ENCODING THESE HUMAN KINASE PROTEINS, AND USES THEREOF

TITLE OF INVENTION: ENCODING THESE HUMAN KINASE PROTEINS, AND USES THEREOF

CURRENT PAPLICATION NUMBER: US/60/192,737

CURRENT FILING DATE: 2000-03-28

NUMBER OF SEQ ID NOS: 1342

SEQ ID NO 1135

LENGTH: 149
 US-60-194-106-704

Sequence 704, Application US/60194106

Sequence 704, Application US/60194106

GENERAL INFORMATION:
TOTAL OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF SECONDALIA
FILE REFERENCE: CL000413

FILE REFERENCE: CL000413

CURRENT FILING DATE: 2000-04-03

NUMBER OF SEQ ID NOS: 826

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 704

LENGTH: 149
 Gaps
 Gaps.
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 Length 622;
 Score 53; DB 24; Length 149;
Pred. No. 6.7;
 Indels
 Score 105; DB 4;
Pred. No. 3.8e-07;
 Mismatches
 Mismatches
 ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION UNBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 amin acids
 3;
 ö
 100.0%;
100.0%;
 50.5%;
64.3%;
 348 DQPKQYEQHLTDYEKIKEG 366
 1 DQPKQYEQHLTDYEKIKEG 19
 Query Match 100.
Best Local Similarity 100.
Matches 19; Conservative
 Conservative
 TYPE: amino acid
STRANDEDNESS: single
 4 KOYEQHLTDYEKIK 17
 68 KQYKHHLTAYEKLE 81
 ; TOPOLOGY: linear
US-08-075-783-9
 Query Match
Best Local Similarity
Matches 9; Conserv
 ; TYPE: PRT
; ORGANISM: HUMAN
US-60-194-106-704
 ; ORGANISM: HUMAN US-60-192-737-1135
 US-60-192-737-1135
 TYPE: PRT
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 Gaps
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 NESOL 105-783-9

Sequence 9, Application US/08075783

Sequence 9, Application US/08075783

Sequence 9, Application US/08075783

SEQUENCE 1 NEORATION:

APPLICANT: Paoletti, Enzo

APPLICANT: Tine, John A.

TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE

NUMBER OF SEQUENCES: 124

CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris & Safford

ADDRESSEE: C/O William S. Frommer

STREET: 530 Fifth Avenue

CITY: New York
 Length 622;
APPLICANT: Paoletti, et al TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE NUMBER OF SEQUENCES: 74 CORRESPONDENCE ADDRESS:
 Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/072,867
 100.0%; Score 105; DB 4;
100.0%; Pred. No. 3.8e-07;
Live 0; Mismatches 0;
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/852,305
FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 25,506
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
 ADDRESSEE: Curtis, Morris, and Safford ADDRESSEE: c/o William S. Frommer STREET: 530 Fifth Avenue CITY: New York STATE: New York
 New York : United States of America
 APPLICATION NUMBER: US/08/075,783
FILING DATE: 11-JUN-1993
 TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 8:
 Query Match
Best Local Similarity 100.0%;
Matches 19; Conservative (
 348 DQPKQYEQHLTDYEKIKEG 366
 1 DQPKQYEQHLTDYEKIKEG 19
 SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
 STRANDEDNESS: single
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
 TYPE: amino acid
 TOPOLOGY: linear
 USA
 FILING DATE:
 10036
 10036
 COUNTRY:
ZIP: 100
 COUNTRY:
 STATE:
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85 KQYKHHLTAYEKLE 98
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 US-60-192-737-1317

Sequence 1317, Application US/60192737

Sequence 1317, Application US/60192737

Sequence 1317, Application US/60192737

GENERAL INFORMATION:

TOTALE INVENTION: ISOLATED HUMAN KINASE PROTEINS OF THE TITLE OF INVENTION: SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES TITLE OF INVENTION: ENCODING THESE HUMAN KINASE PROTEINS, AND USES THEREOF FILE REFERENCE: CLO00402

CURRENT APPLICATION NUMBER: US/60/192,737

CURRENT FILING DATE: 2000-03-28

NUMBER OF SEQ ID NOS: 1342

SOFTWARE: FastSEQ for Windows Version 4.0
 ;
0
 Sequence 808, Application US/60194106
Sequence 808, Application US/60194106
GENERAL INFORMATION:
APPLICANT: BONAZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: UMBER: US/60/194,106
CURRENT APPLICATION NUMBER: US/60/194,106
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 826
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 808
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 Score 53; DB 24; Length 160; Pred. No. 7.3;
 Score 53; DB 24; Length 160; pred. No. 7.3; 3; Mismatches 2; Indels
 DB 24; Length 149; 6.7;
 3; Mismatches
 Score 53; DB;
Pred. No. 6.7;
3; Mismatches
 ; LOCATION: (1)...(160)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-60-194-106-808
 NAME/KEY: VARIANT
LOCATION: (1)...(160)
OTHER INFORMATION: Xaa = Any Amino Acid
 50.5%;
 50.5%;
64.3%;
 50.5%;
 Conservative
 Query Match 50.5
Best Local Similarity 64.3
Matches 9; Conservative
 Query Match 50.5
Best Local Similarity 64.3
Matches 9; Conservative
 |||: ||| |||::
85 KQYKHHLTAYEKLE 98
 4 KQYEQHLTDYEKIK 17
 4 KQYEQHLTDYEKIK 17
 |||: ||| |||::
68 KQYKHHLTAYEKLE 81
 Query Match
Best Local Similarity
Matches 9; Conserv
 NAME/KEY: VARIANT
 ORGANISM: HUMAN
 ORGANISM: HUMAN
 US-60-192-737-1317
 RESULT 10
US-60-194-106-808
 SEQ ID NO 1317
 TYPE: PRT
 TYPE: PRT
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4 KQYEQHLTDYEKIK 17

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Sequence 1176, Application US/60213847

GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: SIGNATED HUMAN KINASE PROTEINS OF THE
TITLE OF INVENTION: SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING THESE HUMAN KINASE PROTEINS, AND USES THEREOF
FILE REPERRNE: CLOONOO4
CURRENT APPLICATION NUMBER: US/60/213,847
CURRENT APPLICATION NUMBER: US/60/213,847

SOFTWARE: FALLING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 1824
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1176
LENGTH: 471
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 Gaps
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 50.5%; Score 53; DB 24; Length 471; 64.3%; Pred. No. 28;
 Score 53; DB 24; Length 360;
Pred. No. 20;
2; Mismatches 4; Indels
 Indels
 3; Mismatches
 ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7476908CD1
US-60-221-679-2
 APPLICANT: BUATOR, Neil
APPLICANT: Wang, Yu-mei E.
APPLICANT: Stewart, Elizabeth A.
APPLICANT: Stewart, Elizabeth A.
APPLICANT: Gandhi, Amena R.
APPLICANT: Patterson, Chandra
APPLICANT: Lee, Ernestine A.
APPLICANT: Lee, Ernestine A.
APPLICANT: Lu, Dyung Aina M.
TITLE OF INVENTION: PROTEIN PHOSPHATASES
FILE REFERENCE: PI-OLT3 P
CURRENT FILING DATE: 2000-07-28
CURRENT FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PERL PROGIAM
Sequence 2, Application US/60221679 GENERAL INFORMATION:
 50.5%;
 Tang, Y.Tom
Elliott, Vicki S.
Ramkumar, Jaya
Yao, Monique G.
 |: :||| |||| |||
144 PEALKQHLQDYEKDKE 159
 Query Match 50.5
Best Local Similarity 64.3
Matches 9; Conservative
 Query Match 50.5
Best Local Similarity 62.5
Matches 10; Conservative
 3 PKQYEQHLTDYEKIKE 18
 4 KQYEQHLTDYEKIK 17
 31 KQYKHHLTAYEKLE 44
 ORGANISM: Homo sapiens
 ; ORGANISM: HUMAN US-60-213-847-1176
 SOFTWARE: PEI
SEQ ID NO 2
LENGTH: 360
 TYPE: PRT
 TYPE: PRT
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APPLICANT: Creasy, Caretha
 US-09-371-674-4
 g
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 APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM PLC
TITLE OF INVENTION: YAKI, YAK3A, AND YAK3B AND YEAST YAKI PROTEIN KINASES
TITLE OF INVENTION: YAKI, YAK3A, AND YAK3B AND YEAST YAKI PROTEIN KINASES
FILE REPERENCE: GH-70650W
CURRENT APPLICATION NUMBER: PCT/US00/30542
CURRENT FILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: TO BE ASSIGNED
PRIOR APPLICATION NUMBER: TO BE ASSIGNED
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 9
SEQ ID
 Gaps
 Gaps
 ;
0
 ;
0
 50.5%; Score 53; DB 1; Length 568; 64.3%; Pred. No. 35;
 Query Match 50.5%; Score 53; DB 1; Length 568; Best Local Similarity 64.3%; Pred. No. 35; Matches 9; Conservative 3; Mismatches 2; Indels
 Indels
 TITLE OF INVENTION: A METHOD OF TREATION
TITLE OF INVENTION: A METHOD OF TREATING ANEMIA
FILE REPERENCE: GH-50041
CURRENT APPLICATION NUMBER: PCT/US00/02544
CURRENT FILING DATE: 2000-02-01
EARLIER APPLICATION NUMBER: 09/40,236
EARLIER APPLICATION NUMBER: 09/371,674
EARLIER PILING DATE: 1999-18-10
EARLIER FILING DATE: 1999-08-10
EARLIER FILING DATE: 1999-08-10
EARLIER FILING DATE: 1999-08-10
SEATION OF SEQ ID NOS: 9
SEQ ID NO 4
LEARLIER FILING DATE: 1999-02-01
SEQ ID NO 4
LEARLIER FILING DATE: 1999-02-01
SEQ ID NO 4
LEARLIER FILING DATE: 1999-02-01
SEQ ID NO 4
 3; Mismatches
 Sequence 8, Application PC/TUS0030542 GENERAL INFORMATION:
 Sequence 4, Application PC/TUS0002544 GENERAL INFORMATION:
 Sequence 4, Application US/09371674
GENERAL INFORMATION:
APPLICANT: Lord, Kenneth A.
APPLICANT: Dillion, Susan B.
 Conservative
 |||: ||| |||:
| 128 KQYKHHLTAYEKLE 141
 ||||: ||| |||::
128 KQYKHHLTAYEKLE 141
 4 KQYEQHLTDYEKIK 17
 4 KQYEQHLTDYEKIK 17
 ; ORGANISM: HOMO SAPIENS
PCT-US00-30542-8
 ; ORGANISM: HOMO SAPIENS
PCT-US00-02544-4
 Query Match
Best Local Similarity
Matches 9; Conserv
 RESULT 14
PCT-US00-30542-8
 PCT-US00-02544-4
 RESULT 15
US-09-371-674-4
 TYPE: PRT
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TITLE OF INVENTION: AMERICAL AND FOR TREATING ANEMIA
FILE REPERENCE: GH50041
CURRENT APPLICATION NUMBER: US/09/371,674
CURRENT FILING DATE: 1999-08-10
EARLIER APPLICATION NUMBER: 60/119.045
EARLIER FILING DATE: 1999-02-01
SOFTWARE: FESTE OF WINDOWS VERSION 3.0
SOFTWARE: FOR ON O 4
LENGTH: 568
TYPE: PRT
ONCANISM: Human
US-09-371-674-4

Query Match
SO.5%; Score 53; DB 17; Length 568;
Best Local Similarity 64.3%; Pred. No. 35;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps

Qy 4 KOYEQHITDYEKIK 17
III: || || || || || ||
Db 128 KOYKHHLTAYEKLE 141
Search completed: January 29, 2002, 10:56:11
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Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

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Sequence 25, Appl Sequence 1656, Appl Sequence 1656, App Sequence 1192, App Sequence 154, App Sequence 154, App Sequence 154, App Sequence 26645, A Sequence 26644, A Sequence 5544, App Sequence 5544, App Sequence 5643, App Sequence 5643, App Sequence 5643, App Sequence 5544, App Sequence 5543, App
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US-09-760-446A-1195
US-09-760-446A-1195
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US-09-760-427-50449
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US-09-817-516-7930
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 US-09-708-427-26643
US-09-708-427-5543
US-09-708-427-5542
 APPLICANT: Katsutoshi Ozaki
TITLE OF INVENTION: MAMALLAN POLYPEPTIDES AND
TITLE OF INVENTION: POLYNUCLEOTIDES
FILE REFERENCE: GP-707798-C1
 ALIGNMENTS
 SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 24
LENGTH: 551
 CURRENT APPLICATION NUMBER: US/10/016,333 CURRENT FILING DATE: 2001-12-06
 Sequence 24, Application US/10016333
GENERAL INFORMATION:
APPLICANT: Ian Edward James
 Michael N. Cook
Kathleen T. Gallagher
Kristine Kay Kikly
 Brian Michael Burns
Kimberly A. Brun
Richard James Chenery
 Randall Forrest Smith
 Alexander H. Taylor
Donald M. Wojchowski
 Peter R. Young
Peter C. McDonnell
Wendy S. Halsey
Han N. Trinh
 Tania Tamson Testa
John Anthony Feild
Caretha Lee Creasy
 Stephen A. Hüghes
David J. Powell
Gary Christie
 David Michalovich
 Warren J. Leonard
Katsutoshi Ozaki
 Zunxuan Chen
Todd Fredrickson
 Michael W. Lark
Harma Ellens
 NUMBER OF SEQ ID NOS: 34
 Xiaotong Li
) ORGANISM: MUS MUSCULUS
US-10-016-333-24
 Erding Hu
 Yuan Zhu
 Lin Yue
 US-10-016-333-24
 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
 APPLICANT:
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 APPLICANT
 Sequence 6793, Ap Sequence 30615, A Sequence 33993, A Sequence 33993, A Sequence 33993, A Sequence 18, Appl Sequence 1240, Ap Sequence 12540, Ap Sequence 2270, Ap Sequence 21194, A Sequence 21195, A Sequence 1305, Ap Sequence 12277, A Sequence 1305, Ap Sequence 12277, A Sequence 12277, A Sequence 1206, Ap Sequence 15015, Ap Sequence 15016, Ap Seq
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5.749 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 ; Search time 120.95 Seconds
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7: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*
 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-087-30615
US-09-708-427-30615
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 January 29, 2002, 10:58:16
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

 protein search, using sw model

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Gapop 10.0 , Gapext 0.5
 US-09-763-397A-18
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
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4445
11485
3321
355
360
412
4412
434
434
436
670
120
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Database :

Score

Result

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APPLICANT: N. ALEXANDROW et al.
APPLICANT: N. ALEXANDROW et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILLE REFERENCE: 275612438
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: 2000-11-09
NUMBER OF SEQ ID NOS: 85564
SEQ ID NO 30614
LENGTH: 222
 ;
0
 ö
 APPLICANT: Bower.

APPLICANT: Bower.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

TITLE OF INVENTION: Sphingomonas elodea genome sequences and uses thereof FILE REFERENCE: 38-10(15806)B

CURRENT APPLICATION NUMBER: US/10/015,127

CURRENT APPLICATION NUMBER: US 60/252,455

PRIOR FILING DATE: 2000-11-22

NUMBER OF SEQ ID NOS: 14357

SEQ ID NO 13974

LENGTH: 575
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 Gaps
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0
 Score 45; DB 6; Length 575;
pred. No. 52;
6; Mismatches 5; Indels
 Length 222;
 Indels
 DB 5;
13;
 2; Mismatches
 COHER INFORMATION: Xaa is any amino acid

NAME/KEY: misc_feature

LOCATION: 1.222

COTHER INFORMATION: Ceres Seq. ID 1829599

US-09-708-427-30614
 Score 46;
Pred. No.
 RESULT 5
Sequence 13974, Application US/10015127
GENERAL INFORMATION:
 Sequence 30614, Application US/09708427; GENERAL INFORMATION:
 42.9%;
 TYPE: PRT . . ORGANISM: Arabidopsis thaliana
 43.8%;
 ; TYPE: PRT ; ORGANISM: Sphingomonas elodea US-10-015-127-13974
 449 DLPENYEKHLAAFOFIRD 466
 1 DOPKOYEQHLTDYEKIKE 18
 Ouery Match
Best Local Similarity 38.5.
Local Similarity 38.5.
Conservative
 Query Match
Best Local Similarity 61.55
Matches 8; Conservative
 | || || || :: ||
176 YAQHWTDYDQSKE 188
 NAME/KEY: misc_feature LOCATION: 1..222
 6 YEQHLTDYEKIKE 18
 6 YEQHLTDYEKIKE 18
 | || || || || || || 84 YAQHWTDYDQSKE 96
 RESULT 6
US-09-708-427-33993
 US-09-708-427-30614
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 APPLICANT: Corbin, David R.
APPLICANT: Corbin, David R.
APPLICANT: Goldman, Barry S.
APPLICANT: Hoshing, Joseph E.
APPLICANT: Hassing, Joseph E.
APPLICANT: Hassing, Joseph E.
APPLICANT: Assomil-Osterfeld, Karina C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, S
 Gaps
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 Length 130;
 Indels
Length 551;
 DB 5; Length 77;
 2; Indels
 2; Indels
 Query Match

43.8%; Score 46; DB 5;
Best Local Similarity 61.5%; Pred. No. 6.9;
Matches 8; Conservative 2; Mismatches
 DB 6;
 Score 46; DB Pred. No. 3.8; 5; Mismatches
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 NAME/KEY: misc_feature
LOCATION: 1..130
CTHER THORMATION: Xaa is any amino acid;
NAME/KEY: misc_feature
LOCATION: 1..130
COTHER INFORMATION: Ceres Seq. ID 1829600
US-09-708-427-30615
 Score 53;
Pred. No.
 Sequence 6793, Application US/09897516 GENERAL INFORMATION:
 ORGANISM: Arabidopsis thaliana
 43.8%;
50.0%;
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Matches 9; Conservative
 Query Match 43.8
Best Local Similarity 50.0
Matches 7; Conservative
 ; TYPE: PRT
; ORGANISM: Xenorhabdus sp.
US-09-897-516-6793
 112 KQYKHHLTAYEKLE 125
 6 YEQHLTDYEKIKEG 19
 |::| ||: ||::|
55 YKKHSTDFMKIRQG 68
 4 KQYEQHLTDYEKIK 17
 US-09-897-516-6793
 TYPE: PRT
 FEATURE:
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Gaps
 Gaps
 APPLICANT: Corbin, David R.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Huesing, Joseph E.
APPLICANT: Krasomil-Osterfeld, Karina C.
APPLICANT: Malvar, Thomas M.
APPLICANT: Slater, Steven C.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorabdus sp. Genome Sequences And Uses Thereof
FILE REFERENCE: 38-21(51847)B
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 TITLE OF INVENTION: Methods for Analyzing Biological Elements FILE REFERENCE: 16517.246/38-10(52045)A
CURRENT APPLICATION NUMBER: US/60/325,537
CURRENT FILING DATE: 2001-10-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
LENGTH: 715
 Score 42; DB 7; Length 715;
pred. No. 1.9e+02;
3; Mismatches 5; Indels
 Length 256;
 Indels
 APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
TITLE REFERENCE: ELITRA.011A
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 DB 5;
 Score 41; DB Pred. No. 81; 3; Mismatches
 CURRENT APPLICATION NUMBER: US/09/897,516 CURRENT FILING DATE: 2001-06-29
 PRIOR APPLICATION NUMBER: US 60/215, 161
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
SEQ ID NO 8110
 Sequence 5240, Application US/09815242
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
 Sequence 8110, Application US/09897516 GENERAL INFORMATION:
 TYPE: PRT CORGANISM: Arabidopsis thaliana US-60-325-537-18
 Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
 APPLICANT: Carr, Grant J. APPLICANT: Yamamoto, Robert T.
 40.0%;
 39.0%;
53.8%;
 Query Match 39.0
Best Local Similarity 53.8
Matches 7; Conservative
 Best Local Similarity 46.7
Matches 7; Conservative
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142 QYQQHVAEMEAAKAG 156
 TYPE: PRT
ORGANISM: Xenorhabdus sp.
US-09-897-516-8110
 5 OYEQHLTDYEKIKEG 19
 :||:| | || :|
48 RQYDQMLADYNQI 60
 4 KQYEQHLTDYEKI 16
 RESULT 10
US-09-815-242-5240
 US-09-897-516-8110
 APPLICANT:
 APPLICANT:
 Query Match
 APPLICANT
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Sequence 33993, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85564
SOFTWARE: PATENTI VERSION 3.1
 Sequence 31392, Application US/09708427
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: N. ALEXANDENCE tal.
APPLICANT: N. ALEXANDENCE tal.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SEQ ID NOS: 85364
SEQ ID NOS: 33992
LENGTH: 655
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 Score 42; DB 5; Length 587;
Pred. No. 1.5e+02;
2; Mismatches 7; Indels
 Length 655;
 Score 42; DB 5; Le
Pred. No. 1.7e+02;
 2; Mismatches
 NAME/KEY: misc_feature
LOCATION: 1..655
OTHER INFORMATION: Xaa is any amino acid
 CTHER INFORMATION: Xaa is any amino acid

NAME/KEY: misc_feature

LOCATION: 1..587

UCHER INFORMATION: Ceres Seq. ID 1837602

US-09-708-427-33993
 NAME/KEY: misc_feature
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US-09-708-427-33992
 US-60-325-537-18
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; GENERAL INFORMATION:
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ORGANISM: Arabidopsis thaliana
 ORGANISM: Arabidopsis thaliana
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50.0%;
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 1 DQPKQYEQHLTDYEKIKE 18
 1 DOPKOYEQHLTDYEKIKE 18
 36 DPPKQPSGPLTNYSKLVE 53
 9; Conservative
 Conservative
 APPLICANT: Stein, Joshua C
 NAME/KEY: misc_feature
LOCATION: 1..587
 Query Match
Best Local Similarity
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Best Local Similarity
 US-09-708-427-33992
 SEQ ID NO 33993
LENGTH: 587
 Matches
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Length 445;

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WAKAMATSU, AI
SUGIYAMA, TOMOYASU
NAGAI, KEIICHI
KOJIMA, SHINICHI
 :| ::::||: | |:
286 EQQRKHVEHLSSYYKFKQ 303
39.0%;
 1 DOPKOYEQHLTDYEKIKE 18
 ISOGAI, TAKAO
HAYASHI, KOJI
ISHII, SHIZUKO
KAWAI, YURI
 :| ::::||: | |:
286 EQQRKHVEHLSSYYKFKQ 303
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Best Local 6; Conservative
 1 DQPKQYEQHLTDYEKIKE 18
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Best Local Similarity 33.33
Matches 6; Conservative
 RESULT 13
US-09-611-526-2980
 APPLICANT:
APPLICANT:
APPLICANT:
 APPLICANT:
 APPLICANT
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 APPLICANT: Trawarch, John D.
APPLICANT: Trawarch, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: DEPORTED OF THE CONTROL OF TREAD OF THE COURSENGE ELITRA OILA
FILE REPERENCE: ELITRA OILA
CURRENT FILING DATE: 2001-03-21
PRIOR PELICATION NUMBER: 60/191,078
PRIOR PELICATION NUMBER: 60/206,848
PRIOR PELICATION NUMBER: 60/206,848
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PRIOR FILING DATE: 2000-05-23
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PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-12-22
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PRIOR PELING DATE: 2000-05-28

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PRIOR PILING DATE: 2001-02-16

NUMBER OF SED ID NOS: 14110
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 Sequence 12582, Application US/09815242 GENERAL INFORMATION:
 , ORGANISM: Staphylococcus aureus
US-09-815-242-12582
 ORGANISM: Staphylococcus aureus US-09-815-242-5240
 Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
 283 EQQRKHVEHLSSYYKFKQ 300
 APPLICANT: Haselbeck, Robert
 1 DOPKOYEQHLTDYEKIKE 18
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 Dp
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 Gaps
 Gaps
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 .;
0
 Length 445;
 APPLICANT: Haselbeck, Koust.
APPLICANT: Oblisen, Kari L.
APPLICANT: 2yskind, Judith W.
APPLICANT: Existind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trammorto, Robert T.
APPLICANT: Vamemorto, Robert T.
CURRENT FILING DATE: 2001-03-21
PRIOR PILICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-26
PRIOR PILICATION NUMBER: 60/207,727
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PRIOR
 5; Indels
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 Score 41; DB 5;
Pred. No. 1.5e+02;
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Pred. No. 1.5e+02;
 7; Mismatches
 Sequence 2980, Application US/09611526 GENERAL INFORMATION: APPLICANT: OTA, TOSHIO APPLICANT: NISHIKAWA, TETSUO
 Sequence 12940, Application US/09815242; GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
 , ORGANISM: Staphylococcus aureus
US-09-815-242-12940
 39.0%;
33.3%;
```

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Zelder, Oskar
 SEQ ID NO 2270
LENGTH: 306
 ò
 ö
 ö
 Gaps
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 APPLICANT: Corbin, David R.
APPLICANT: Corbin, David R.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Huesing, Joseph E.
APPLICANT: Krasomil-Osterfeld, Karina C.
APPLICANT: Slater, Thomas M.
APPLICANT: Slater, Steven C.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof FILE REPERENCE: 38-21(51847)8
CURRENT APPLICATION UNMBER: US/09/897,516
CURRENT FILING DATE: 2001-06-29
 TITLE OF INVENTION: PREMERS FOR SYNTHESIS OF FULL LENGTH CDNAS
TITLE OF INVENTION: AND THEIR USES
FILE REFERENCE: 08335/0122
CURRENT APPLICATION NUMBER: US/09/611,526
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CURRENT FILING DATE: US/00-07-07
PRIOR FILING DATE: 1999-194486
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PRIOR FILING DATE: 2000-01-11
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PRIOR FILING DATE: 2000-01-12
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FRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 4484
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LENGTH: 540
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 Score 41; DB 5; Length 1485;
Pred. No. 6e+02;
 Length 540;
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PRIOR FILING DATE: 2000-06-30
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; GENERAL INFORMATION:
APPLICANT: Pompedus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
 Sequence 7774, Application US/09897516 GENERAL INFORMATION:
 39.0%;
50.0%;
 39.0%;
53.3%;
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 ORGANISM: Xenorhabdus sp. US-09-897-516-7774
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 ORGANISM: Homo sapiens
US-09-611-526-2980
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 US-09-897-516-7774
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January 29, 2002, 10:56:09; Search time 1760.55 Seconds (without alignments) 2.839 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
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 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
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 US-09-763-397A-17
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Maximum DB seq length: 200000000
 Title:
Perfect score:
Sequence:
 Scoring table:
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 Searched:
 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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|--------|-------|-------|--------------------|----|---------------------|-------------------|
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| Result |       | Query |                    |    |                     |                   |
| NO.    | Score | Match | Match Length DB ID | DB | ID                  | Description       |
|        | 102   | 100.0 | 18                 | 21 | US-09-763-397A-17   | Sequence 17, Appl |
| 7      | 102   | 100.0 | •••                | 21 | US-09-763-397A-2    | Sequence 2, Appli |
| m      | 93    | 91.2  |                    | -  | PCT-US92-02207-8    | Sequence 8, Appli |
| 4      | 93    | 91.2  |                    | m  | US-07-672-183A-8    | Sequence 8, Appli |
| S      | 93    | 91.2  |                    | 4  | US-08-072-867-8     | Sequence 8, Appli |
| 9      | 93    | 91.2  |                    | 4  | US-08-075-783-9     | Sequence 9, Appli |
| 7      | 47    | 46.1  | 104                | 24 | US-60-171-489-1218  | Sequence 1218, Ap |
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| 6      | 44    | 43.1  |                    | 16 | US-09-270-767-60056 | Sequence 60056, A |

|                                               |        | Sequence 3482, Ap                        | 2, Ap  | 2767        | 2228 | 604,              | 14129               |                     | 1365                | 4, A              | e 3571              | 4932,              | 6829,              | Sequence 2663, Ap  | 2, Ap           | 797                | 8823,               | Sequence 23126, A   | 2312                | 1939                | 19397               | Sequence 6652, Ap  | 710, 2             | Sequence 710, App | 15389               |                    |                     | 1010,              | 26726,               |                    | 8243,     | 830            | Sequence 43442, A   |
|-----------------------------------------------|--------|------------------------------------------|--------|-------------|------|-------------------|---------------------|---------------------|---------------------|-------------------|---------------------|--------------------|--------------------|--------------------|-----------------|--------------------|---------------------|---------------------|---------------------|---------------------|---------------------|--------------------|--------------------|-------------------|---------------------|--------------------|---------------------|--------------------|----------------------|--------------------|-----------|----------------|---------------------|
| US-09-270-849B-189090<br>US-09-252-991A-24400 | -09-27 | US-60-316-362-3482<br>US-60-215-161-6098 | -09-72 | -60-191-637 | -09- | US-60-167-245-604 | US-60-173-464-14129 | US-60-191-637-17243 | US-60-191-681-13652 | PCT-US99-26796-44 | US-09-417-507-35717 | US-60-128-476-4932 | US-60-215-161-6859 | US-09-540-236-2663 | US-09-543-091-2 | US-09-328-352-7970 | US-09-489-039A-8823 | US-09-733-089-23126 | US-09-816-660-23126 | US-09-733-089-19397 | US-09-816-660-19397 | US-09-134-000-6652 | PCT-US00-00724-710 | US-60-162-866-710 | US-09-248-796-15389 | US-60-312-544-9416 | US-09-198-452A-1081 | US-09-438-185-1010 | US-09-252-991A-26726 | US-09-328-352-6123 | 0-312-544 | -60-312-544-89 | US-09-270-767-43442 |
| 16                                            | 16     | 24                                       | 21     | 24          | 24   | 24                | 24                  | 24                  | 24                  | Н                 | 18                  | 24                 | 24                 | 13                 | 13              | 17                 | 18                  | 21                  | 22                  | 21                  | 22                  | 15                 | ~                  | 24                | _                   | 7                  | ٦                   | _                  | ٦                    | 17                 | 7         | 24             | 16                  |
| 480                                           | 635    | 133                                      | 196    | 226         | 226  | 327               | 327                 | 339                 | 339                 | 508               | 990                 | 405                | 519                | 554                | 592             | 622                | 764                 | 168                 | 768                 | 1443                | 1443                | 160                | 187                | 187               | 242                 | 284                | 294                 | 300                | 363                  | 948                | 260       | 271            | 367                 |
| 43.1                                          | 43.1   | 43.1                                     |        |             |      | 42.2              |                     |                     | 42.2                | 42.2              | 41.7                | 41.2               | 41.2               | 41.2               | 41.2            | 41.2               | 41.2                | 41.2                |                     | 41.2                | 41.2                | 40.7               | 40.2               | 40.2              | 40.2                | 40.2               | 40.2                | 40.2               | 40.2                 | 40.2               | 39.7      | 39.7           | 39.7                |
| 44                                            | 44     | 4 4                                      | 43     | 43          | 43   | 43                | 43                  | 43                  | 43                  | 43                | 42.5                | 42                 |                    | 42                 |                 | 42                 | 42                  | 42                  | 42                  | 42                  | 42                  | 41.5               | 41                 | 41                | 41                  | 41                 | 41                  | 41                 | 41                   | 41                 |           | 40.5           |                     |
| 11                                            | 12     | 13                                       | 15     | 16          | 17   | 18                | 19                  | 20                  | 21                  | 22                | 23                  | 24                 | 25                 | 26                 | 27              | 28                 | 29                  | 30                  | 31                  | 32                  | 33                  | 34                 | 35                 | 36                | 37                  | 38                 | 39                  | 40                 | 41                   | 42                 | 43        | 44             | 45                  |

## ALIGNMENTS

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APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the Department of Health and Human Services, Centers for APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A.
APPLICANT: Ping Shi, Ya
APPLICANT: Hasnain, Seyed E.
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Fa
CURRENT FILING DATE: 2001-02-16
CURRENT FILING DATE: 1998-08-21
PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR APPLICATION NUMBER: PCT / US99/18869
PRIOR FILING DATE: 1999-08-19
 Length 18;
 100.0%; Score 102; DB 21;
100.0%; Pred. No. 2.6e-09;
Live 0; Mismatches 0;
 Sequence 17, Application US/09763397A GENERAL INFORMATION:
 ORGANISM: Plasmodium falciparum
 Query Match
Best Local Similarity 100.
Matches 18; Conservative
US-09-763-397A-17
 US-09-763-397A-17
 SEQ ID NO 17
LENGTH: 18
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Gaps

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Indels

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 Length 622;
 NESCUI.
US-07-672-183A-8
Sequence 8, Application US/07672183A
Sequence 8, Application US/07672183A
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Tine, John A.
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
 Score 93; DB 1; Length 622;
Pred. No. 5.7e-06;
0; Mismatches 1; Indels
 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/672,183A FILLING DATE: 19910320 CLASSIFICATION: 424
 Score 93; DB 3; DP ADDRESSEE: William S. Frommer ADDRESSEE: c/o Curtis, Morris & Safford, P.C. STREET: 530 Fifth Avenue
 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Fronmer, William S.
REGISTRATION NUMBER: 25,506
REFERRENCE/DOCKET NUMBER: 454310-2300
TELECHONE: (212) 840-333
TELEPHONE: (212) 840-312
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 8, Application US/08072867 GENERAL INFORMATION:
 1 GNAEKYDKMDEPQHYGKS 18
 : 622 amino acids
AMINO ACID
 LENGTH: 622 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US92-02207-8
 Query Match
Best Local Similarity 94.4
Matches 17; Conservative
 1 GNAEKYDKMDEPQHYGKS 18
 COUNTRY: United States ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dis
 Conservative
 single
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 linear
 Query Match
Best Local Similarity
Matches 17; Conserv
 STATE: New York
 New York
 STRANDEDNESS:
 ;
US-07-672-183A-8
 RESULT 5
US-08-072-867-8
 RESULT
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 APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the Department of Health and Human Services, Centers for Dis APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A.
APPLICANT: Ping Shi, Seyed E.
TILE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falci FILE REFERENCE: 6395-57049
CURRENT APPLICATION NUMBER: US/09/763,397A
CURRENT APPLICATION NUMBER: US 60/097,703
FRIOR APPLICATION NUMBER: PS 60/097,703
FRIOR APPLICATION NUMBER: PS 60/097,703
FRIOR APPLICATION NUMBER: PS 60/097,703
FRIOR RILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN VETSION 3.1
 ö
 Gaps
 ;
0
 Length 350;
 Sequence 8, Application PC/TUS9202207
GENERAL INFORMATION:
APPLICANT: VIRGENETICS, CORPORATION
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
 Indels
 SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
 100.0%; Score 102; DB 21;
100.0%; Pred. No. 9.9e-08;
+ive 0: Mismatches 0;
 0; Mismatches
 ADDRESSEE: Curtis, Morris, and Safford ADDRESSEE: c/o William S. Frommer STREET: 530 Fifth Avenue
 CTHER INFORMATION: Recombinant DNA/Protein US-09-763-397A-2
 NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-5333
TELEFAX: (212) 840-0712
 UMBER: PCT/US92/02207
19-MAR-1992
 Sequence 2, Application US/09763397A GENERAL INFORMATION:
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
 ORGANISM: Artificial Sequence
 ATTORNEY/AGENT INFORMATION:
 158 GNAEKYDKMDEPQHYGKS 175
 1 GNAEKYDKMDEPQHYGKS 18
 SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
 1 GNAEKYDKMDEPQHYGKS 18
 Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
 ZIP: 10036
COMPUTER READABLE FORM:
 APPLICATION NUMBER:
FILING DATE: 19-MAR
CLASSIFICATION:
 CITY: New York STATE: New York
 RESULT 3
PCT-US92-02207-8
 COUNTRY:
 SEQ ID NO 2
LENGTH: 350
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us-09-763-397a-17.rapm

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Sequence 36491, Application US/09417507
GENERAL INFORMATION:
APPLICAMT KEITH G. WEINSTOCK ET AL.
APPLICAMT SETH G. WICLELC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS
TITLE OF INVENTION: FUMIGATUS FOR DIAGNOSTICS AND THERAPEUTICS
FILLS RESERVED: PATH99-10
CURRENT APPLICATION NUMBER: US/09/417,507
CURRENT FILING DATE: 1999-10-14
NUMBER OF SEQ ID NOS: 44312
SEQ ID NO 36491
LENGTH: 393
 US-60-171-489-1218
Sequence 1218, Application US/60171489
Sequence 1218, Application US/60171489
Sequence INFORMATION:
THEORY TO THE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000165
CURRENT FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 1412
SEQ ID NOS: 1412
SEQ ID NO 1218
LENGTH: 104
 Gaps
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 Score 47; DB 24; Length 104;
 Score 93; DB 4; Length 622;
Pred. No. 5.7e-06;
0; Mismatches 1; Indels
 Pred. No. 18;
2; Mismatches
 ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/ROCKET NUMBER: 454310-2500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEPAX: (212) 840-3733
TELEPAX: (212) 840-3712
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-075-783-9
 46.18;
61.58;
 91.28;
 571 GNAEKYDKMDEPQDYGKS 588
 1 GNAEKYDKMDEPQHYGKS 18
 Ouery Match
Best Local Similarity 61.57
 Query Match
Best Local Similarity 94.4
Matches 17; Conservative
 7 KWDTLTEPQSYGK 19
 5 KYDKMDEPQHYGK 17
 ORGANISM: A.fumigatus
 NAME/KEY: UNSURE
LOCATION: (44),(53)
 CLASSIFICATION:
 ; ORGANISM: Human
US-60-171-489-1218
 RESULT 8
US-09-417-507-36491
 TYPE: PRT
 TYPE: PRT
 FEATURE:
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 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Tine, John A.
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
TUTHE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: C/O William S. Frommer
STREET: S30 Fifth Avenue
CITY: New York
APPLICANT: Paoletti, et al
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 74
ANDRESSESSES
 Length 622;
 ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Partentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/075,783
FILING DATE: 11-JUN-1993
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/072,867
 Score 93; DB 4; I
Pred. No. 5.7e-06;
0; Mismatches 1;
 FLLING JAILS.

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILLIG DATE: 18-MAR-1992
ATTORNEY AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2410
TELEPHONE: (212) 840-3333
TELEPHONE: (212) 840-3333
TELEPHONE: (212) 840-3712
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
 ADDRESSEE: Curtis, Morris, and Safford
ADDRESSEE: c/o William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
 COUNTRY: United States of America 2IP: 10036
 91.2%;
94.4%;
 571 GNAEKYDKMDEPQDYGKS 588
 1 GNAEKYDKMDEPQHYGKS 18
 Query Match 91.2
Best Local Similarity 94.4
Matches 17; Conservative
 TYPE: amino acid
STRANDEDNESS: single
 ; TOPOLOGY: linear
US-08-072-867-8
 New York
 FILING DATE:
 10036
 US-08-075-783-9
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Sequence 24400, Application US/09252991A GENERAL INFORMATION:
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515 YDRFERPQHY 524
 293 DGRDQPQHYG 302
 Best Local Similarity
Matches 7; Conserv
 6 YDKMDEPQHY 15
 7 DKMDEPQHYG 16
 US-09-252-991A-24400
 US-09-252-991A-24400
 RESULT 12
US-09-270-767-44609
 RESULT 13
US-60-316-362-3482
 TYPE: PRT
 Query Match
 Matches
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; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknd
US-09-417-507-36491
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 Sequence 60056, Application US/09270767

Sequence 60056, Application US/09270767

GENERAL INFORMATION

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62217

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 60056

LENGTH: 480
 CHTER INFORMATION: Description of Artificial Sequence: Synthetic corner in OTHER INFORMATION: at any location having Xaa, Xaa means any amino acid US-09-270-849B-189090
 Gaps
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 43.1%; Score 44; DB 16; Length 480; 60.0%; Pred. No. 3.5e+02; tive 2; Mismatches 2; Indels
 Length 480;
 Length 393;
 2; Indels
 RESULT 10
US-09-270-849B-189090
; Sequence 189090, Application US/09270849B
; GENERAL INFORMATION:
; APPLICANT: Swimmer et al.
; TITLE OF INVENTION: Insect genome survey devices
; TITLE OF INVENTION: Insect genome survey devices
; TITLE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/270,849B
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 195450
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 189090
; LENGTH: 480
 Score 44; DB 16; L/Pred. No. 3.5e+02;
 43.1%; Score 44; DB 18;
ilarity 53.8%; Pred. No. 2.7e+02;
Conservative 4; Mismatches 2;
 ; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-60056
 2; Mismatches
 ORGANISM: Drosophila melanogaster
 ORGANISM: Artificial Sequence
 43.1%;
 6; Conservative
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 1 GNAEKYDKMDEPQ 13
 360 YDRFERPQHY 369
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 6 YDKMDEPQHY 15
 Best Local Similarity
 Query Match
Best Local Similarity
Matches 6; Conserv
 6 УДКМДЕРОНУ 15
 Best Local Similarity
Matches 7; Conserv
 US-09-270-767-60056
 Query Match
 Query Match
 FEATURE
 Matches
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RESULT

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Sequence 3482, Application US/60316362
Sequence 3482, Application US/60316362
GENERAL INFORMATION:
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M.
TITLE OF INVENTION: Identification of Essential Genes of Aspergillus fumigatus and
TITLE OF INVENTION: Use
FILE REFERENCE: 10182-012-888
CURRENT APPLICANTION NUMBER: US/60/316,362
CURRENT FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 4037
APPLICATE MATC J. Rubenfield et al.
APPLICATE MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24400
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 0;
 Sequence 44609, Application US/09270767

Sequence 44609, Application US/09270767

GENERAL INFORMATION

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: TAS6-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 44609

LENGTH: 635
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 Score 44; DB 16; Length 635;
Pred. No. 5e+02;
2; Mismatches 2; Indels
 Score 44; DB 16; I
Pred. No. 4.9e+02;
1; Mismatches 2;
 CTHER INFORMATION: Xaa means any amino acid US-09-270-767-44609
 Mismatches
 ORGANISM: Drosophila melanogaster
 ORGANISM: Pseudomonas aeruginosa
 43.1%;
60.0%;
 43.18;
70.08;
 Query Match 43.1
Best Local Similarity 60.0
Matches 6; Conservative
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 FILE REFERENCE: 38-21(51847)A
CURRENT APPLICATION NUMBER: US/60/215,161
CURRENT FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
SEQ ID NO 6098
LENGTH: 133
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 Gaps
 Gaps
 Gaps
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 Ouery Match 43.1%; Score 44; DB 24; Length 740; Best Local Similarity 53.8%; Pred. No. 6e+02; Matches 7; Conservative 4; Mismatches 2; Indels
 Score 43; DB 24; Length 133;
Pred. No. 1.1e+02;
4; Mismatches 5; Indels
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 Sequence 2.7 Application US/09723229
GENERAL INFORMATION:
APPLICANT: Douglas, James O.
TITLE OF INVENTION: Hypothalamic-Secreted Polypeptide
FILE REFERENCE: 01017/36937
CURRENT APPLICATION NUMBER: US/09/723,229
CURRENT FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 6
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
 Corbin, David R.
Goldman, Barry S.
Huesing, Joseph E.
Krasomil-Osterfeld, Karina C.
 US-60-215-161-6098 Sequence 6098, Application US/60215161 Sequence LINFORMATION: APPLICANT: Corbin, David R. PAPLICANT: Goldman, Barry S.
 APPLICANT: Huesing, Joseph E.
APPLICANT: Krasomil-Osterfeld, P.
APPLICANT: Malvar, Thomas M.
APPLICANT: Slater, Steven C.
APPLICANT: Spiridonov, Sergei, APPLICANT: Hinkle, Gregory J.
TITLE OF INVENTION:
 ; ORGANISM: Aspergillus fumigatus US-60-316-362-3482
SOFTWARE: Patentin version 3.1
SEQ ID NO 3482
LEMCTH: 740
TYPE: PRT
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Best Local Similarity 43.8%;
Matches 7; Conservative
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 ; ORGANISM: Xenorhabdus sp. US-60-215-161-6098
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548 GNAEKYAQVENPE 560
 1 GNAEKYDKMDEPQ 13
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-723-229-2
 SEQ ID NO 2
LENGTH: 196
 US-09-723-229-2
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4 EKYDKMDEPQHYGK 17
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Search completed: January 29, 2002, 10:56:10 Job time: 2406 sec

Mon Feb 4 15:23:39 2002

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|-------------------|------------------|-------------------|---------------------|---------------------|-------------------|---------------------|---------------------|-------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|-------------------|---------------------|---------------------|
| 37                | 37               | 37                | 37                  | 37                  | 37                | 37                  | 37                  | 37                | 37                  | 37                  | 37                  | 37                  | 37                  | 37                  | 37                  | 37                | 38                  | 38                  |
| 36.3              | 36.3             | 36.3              | 36.3                | 36.3                |                   |                     |                     |                   | 36.3                |                     |                     |                     |                     |                     |                     |                   | 37.3                | 37.3                |
| 1003              | 1003             | 1003              | 831                 | 587                 | 544               | 524                 | 513                 | 474               | 412                 | 390                 | 384                 | 361                 | 308                 | 278                 | 232                 | 124               | 1313                | 1304                |
| տ                 | v                | տ                 | Ç                   | σ                   | σ                 | ۍ.                  | υ                   | S                 | υ                   | G                   | Ç                   | Ģ                   | σ                   | G                   | Ç                   | Ģ                 | տ                   | Çī                  |
| US-09-989-730-33  | US-09-989-724-33 | US-09-989-723-33  | US-09-605-703B-1396 | US-09-708-427-10422 | US-09-759-272B-5  | US-09-708-427-10423 | US-09-605-703B-1394 | US-09-545-199D-81 | US-09-708-427-14812 | US-09-708-427-10424 | US-09-708-427-14813 | US-09-708-427-14814 | US-09-708-427-33387 | US-09-708-427-33388 | US-09-708-427-33389 | US-09-995-493-18  | US-09-708-427-15044 | US-09-708-427-15045 |
| Sequence 33, Appl |                  | Sequence 33, Appl | Sequence 1396, Ap   | Sequence 10422, A   | Sequence 5, Appli | Sequence 10423, A   | Sequence 1394, Ap   | Sequence 81, Appl | Sequence 14812, A   | Sequence 10424, A   | Sequence 14813, A   | Sequence 14814, A   | Sequence 33387, A   | Sequence 33388, A   | Sequence 33389, A   | Sequence 18, Appl | Sequence 15044, A   | Sequence 15045, A   |

ALIGNMENTS

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RESULT 2
US-09-897-516-6098
 ; ORGANISM: Acinetobacter sp. US-09-648-004-8
APPLICANT: GOLdman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Huesing, Joseph E.
APPLICANT: Krasomil-Osterfeld, Karina C.
APPLICANT: Krasomil-Osterfeld, Karina C.
APPLICANT: Slater, Thomas M.
APPLICANT: Slater, Steven C.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome SeriLE REFERENCE: 38-21(51847)B
CURRENT APPLICATION NUMBER: US/09/897,516
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215, 161
 US-09-648-004-8
 ; Sequence 8, Application US/09648004; GENERAL INFORMATION:
APPLICANT: CHEN, QIONG
 Sequence 6098, Application US/09897516
GENERAL INFORMATION:
APPLICANT: Corbin, David R.
 NUMBER OF SEQ ID NOS: 32
SOFTWARE: Microsoft Office
SEQ ID NO 8
 Query Match
Best Local Similarity
Matches 9; Conserv
 APPLICANT: THOMAS, STUART
APPLICANT: NAGARAJAN, VASANTHA
TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND
TITLE OF INVENTION: INTERMEDIATES
FILE REFERENCE: CL-1341-A
CURRENT APPLICATION NUMBER: US/09/648,004
CURRENT FILING DATE: 2000-04-25
COURRENT FILING DATE: 2000-04-25
 CURRENT FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/252,553
PRIOR FILING DATE: 1999-02-19
 LENGTH: 572
TYPE: PRT
 206 KYNLDKDSDPQHYG
 5 KY--DKMDEPQHYG
 Conservative
 219
 16
 43.18;
 Score 44;
Pred. No.
 Mismatches
 DB
. 19;
 Sequences And Uses Thereof
 <u>ა</u>
 Length 572;
 Indels
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 Gaps
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<u>ب</u>

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; TYPE: PRT ; ORGANISM: Xenorhabdus sp US-09-897-516-6098
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 NAME/KEY: misc_feature
LOCATION: 1..269
COTHER INFORMATION: Ceres Seq. ID 1936382
US-09-708-427-55948
 US-09-708-427-55947
Sequence 55947, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
 밁
 JS-09-708-427-55948
 Sequence 55948, Application US/09708427

SEQUENCE TITLE OF INVENTION: SEQUENCE DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1

SEQ ID NO 55948

LENGTH: 269
 Query Match
Best Local Similarity
Matches 7; Conserv
 SEQ ID NO 6098
LENGTH: 133
 FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 55947
LENGTH: 281
 Query Match
Best Local
 PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
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 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY
 NAME/KEY: misc_feature
LOCATION: 1..269
OTHER INFORMATION: Xaa is any amino acid
 ORGANISM: Zea mays subsp. mays
 TYPE: PRT
 FEATURE:
 NAME/KEY: misc_feature LOCATION: 1..281
 ORGANISM: Zea mays subsp.
OTHER INFORMATION: Xaa is any amino acid
 FEATURE:
 148 GEGDKYDRQAEKDHLSK 164
 61 AERHRASEEPTHYNRS 76
 Local Similarity les 7; Conserv
 3 AEKYDKMDEPQHYGKS 18
 GNAEKYDKMDEPQHYGK 17
 Conservative
 Conservative
 42.2%;
 41.2%;
 4.
 Score 43;
Pred. No. 5
 Score 42; DB 5;
Pred. No. 17;
2; Mismatches
 Mismatches
 DB 5;
 8;
 Length 133;
 Length 269;
 Indels
 0,:
 0;
 Gaps
 Gaps
 0;
 0;
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CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 55946
LENGTH: 384
TYPE: PRT
ORGANISM: Zea mays subsp. mays
 ; NAME/KEY: misc_feature; LOCATION: 1. 281; OTHER INFORMATION: Ceres Seq. US-09-708-427-55947
 NAME/KEY: misc_feature
LOCATION: 1..384
NAME/KEY: misc_feature
LOCATION: 1..384
OTHER INFORMATION: Ceres Seq. ID 1936380
US-09-708-427-55946
 US-09-708-427-55946
, Sequence 55946, Application US/09708427
; GENERAL INFORMATION:
, APPLICANT: N. ALEXANDROV et al.
 В
 Query Match
Best Local Similarity
Whiches 7; Conserve
 US-09-897-516-6859
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 οy
 RESULT
 PRIOR APPLICATION NUMBER: US 60/215, 161
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEO ID NOS: 8409
SEQ ID NO 6859
TENCENT
 GENERAL INFORMATION:
 Query Match
Best Local Similarity 41.
Matches 7; Conservative
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
 Sequence 6859, Application US/09897516
 APPLICANT:
APPLICANT:
 APPLICANT: Malvar, Thomas M.
APPLICANT: Slater, Steven C.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome
FILE REFERENCE: 38-21(51847)B
 APPLICANT: Corbin, David R. APPLICANT: Goldman, Barry
 CURRENT APPLICATION NUMBER: US/09/897,516
CURRENT FILING DATE: 2001-06-29
 FEATURE:
ORGANISM: Xenorhabdus sp
 LENGTH: 519
 160 GEGDKYDRQAEKDHLSK 176
 263 GEGDKYDRQAEKDHLSK 279
 1 GNAEKYDKMDEPQHYGK 17
 1 GNAEKYDKMDEPQHYGK 17
 Goldman, Barry S.
Hinkle, Gregory J.
Huesing, Joseph E.
Krasomil-Osterfeld,
 Conservative
 41.2%;
 41.2%;
 2
 Score 42; DB
Pred. No. 18;
 ID 1936381
 Score 42;
Pred. No.
 Karina C
 Mismatches
 Mismatches
 DB 5;
 Sequences And Uses Thereof
 5,
 8
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 Length 281
 Length 384;
 Indels
 Indels
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 0;
 Gaps
 Gaps
 0;
 0
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; TYPE: PRT ; ORGANISM: Homo sapiens US-09-832-292-31
 밁
 밁
 US-09-815-242-12798
 US-09-832-292-31
 US-09-897-516-6859
 PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
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PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
 Sequence 31, Application US/09832292
GENERAL INFORMATION:
APPLICANT: Ryazanov, Alexey
 Sequence 12798, Application US/09815242
 SOFTWARE: P
SEQ ID NO 31
 Query Match
Best Local 9
 GENERAL INFORMATION:
 Query Match
 Matches
 TITLE OF INVENTION: MAMMALÍAN ALPHA-KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USES THEREOF FILE REFERENCE: 601-1-098CIP CURRENT APPLICATION NUMBER: US/09/832,292 CURRENT FILING DATE: 2001-04-10
 FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
 APPLICANT:
 PRIOR APPLICATION NUMBER: 09/632,131 PRIOR FILING DATE: 2001-08-03
 TITLE OF INVENTION: Identification of Essential Genes
 APPLICANT:
 APPLICANT:
 APPLICANT:
 NUMBER OF SEQ ID NOS: 45
 ENGTH: 2011
 785 SVKEYDLERGHDEKLDENQHFG 806
 237 GRAQRYFQVYEPAFYDKS
 Local Similarity hes 8; Conserv
 Local Similarity
nes 8; Conserv
 2 NAEKYD-----KMDEPQHYG 16
 1 GNAEKYDKMDEPQHYGKS 18
FILING DATE:
 PatentIn version 3.1
 Haselbeck, Robert
 Carr, Grant J.
Yamamoto, Robert T.
 Zyskind, Judith W.
 Trawick, John D.
 Wall, Danie
 Ohlsen, Kari
 Xu, H. Howard
 Conservative
 Conservative
 41.28;
 39.7%;
 60/269,308
 254
 5
 4.
 Score 40.5; DB 5; Pred. No. 3.1e+02;
 Pred. No.
 Score 42;
 Mismatches
 Mismatches
 DB 5;
37;
 DB 5;
 6;
 Length 519
 Length 2011;
 Indels
 Indels
 'n
 ACIDS AND
 0;
 Gaps
 Gaps
 1;
 0;
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Ş
 뮹
 ; ORGANISM: Staphylococcus aureus US-09-815-242-12798
 US-09-708-427-74488
 US-09-708-427-75548
 US-09-708-427-75548
; Sequence 75548, Application US/0
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
 Ş
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TTPLE OF INVENTION: THERRBY FILE REFERENCE: 2750-1243P CURRENT APPLICATION NUMBER: US/09/708,427 CURRENT PILING DATE: 2000-11-09 NUMBER OF SEQ ID NOS: 85364 SOFTWARE: Patentin version 3.1 SEQ ID NO 75548
 CURRENT FILING DATE: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 74488
LENGTH: 139
 Sequence 74488, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
 NUMBER OF SEO ID NOS: 14110
SOFTWARE: FRASTSEQ for Windows Version 4.0
SEO ID NO 12798
LENGTH: 697
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Best Local Similarity
Matches 7; Conserv
 Query Match
Best Local 9
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 TYPE: PRT ORGANISM: Zea mays subsp. mays FEATURE:
 OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..53
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ORGANISM: Zea mays subsp. mays
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 TYPE: PRT
 NAME/KEY: misc_feature LOCATION: 1..139
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 OTHER INFORMATION: Ceres Seq. ID 1946917
OTHER INFORMATION: Xaa is any amino acid
 LENGTH:
 668 ADKSDEKDEPAH 679
 Local Similarity es 7; Conserv
 32 GHAEEHDVLADGTHSGES 49
 1 GNAEKYDKMDEPQHYGKS 18
 3 AEKYDKMDEPQH 14
 Conservative
 Application US/09708427
 38.2%;
 39.2%;
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 Score 39;
Pred. No.
 Score 40;
Pred. No.
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; NAME/KEY: misc_feature
; LOCATION: 1..139
; OTHER INFORMATION: Ceres Seq. ID 1945476
US-09-708-427-74488
 Š
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 US-09-708-427-84690
 RESULT 12
US-09-708-427-73364
; Sequence 73364, Application US/09708427
; GENERAL INFORMATION:
 Sequence 84690, Application US/09708427

GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION UNMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 84690
LENGTH: 139
TYPPE- DEPT
 B
 δÃ
 US-09-708-427-84690
 Query Match
Best Local Similarity
 APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1143P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 73364
LENGTH: 158
TYPE: PRT
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Best Local :
 FEATURE: misc_feature
LOCATION: 1..139
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..139
OTHER INFORMATION: Ceres Seq. ID 1964740
 ORGANISM: Zea mays subsp. mays
 TYPE: PRT
 FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..158
OTHER INFORMATION: Xaa is
 ORGANISM: Zea mays subsp.
 NAME/KEY: misc_feature LOCATION: 1..158
 114 HAESYDWVDIPDH 126
 114 HAESYDWVDIPDH 126
 y Match 38.2%;
Local Similarity 53.8%;
hes 7; Conservative
 2 NAEKYDKMDEPQH 14
 2 NAEKYDKMDEPQH 14
INFORMATION: Ceres Seq. ID 1943726
 Conservative
 38.2%;
 mays
 any amino acid
 Score 39;
Pred. No.
 2;
 Score 39;
Pred. No.
 Mismatches
 Mismatches
 DB
25;
 5
 رب
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 4.
 Length 139;
 Length 139;
 Indels
 Indels
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 0;
 Gaps
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 0;
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CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 73363
LENGTH: 212
TYPE: PRT
ORGANIEM: Zee mays subsp. mays
 망
 Qy
 US-09-708-427-73364
 OTHER INFORMATION: Ceres US-09-708-427-73363
 US-09-708-427-73363
 US-09-708-427-73362
US-09-708-427-73362
SEQUENCE 73362, Application US/09708427
SEQUENCE TI INFORMATION:
GENERAL INFORMATION: SEQUENCE - DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT ETLING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
 맑
 γ
 Sequence 73363, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
 Query Match
Best Local Similarity
Matches 7; Conserv
 SOFTWARE: PatentIn version 3.1 SEQ ID NO 73362
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 Matches
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY
 FILE REFERENCE: 2750-1243P
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 NAME/KEY: misc_feature LOCATION: 1..212
 FEATURE:
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 TYPE: PRT
ORGANISM: Zea mays subsp. mays
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 LENGTH: 246
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 86 HAESYDWVDIPDH
 2 NAEKYDKMDEPQH 14
 NAEKYDKMDEPQH 14
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7; Conserva
 Conservative
 Conservative
 44
 98
 38.2%;
 38.2%;
53.8%;
 S,
 is any amino
 Seq.
 any amino acid
 Score 39; DB pred. No. 29;
 ?
 Score 39;
Pred. No.
 ID 1943725
 Mismatches
 Mismatches
 DB 5;
 ა
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 Indels
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; Sequence 66583, Application US/09708427
; GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THERRBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
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SOFTWARE: PATENTIN VERSION 3.1
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LENGTH: 316
 TYPE: PRT
ORGANISM: Zea mays subsp. mays
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NAME/KEY: misc_feature
LOCATION: 1..316
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NAME/KEY: misc_feature
LOCATION: 1..316
COCATION: 1..316
OTHER INFORMATION: Ceres Seq. ID 1930901
US-09-708-427-66583
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 밁
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Matches 6; Conservative
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120 HAESYDWVDIPDH 132
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 6 YDKMDEPQH 14
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Mon Feb

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Sequence 8, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 783, Appli
Sequence 753, Appli
 Sequence 16, Appl
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 ; Search time 1760.55 Seconds
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-07-672-183A-8

US-08-072-867-8

US-08-075-783-9

US-09-248-795-18857

US-09-248-795-18857

US-09-388-092-753
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Listing first 45 summaries
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Perfect score:
 Score
 Scoring table:
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 Sequence:
 Run on:
 Result
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| equence 1245,<br>equence 251689<br>equence 251689<br>equence 1244,<br>equence 1244,<br>equence 1293,<br>equence 41784<br>equence 5065,<br>equence 5065,<br>equence 20159<br>equence 20159<br>equence 20159<br>equence 20159<br>equence 20159<br>equence 20159<br>equence 20159<br>equence 20169<br>equence 20169                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Sequence 1590, App<br>Sequence 1573, Ap<br>Sequence 16, Appl<br>Sequence 1835, Ap<br>Sequence 22, Appl<br>Sequence 22277, A |
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| US-09-689-<br>US-60-324-<br>US-60-324-<br>US-60-324-<br>US-60-314-<br>US-60-191-<br>US-60-191-<br>US-60-213-<br>US-60-213-<br>US-60-213-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191-<br>US-60-191- | US-09-573-655A-3<br>US-09-573-655A-1<br>US-09-577-711-16<br>US-09-597-771-12<br>US-09-597-771-12<br>US-60-324-109-23        |
| 160<br>1160<br>1160<br>1160<br>1160<br>1160<br>1160<br>1160                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                                                                                                                             |
| 44444444444444444444444444444444444444                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                                             |
| 444444444444444444444444444444444                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4                                                                                       |
| 01111111111111111111111111111111111111                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 30<br>44<br>44<br>44<br>44<br>44<br>44                                                                                      |

## ALIGNMENTS

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Sequence 16, Application US/09763397A
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the Department of Health and Human Services, Centers for APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A.
APPLICANT: Hasnain, Ya
APPLICANT: Hasnain, Seyed E.
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Fa
FILE REPERENCE: 6395-57049
CURRENT APPLICATION NUMBER: US/09/763,397A
 ö
 Gaps
 ö
 Length 18;
 Indels
 Query Match 100.0%; Score 100; DB 21; Best Local Similarity 100.0%; Pred. No. 8.5e-10; Matches 18; Conservative 0; Mismatches 0;
 PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR FILING DATE: 1998-08-21
PRIOR APPLICATION NUMBER: PCT / US99/18869
PRIOR FILING DATE: 1999-08-19
 ; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-09-763-397A-16
 NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
US-09-763-397A-16
 LENGTH: 18
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 Gaps
 ;
0
 ö
 Length 622;
 US-07-672-183A-8
Sequence 8, Application US/07672183A
Sequence 8, Application US/07672183A
Sequence 8, Application
Sequence 8, Application
Sequence 8, Application
Applicant: Paloetti, Enzo
Applicant: de Taisne, Charles
Applicant: Tine, John A.
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
 Length 622;
 1; Indels
 STATE: New York
CONNTRY: United States
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/672,183A
FILING APTE: 19910320
 ADDRESSEE: William S. Frommer ADDRESSEE: c/o Curtis, Morris & Safford, P.C. STREET: 530 Fifth Avenue
 4.3e-07;
 Score 95; DB 1; I
Pred. No. 4.3e-07;
 DB 3;
 Mismatches
 Mismatches
 REFERENCE/DOCKET NUMBER: 454310-2300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
 Score 95;
Pred. No.
 US-08-072-867-8; Sequence 8, Application US/08072867; GENERAL INFORMATION:
 FILING DATE: 19910320
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
 95.0%;
94.4%;
 95.0%;
94.4%;
 317 DGNCEDIPHVNEFPAIDL 334
 TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
 317 DGNCEDIPHVNEFPAIDL 334
 1 DGNCEDIPHVNEFSAIDL 18
 1 DGNCEDIPHVNEFSAIDL 18
 622 amino acids
 Conservative
INFORMATION FOR SEQ ID NO:
 Conservative
 SEQUENCE CHARACTERISTICS
 single
 AMINO ACID
 linear
 Query Match
Best Local Similarity
Matches 17; Conserv
 amino acid
 linear
 Query Match
Best Local Similarity
Matches 17; Conserv
 New York
 STRANDEDNESS:
 STRANDEDNESS:
TOPOLOGY: lin
 TOPOLOGY:
US-07-672-183A-8
 ;
PCT-US92-02207-8
 LENGTH:
 RESULT
 q
 qq
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 APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the Department of Health and Human Services, Centers for Dis APPLICANT: Centrol and Prevention APPLICANT: Control and Prevention APPLICANT: Control and Prevention APPLICANT: Plan, Altaf A. APPLICANT: Ping Shi, Ya APPLICANT: Hashain, Seyed E. APPLICANT: Hashain, Seyed E. TIVER RECENSION: 6395-57049 CURRENT APPLICATION NUMBER: US/09/763,397A CURRENT FILING DATE: 1998-08-21 PRIOR FILING DATE: 1998-08-21 PRIOR FILING DATE: 1999-08-19 PRIOR FILING DATE: 1999-08-19 PRIOR SEQ ID NOS: 26 NUMBER OF SEQ ID NOS: 26 NUMBER OF SEQ ID NOS: 26 NUMBER PATCH OF SEQ ID NOS: 26 NUMBER PATCH OF SEQ ID NOS: 26 NUMBER OF SEQ
 ö
 Gaps
 ;
0
 Length 350;
 Sequence 8, Application PC/TUS9202207
GENERAL INFORMATION:
APPLICANT: VIROGENETICS, CORPORATION
TILLE OF INVENTION: MALBRIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
 Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 DB 21;
 ö
 100.0%; Score 100; DB 2
100.0%; Pred. No. 3e-08;
 0; Mismatches
 ADDRESSEE: Curtis, Morris, and Safford ADDRESSEE: C/O William S. Frommer STREET: 530 Fifth Avenue CITY: New York STATE: New York
 OTHER INFORMATION: Recombinant DNA/Protein US-09-763-397A-2
 ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
 UMBER: PCT/US92/02207
19-MAR-1992
 Sequence 2, Application US/09763397A GENERAL INFORMATION:
 ORGANISM: Artificial Sequence
 140 DGNCEDIPHVNEFSAIDL 157
 1 DGNCEDIPHVNEFSAIDL 18
 1 DGNCEDIPHVNEFSAIDL 18
 18; Conservative
 APPLICATION NUMBER:
 Query Match
Best Local Similarity
 CLASSIFICATION:
 USA
 FILING DATE:
 ZIP: 10036
 RESULT 3
PCT-US92-02207-8
 COUNTRY:
 US-09-763-397A-2
 LENGTH: 350
 SEQ ID NO 2
 Matches
 QQ
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APPLICANT: Keith Weinstock et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBI TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS FILE REFERENCE: 107196.132 CURRENT APPLICATION NUMBER: US/09/248,796 CURRENT FILING DATE: 1999-02-12 NUMBER OF SEQ ID NOS: 28206 SEQ ID NOS: 28206 LENGTH: 301
 COCATION: (221),(244); OTHER INFORMATION: Identity of amino acid sequences at the above locations are un US-09-248-796-18857
 Sequence 7548, Application US/60314050
GENERAL INFORMATION:
APPLICANT: Roemer, Terry
APPLICANT: Boone, Charles
APPLICANT: Boone, Charles
APPLICANT: Bone, Charles
APPLICANT: Bone, Charles
APPLICANT: Bussey, Howard
APPLICANT: Ohisen, Kari L.
TITLE OF INVENTION: GENE DISRUPTION METHODOLOGIES FOR DRUG TARGET DISCOVERY
FILE REFERENCE: 10182-013-888
CURRENT APPLICATION NUMBER: US/60/314,050
CURRENT FILING DATE: 2001-08-22
NUMBER OF SEQ ID NOS: 7834
 Gaps
 Gaps
 ö
 5;
 Length 301;
 DB 4; Length 622;
 Score 95; DB 4; Length 622
Pred. No. 4.3e-07;
0; Mismatches 1; Indels
 Indels
 Query Match . 51.5%; Score 51.5; DB 16;
Best Local Similarity 52.4%; Pred. No. 5.5;
Matches 11; Conservative 2; Mismatches 3;
 NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
TYPE: amino acids
TOPOLOGY: single
 US-09-248-796-18857
; Sequence 18857, Application US/09248796
; GENERAL INFORMATION:
 89 DFNCQDIPEFFEDHMNELMAI 109
 1 DGNCEDIP-----HVNEFSAI 16
 SOFTWARE: PatentIn version 3.1 SEQ ID NO 7648
 95.0%;
 ATTORNEY/AGENT INFORMATION:
 317 DGNCEDIPHVNEFPAIDL 334
 1 DGNCEDIPHVNEFSAIDL 18
 Query Match
Best Local Similarity 94.4
Matches 17; Conservative
 TYPE: PRT
ORGANISM: Candida albicans
 NAME/KEY: UNSURE
 US-60-314-050-7648
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 Gaps
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 Sequence 9, Application US/08075783
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: De Taisne, Charles
APPLICANT: Tine, John A.
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
APPLICANT: Paoletti, et al TITLE OF INVENTION MALARIA RECOMBINANT POXVIRUS VACCINE NUMBER OF SEQUENCES: 74 CORRESPONDENCE ADDRESS:
 Length 622;
 1; Indels
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
AURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/072,867
FILING DATE:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/075,783
FILING DATE: 11-JUN-1993
 Score 95; DB 4; 1 Pred. No. 4.3e-07;
 0; Mismatches
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PAPLICATION DATA:
PAPLICATION DATA:
FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 25,506
TELECOMMUNICATION INFORMATION:
 ADDRESSEE: Curtis, Morris, and Safford ADDRESSEE: c/o William S. Frommer STRET: 330 Fifth Avenue CITY: New York
 ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o William S. Frommer
STREET: 530 Fifth Avenue
 United States of America
 | TELEPHONE: (212) 840-3333
| TELEFAX: (212) 840-0712
| INFORMATION FOR SEQ ID NO: 8:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 612 anino acids
| TYPE: amino acid
| STRANDEDNESS: single
| US-08-072-867-8
 95.0%;
94.4%;
 317 DGNCEDIPHVNEFPAIDL 334
 1 DGNCEDIPHVNEFSAIDL 18
 Best Local Similarity 94.4 Matches 17; Conservative
 ZIP: 10036
COMPUTER READABLE FORM:
 New York
 New York
 New York
 USA
 COUNTRY: Ur
 RESULT 6
US-08-075-783-9
 COUNTRY:
 CITY: N
STATE:
 CITY: N
 Query Match
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5
 Gaps
 Gaps
 APPLICANT: Gao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Bdgerton, Michael D
APPLICANT: Bdgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Liu, Jingdong
APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFREENCE: 38-10(52726)8
CURRENT APPLICATION NUMBER: US/60/324,109
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 33196
SEQ ID NO 25459
LENGTH: 177
 APPLICANT: Cao, Yongwei
APPLICANT: Edgerton, Michael D
APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REPERENCE: 38-10(52726)B
CURRENT APPLICATION NUMBER: US/60/324,109
CURRENT APPLICATION NUMBER: US/60/324,109
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 33196
SEQ ID NO 18127
LENGTH: 160
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 Length 160;
 Length 160;
 Indels
 Indels
 DB 24;
 DB 20;
 Score 47.5; Di
Pred. No. 13;
2; Mismatches
 2; Mismatches
 TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
1..160
OCHER INFORMATION: Xaa is any amino acid
MAME/KEY: misc_feature
1.004TON: 1..160
COCATION: 1..160
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US-09-689-980-1245
 Score 47.5;
 ; Sequence 25459, Application US/60324109; GENERAL INFORMATION:
 ; Sequence 18127, Application US/60324109; GENERAL INFORMATION:
 47.5%;
61.1%;
 47.58;
 3 NCEDIPHVN--EFSAIDL 18
 3 NCEDIPHVN--EFSAIDL 18
 || |||||| |: ||:
81 NC-DIPHVNRTEYQLIDI 97
 Query Match 47.5 Best Local Similarity 61.1 Matches 11; Conservative
 Query Match 47.5
Best Local Similarity 61.1
Matches 11; Conservative
 TYPE: PRT
ORGANISM: Zea mays
 RESULT 11
US-60-324-109-18127
 US-60-324-109-18127
SEQ ID NO 1245
LENGTH: 160
 g
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 APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-1237P
CURRENT APPLICATION NUMBER: US/09/689,980
CURRENT FILING DATE: 2000-10-13
**QUABER CF- SEQ ID NOS: 3877
 0;
 Sequence 73.3 Application US/09538092

Sequence 73.3 Application US/09538092

Sequence 73.3 Application.

APPLICANT: Giot, Loic

APPLICANT: Mansfeld, Traci A.

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 1596-542

CURRENT APPLICATION NUMBER: 05/09/538,092

CURRENT APPLICATION NUMBER: 60/127,352

PRIOR FILING DATE: 1099-04-01

PRIOR PLLING DATE: 2000-03-29

PRIOR PLLING DATE: 2000-03-01

NUMBER OF SEQ ID NOS: 1387

SOFTWARE: CuraPatSeqFormatter Version 0.9

SOFTWARE: CuraPatSeqFormatter Version 0.9
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 Score 51; DB 19; Length 347;
Pred. No. 8;
 Indels
 COCATION: (0)...(0)
COTHER INFORMATION: Polypeptide Accession Number YOR262W
US-09-538-092-753
 3; Mismatches
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COTHER INFORMATION: X-any amino acid
NAME/KEY: MISC_FEATURE

LOCATION: (617)...(617)

COHER INFORMATION: X-any amino acid
NAME/KEY: MISC_FEATURE

LOCATION: (625)...(625)

COTHER INFORMATION: X-any amino acid
US-60-314-050-7648
 Sequence 1245, Application US/09689980; GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai
 ORGANISM: Saccharomyces cerevisiae
 5;
 220 DFNCQDIPEFEDHMNELMAI 240
 1 DGNCEDIP----HVNEFSAI 16
 51.0%;
61.5%;
 Ouery Match
Best Local Similarity 61...
Best Conservative
 TYPE: FKI
ORGANISM: Candida albicans
 11; Conservative
 |:||:| || ||:
167 DLPHINVFSKIDM 179
 NAME/KEY: misc_feature
 6 DIPHVNEFSAIDL 18
 NAME/KEY: MISC_FEATURE
 Query Match
Best Local Similarity
 RESULT 10
US-09-689-980-1245
 US-09-538-092-753
 LENGTH: 1042
 Matches
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RESULT 15
US-09-688-546-4
Sequence 4, Application US/09858546
SERVERAL INFORMATION:
APPLICANT: SHAO, Wei et al
TITLE OF INVENTION: ISOLAHED HUWAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILLE REFERENCE: CL001232
CURRENT APPLICATION NUMBER: US/09/858,546
CURRENT APPLIANG DATE: 2001-05-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
 Gaps
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 3
 DB 22; Length 510; 62;
 Indels
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 5.
 Score 47; DB;
Pred. No. 62;
0; Mismatches
 61.1%; Pred. No. 16; ive 2; Mismatches
 Search completed: January 29, 2002, 10:56:09 Job time: 2405 sec
 47.0%;
58.8%;
 113 NC-DIPHVNRTEYQLIDI 129
 3 NCEDIPHVN--EFSAIDL 18
 335 GNCECFGHSNRCSYIDL 351
 2 GNCEDIPHVNEFSAIDL 18
 Best Local Similarity 61.1
Matches 11; Conservative
 Query Match 47.0
Best Local Similarity 58.8
Matches 10; Conservative
 TYPE: PRT
ORGANISM: Mus musculus
US-09-858-546-4
 SEQ ID NO 4
 QQ
 ò
 ŏ
 APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BROVEN, Vyacheslav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
CURRENT APPLICATION NUMBER: US/09/689,980
CURRENT APPLICATION NUMBER: US/09/689,980
CURRENT FILING DATE: 2000-10-13
SEQ ID NOS: 3877
LENGTH: 192
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 5
 Gaps
 Gaps
 US-60-324-109-25168

Sequence 25168, Application US/60324109

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Edgerton, Michael D

APPLICANT: Hinkle, Gregory J.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Liu, Jingdong

APPLICANT: Stein, Joshua

TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT

FILE REFERENCE: 38-10(5278)

CURRENT FILING DATE: 2001-09-21

NUMBER OF SEQ ID NOS: 33196

SEQ ID NO 25168

LENGTH: 182
 DB 24; Length 177;
 Length 182;
 47.5%; Score 47.5; DB 20; Length 192;
 Indels
 Indels
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 DB 24;
 Score 47.5; DE Pred. No. 14; 2; Mismatches
 Score 47.5; Di
Pred. No. 15;
2; Mismatches
 NAME/KEY: misc_feature
LOCATION: 1..192
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..192
OTHER INFORMATION: Ceres Seq. ID 1597431
 ; Sequence 1244, Application US/09689980; GENERAL INFORMATION:
 ORGANISM: Arabidopsis thaliana
 47.5%;
61.1%;
 103 NC-DIPHVNRTEYQLIDI 119
 3 NCEDIPHVN--EFSAIDL 18
 3 NCEDIPHVN--EFSAIDL 18
 Query Match
Best Local Similarity 61.1
Matches 11; Conservative
 Query Match 47.5
Best Local Similarity 61.1
Matches 11; Conservative
ORGANISM: Zea mays
 TYPE: PRT
ORGANISM: Zea mays
 ; FEATURE:
US-60-324-109-25459
 ; FEATURE:
US-60-324-109-25168
 US-09-689-980-1244
 Query Match
 FEATURE:
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Run on:

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Sequence 49966, Application US/09708427
GENERAL INFORMATION:
APPLICAMT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REPERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 49966
LENGTH: 135
 Sequence 49942, Application US/09708427
GENERAL INFORMATION:
APPLICAMT:
APPLICAMT:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID;
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: US/09/708,427
SOURCENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SSEQ ID NO 49942
LENGTH: 146
Sequence 3887, Ap Sequence 19776, A Sequence 19776, A Sequence 19775, A Sequence 28967, A Sequence 28967, A Sequence 2965, A Sequence 2965, A Sequence 515, App Sequence 513, App Sequence 3111, App Sequence 28457, A Gaps
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 Length 135;
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 US-09-708-427-19775
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US-09-708-427-19775
US-09-708-427-28967
US-09-708-427-28966
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| US-09-708-427-49966
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61.1%;
 3 NCEDIPHVN--EFSAIDL 18
 Best Local Similarity 61.1
Matches 11; Conservative
 ORGANISM: Zea mays subsp.
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 RESULT 2
US-09-708-427-49942
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US-09-708-427-49966
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5.446 Million cell updates/sec
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7: /cgn2_6/ptcdata/2/paa/USO0_NEW_COMB.pep:*
 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-708-427-11605
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 January 29, 2002, 10:58:15
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 BLOSUM62
 Query
Match
 Total number of
 47.5
47.5
47.5
47.5
47.5
43.5
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 Perfect score:
 Scoring table:
 Searched:
 Seguence:
 Database
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Result

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Gaps
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ب
 TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants FILE REFERENCE: 38-15(52796)A CURRENT APPLICATION NUMBER: US/60/337,358
CURRENT FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 745
 Length 160;
 Indels
 Score 47.5; DB 5;
Pred. No. 0.8;
2; Mismatches 2;
NAME/KEY: misc_feature
COATION: 1..160
MIRER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..160
COTHER INFORMATION: Ceres Seq. ID 1921936
US-09-708-427-49467
 Sequence 461, Application US/60337358 (GENERAL INFORMATION: APPLICANT: Aprens, Jeffrey E.
 Lund, Adrian
Madson, Linda L.
Malloy, Kathleen A.
McKiel, Christine L.
Miller, Philip W.
 Ball, James A.
Banu, G.
Ball, Erin
Boddupalli, Raghava
Chomet, Paul S.
Daly, MacKenzie
Deikman, Jill
Deng, Jinzhuo
Duff, Stephen M.
 Padmathi, Machikanti
 Kretzmer, Keith A.
Laccetti, Lucille B.
 Parnell, Laurence D.
 Edgerton, Michael D
 Johnson, Richard G.
Jung, Vincent
 Galligan, Meghan M
 Hinchey, Brenda S.
 Liu, Jingdong
Lu, Bin
Luethy, Michael M.
 47.5%;
illarity 61.1%;
Conservative
 Sheridan, Paul
Sherman, Paul L.
Start, William G.
 Shihshieh
 3 NCEDIPHVN--EFSAIDL 18
 81 NC-DIPHVNRTEYQLIDI 97
 Lai, Chao-Qiang
 Yang, Chunzhi
Zeng, Xiaoping
 Tennesen, Dan
Vidya, K.R.
 Zhang, Qiang
Zhao, Yajuan
Zhou, Li
 Wang, Haiyun
 Xin, Zhanguo
Xu, Nanfei
 Jie-Yi
 Query Match
Best Local Similarity
Matches 11; Conserv
 Huang,
 APPLICANT:
 APPLICANT
 APPLICANT
 APPLICANT
 APPLICANT
 APPLICANT
 qq
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 Sequence 19467, Application US/09708427

GENERAL INFORMATION:
APPLICANT: N. ALEXANDROW et al.
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PACENTIN VERSION 3.1
 APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 79333
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 Gaps
 Gaps
 3;
 Length 149;
 Score 47.5; DB 5; Length 146; Pred. No. 0.72;
 2; Indels
 Indels
 Score 47.5; DB 5;
Pred. No. 0.73;
2; Mismatches 2;
 Mismatches
 FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..149
OTHER INFORMATION: Xaa is any amino acid
 NAME/KEY: misc_feature
CATTON: 1.149
COTHER INFORMATION: Ceres Seq. ID 1965146
018-09-708-427-9933
 NAME/KEY: misc_feature
COATION: 1..146
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..146
OTHER INFORMATION: Ceres Seq. ID 1923441
US-09-708-427-49942
 Sequence 79333, Application US/09708427 GENERAL INFORMATION:
 2;
 SEQ ID NO 49467
LENGTH: 160
TYPE: PRT
ORGANISM: Zea mays subsp. mays
 ORGANISM: Zea mays subsp. mays
 ORGANISM: Zea mays subsp. mays
 Query Match
Best Local Similarity 61.1%;
Matches 11; Conservative
 Query Match
Best Local Similarity 61.1%;
Matches 11; Conservative
 3 NCEDIPHVN--EFSAIDL 18
 3 NCEDIPHVN--EFSAIDL 18
 US-09-708-427-49467
 US-09-708-427-79333
 LENGTH: 149
 FEATURE:
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY TITLE OF INVENTION: THEREBY TITLE OF INVENTION: THEREBY PILE REFERENCE: 2750-1243P CURRENT APPLICATION NUMBER: US/09/708,427 CURRENT FILING DATE: 2000-11-09 NUMBER OF SEQ ID NOS: 85364 SEQ ID NOS: 85364 SEQ ID NOS: 85364 SEQ ID NO 15548 LENGTH: 158
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 Gaps
 Gaps
 3,
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 Length 173;
 Length 283;
 Indels
 Indels
 5,
 DB 5;
 Score 47.5; DB
Pred. No. 0.87;
 Score 45; DB 9
Pred. No. 4;
2; Mismatches
 2; Mismatches
 CTHER INFORMATION: Xaa is any amino acid;
NAME/KEY: misc_feature
LOCATION: 1..158
. OTHER INFORMATION: Ceres Seq. ID 1829388
US-09-708-427-15548
; OTHER INFORMATION: Ceres Seq. ID 1923440 US-09-708-427-49941
 Sequence 15548, Application US/09708427 GENERAL INFORMATION:
 ; ORGANISM: Corynebacterium glutamicum US-09-605-703B-2242
 ORGANISM: Arabidopsis thaliana
 47.5%; 61.1%;
 Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
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108 NC-DIPHVNRTEYQLIDI 124
 3 NCEDIPHVN--EFSAIDL 18
 Query Match 47.5
Best Local Similarity 61.1
Matches 11; Conservative
 NAME/KEY: misc_feature
 6 DIPHVNEFSAI 16
 | ||:||| |:
9 DAPHINEFPAL 19
 LOCATION: 1..158
 RESULT 8
US-09-605-703B-2242
 US-09-708-427-15548
 TYPE: PRT
 FEATURE:
 Sequence 4991, Application US/09708427
GREERAL INFORMATION:
APPLICANT: N ALEXANDROUGH al.
APPLICANT: N ALEXANDROUGH al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REPERENCE: 2750-1243P
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 49941
 Sequence 4964, Application US/09708427
GRNERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
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 Length 163;
 Length 160
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 Score 47.5; DB 7;
Pred. No. 0.8;
2; Mismatches 2;
 Score 47.5; DB 5;
Pred. No. 0.81;
2; Mismatches 2;
 NAME/KEY: misc_feature
LOCATION: 1..173
VOTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..173
 COCATION: 1..163
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..163
COTHER INFORMATION: Ceres Seq. ID 1923496
US-09-708-427-49964
 TYPE: PRT
ORGANISM: Zea mays subsp. mays
 47.5%;
61.1%;
 47.5%;
61.1%;
 3 NCEDIPHVN--EFSAIDL 18
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 Query Match 47.5
Best Local Similarity 61.1
Matches 11; Conservative
 Best Local Similarity 61.1 Matches 11; Conservative
 ORGANISM: Zea mays subsp.
 NAME/KEY: misc_feature
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US-60-337-358-461
 RESULT 6
US-09-708-427-49964
 RESULT 7
US-09-708-427-49941
 SEQ ID NO 49964
LENGTH: 163
 LENGTH: 160
 SEQ ID NO 461
 TYPE: PRT
 TYPE: PRT
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Sequence 32251, Application US/09708427
Sequence 32251, Application US/09708427
SEQUENCE APPLICANT: N ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SEQ ID NO 32251
LENGTH: 679
 GENERAL INFORMATION:
Sequence 574, Application US/09637780B
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BLEXANDROV, Nickolai
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
TITLE OF INVENTION: Thereby
TITLE REFERENCE: 2750-1096P
CURRENT APPLICATION NUMBER: US/09/637,780B
CURRENT FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 1401
SEQ ID NO 574
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 43.0%; Score 43; DB 5; Length 679; 100.0%; Pred. No. 24; O; Indels iive 0; Mismatches 0; Indels
 Length 182;
 Indels
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 Score 43; DB 5;
Pred. No. 5.4;
 2; Mismatches
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 COCATION: 1..679
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..679
COTHER INFORMATION: Ceres Seq. ID 1833855
US-09-708-427-32251
 OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
COCATION: 1.182
OTHER INFORMATION: Ceres Seq. ID 1482445
US-09-637-780B-574
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 ORGANISM: Arabidopsis thaliana
 TYPE: PRT
ORGANISM: Arabidopsis thaliana
 43.0%;
61.5%;
 Conservative
 Query Match 43.0
Best Local Similarity 61.5
Matches 8; Conservative
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 NAME/KEY: misc_feature
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LOCATION: 1..182
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49 ELPHVNILSKIDL 61
 6 DIPHVNEFSAIDL 18
 S ELPHVNILSKIDL 17
 Query Match
Best Local Similarity
Matches 7; Conserva
 4 CEDIPHV 10
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 TYPE: PRT
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Sequence 576, Application US/09637780B
Sequence 576, Application US/09637780B
GENERAL IRRORMATION:
SEQUENCE 576, Application US/09637780B
GENERAL IRRORMATION:
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: ALEXANDROV, Nickolai
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-1096P
CURRENT APPLICATION NUMBER: US/09/637,780B
CURRENT FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 1401
SEQ ID NO 576
LENGTH: 135
 APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-1096P
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 Length 158;
 Length 138;
 Length 135;
 3; Indels
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 Score 43.5; DB 5;
Pred. No. 3.8;
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LOCATION: 1..135
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NAME/KEY: misc_feature
LOCATION: 1..135
OTHER INFORMATION: Ceres Seq. ID 1482447
US-09-637-7808-576
 ID 1482446
 Score 43;
Pred. No.
 Sequence 575, Application US/09637780B GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai
 NAME/KEY: misc_feature
CATATON: 1..138
CTHER INFORMATION: Xaa is any am;
NAME/KEY: misc_feature
CATATON: 1..138
CTHER INFORMATION: Ceres Seq. III
US-09-637-780B-575
 ORGANISM: Arabidopsis thaliana
 TYPE: PRT
ORGANISM: Arabidopsis thaliana
 43.0%;
 43.0%;
 43.5%;
 || |:|||| :: ||:
79 NC-DVPHVNRTDYQLIDI 95
 3 NCEDIPHVN--EFSAIDL 18
 Query Match 43.59
Best Local Similarity 50.09
Matches 9; Conservative
 Best Local Similarity 61.5
Matches 8; Conservative
 6 DIPHVNEFSAIDL 18
 ELPHVNILSKIDL 14
 Query Match
Best Local Similarity
 RESULT 11
US-09-637-780B-575
 Query Match
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Search completed: January 29, 2002, 10:58:15 Job time: 2511 sec
 RESULT 14
US-09-708-427-32250
US-09-708-427-32250
Sequence 32250, Application US/09708427
GENERAL INFORMATION:
TILLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION UNMERS: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SEQ ID NO 32250
LENGTH: 741
 Sequence 32249, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARR: PATENTIN VERSION 3.1
SEQ ID NO 32249
LENGTH: 827
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 Gaps
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 ;
0
 Query Match 43.0%; Score 43; DB 5; Length 741; Best Local Similarity 100.0%; Pred. No. 26; Matches 7; Conservative 0; Mismatches 0; Indels
 Query Match . 43.0%; Score 43; DB 5; Length 827; Best Local Similarity 100.0%; Pred. No. 30; Matches 7; Conservative 0; Mismatches 0; Indels
 NAME/KEY: misc_feature
CCATION: 1..74
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LCCATION: 1..741
COTHER INFORMATION: Ceres Seq. ID 1833854
US-09-708-427-32250
 NAME/KEY: misc_feature
LOCATION: 1..827
OTHER INFORMATION: Xaa is any amino acid
 NAME/KEY: misc_feature
CCATION: 1..827
S. OTHER INFORMATION: Ceres Seq. ID 1833853
US-09-708-427-32249
 TYPE: PRT ORGANISM: Arabidopsis thaliana
 TYPE: PRT
ORGANISM: Arabidopsis thallana
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160 CEDIPHV 166
 4 CEDIPHY 10
12 CEDIPHV 18
 4 CEDIPHV 10
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74 CEDIPHV 80
 US-09-708-427-32249
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; Search time 1760.55 Seconds
(without alignments)
1.262 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd
 Total number of hits satisfying chosen parameters:
 3148936 seqs, 277657034 residues
 January 29, 2002, 10:56:07
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 US-09-763-397A-15
52
1 GQHGHMHG 8
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 Title:
Perfect score:
 Scoring table:
 Database :
 Sequence:
 Searched:
 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2\_6/ptodata/2/paa/US097\_COMB.pep:\* /cgn2\_6/ptodata/2/paa/US098\_COMB.pep:\* /cqn2\_6/ptodata/2/paa/US099\_COMB.pep:\*

/cgn2\_6/ptodata/2/paa/US093\_COMB.pep:\* /cgn2\_6/ptodata/2/paa/US094\_COMB.pep:\*

/ptodata/2/paa/US095\_COMB.pep:\*/ptodata/2/paa/US096\_COMB.pep:\*

|               |       | æ              |                          |    | SUMMARIES            |                   |
|---------------|-------|----------------|--------------------------|----|----------------------|-------------------|
| Result<br>No. | Score | Query<br>Match | Query<br>Match Length DB | DB | ID                   | Description       |
| -             | 52    | 100.0          | 8                        | 21 | US-09-763-397A-15    | Sequence 15, Appl |
| 7             | 52    | 100.0          |                          |    | PCT-US99-26796-59    | Sequence 59, Appl |
| ٣             | 52    | 100.0          |                          | 21 | US-09-763-397A-2     | Sequence 2, Appli |
| 4             | 43    | 82.7           |                          | 23 | US-09-902-540-15333  | Sequence 15333, A |
| ഗ             | 41    | 78.8           | 157                      | 23 | US-09-902-540-16719  | Sequence 16719, A |
| 9             | 41    | 78.8           |                          | 1  | PCT-US01-08631-41146 | Sequence 41146, A |
| 7             | 41    | 78.8           |                          | 24 | US-60-161-932-1547   | Sequence 1547, Ap |
| 80            | 41    | 78.8           |                          | 24 | US-60-167-217-241    | Sequence 241, App |
| 6             | 41    | 78.8           |                          | 24 | US-60-173-464-228    | Sequence 228, App |

1 СОНСИМНС 8

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| Sequence 1944, Ap | Sequence    | Sequence 26251 | Sequence  | Sequence    | Sequence 20860 | Sequence    | Sequence 19253 | Sednen | Sequen   | Sequen |                       | Seguen | Seguen                | Sequen   | Seguen                | Seguen   | Sequen             | Sequen             | Sequen | Sequen | Sequen             | Seguen | Sednenc          | Seguenc | 4 Sednen           |    |    |    |    |    | 5 Seguence 14585, A | 0 Sequence 11480, A |             | Sequence 1632, Ap | Common 2041 An     |
|-------------------|-------------|----------------|-----------|-------------|----------------|-------------|----------------|--------|----------|--------|-----------------------|--------|-----------------------|----------|-----------------------|----------|--------------------|--------------------|--------|--------|--------------------|--------|------------------|---------|--------------------|----|----|----|----|----|---------------------|---------------------|-------------|-------------------|--------------------|
| -60-167-324       | -60-191-637 | 0 - 191 - 637  | 0-191-637 | -60-191-681 | -60-191-681    | -60-173-464 | -60-173-464-   | 32     | -60 - 19 | -60-19 | 4 US-60-173-464-30035 | 0-19   | 4 US-60-191-681-30544 | US-09-25 | 8 US-09-417-507-30578 | -60-167- | US-60-173-464-6289 | US-60-191-637-7785 | -60-19 | -60-19 | US-60-191-700-1149 | 0-16   | US-08-390-207-36 | 2       | US-09-489-039A-108 | ם  | D  | D  | ם  | ם  | US-60-191-637-1     | US-60-191-681-1148  | -16450-1632 | 50A-163           | US-09-488-725A-204 |
|                   | 449 24      |                |           |             |                |             | ñ              |        | Ñ        | ñ      | Ň                     | ñ      | Ñ                     | 7        | 1                     | 7        |                    | 472 24             |        |        |                    |        |                  |         |                    | •  |    | •  | •  | •  | 366 24              | •                   | 376 1       | 376 1             | 376 18             |
| 78.8              | 78.8        |                |           |             |                |             |                |        |          |        |                       |        |                       |          |                       |          |                    |                    |        |        |                    |        |                  |         |                    |    |    |    |    |    | 75.0                |                     |             |                   | 75.0               |
| 41                | 41          | 41             | 41        | 41          | 41             | 41          | 41             | 41     | 41       | 41     | 40                    | 40     | 40                    | 40       | 40                    | 40       | 40                 | 40                 | 40     | 40     | 40                 | 40     | 38               | 38      | 38                 | 39 | 39 | 38 | 33 | 39 | 38                  | 36                  | 39          | 39                | 39                 |
| 10                | 11          | 12             | 13        | 14          | 15             | . 16        | 17             | 18     | 19       | 20     | 21                    | 22     | 23                    | 24       | 25                    | 56       | 27                 | 28                 | 29     | 30     | 31                 | 32     | 33               | 34      | 35                 | 36 | 37 | 38 | 39 | 40 | 41                  | 42                  | 43          | 44                | 4.5                |

## ALIGNMENTS

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SUBJECT THE GOVERNMENT Of the United States of America, as represented by the APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for APPLICANT: Control and Prevention APPLICANT: Lal, Altaf A. APPLICANT: Lal, Altaf A. APPLICANT: Hasnain, Seyed E. TITLE OF INNENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Fa. TITLE REFERENCE: 6395-57049

CURRENT FILING DATE: 1098-08-21

PRIOR FILING DATE: 1998-08-21

PRIOR FILING DATE: 1999-08-19

PRIOR FILING DATE: 1999-08-19

PRIOR FILING DATE: 1999-08-19

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin version 3.1

FEMALE APPLICATION OF SEQ ID NOS: 26

SEQ ID NO 15
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 Gaps
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 Length 8;
 Indels
 Query Match 100.0%; Score 52; DB 21; Best Local Similarity 100.0%; Pred. No. 2.9e+06; Matches 8; Conservative 0; Mismatches 0;
Sequence 15, Application US/09763397A GENERAL INFORMATION:
 ; ORGANISM: Plasmodium falciparum US-09-763-397A-15
 LENGTH: 8
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US-09-902-540-16719
; Sequence 16719, Application US/09902540
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Glodman, Barry S.
; APPLICANT: Blater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococus xanthus Genome Sequences and Uses Thereof; TITLE OF INVENTION: Myxococus xanthus Genome Sequences and Uses Thereof; TITLE OF INVENTION: Myxococus xanthus Genome Sequences and Uses Thereof; TITLE OF INVENTION: Myxococus xanthus Genome Sequences and Uses Thereof; TITLE OF INVENTION: Mymber OF 101-07-10
; PRIOR PILICATION NUMBER: 60/217,883
; SEQ ID NOS: 16825
; SEQ ID NO 16719
 ö
 Sequence 15333, Application US/09902540

Sequence 15333, Application US/09902540

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Wyxococcus xanthus Genome Sequences and Uses Thereof FILE REPERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT APPLICATION NUMBER: 06/217,883
PRIOR FILING DATE: 2001-07-10
PRIOR PILING DATE: 2001-07-10
PRIOR PILING DATE: 2001-07-10
PRIOR PILING DATE: 2001-07-10
 Gaps
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 ;
 0;
 Length 157;
 Score 43; DB 23; Length 198;
Pred. No. 93;
1; Mismatches 1; Indels
 RESULT 6
PCT-USO1-08631-41146
; Sequence 41146, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFRENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
 Score 41; DB 23;
Pred. No. 1.5e+02;
 1; Mismatches
 PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
 78.8%;
75.0%;
 82.7%;
75.0%;
 TYPE: PRT ORGANISM: Myxococcus xanthus
 ORGANISM: Myxococcus xanthus US-09-902-540-15333
 NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 15333
LENGTH: 198
 Conservative
 6; Conservative
 Query Match
Best Local Similarity
Matches 6; Conserv
 Query Match
Best Local Similarity
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142 GEHGHDHG 149
 1:111 | 1 | 136 GEHGHAHG 143
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 1 сонсимис 8
 US-09-902-540-16719
 1 GQHGHMHG
 JS-09-902-540-15333
 Matches
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 Sequence 2, Application US/09763397A

Sequence 2, Application US/09763397A

GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Control and Prevention
APPLICANT: Control and Prevention
APPLICANT: Ping Shi, Ya
APPLICANT: Ping Shi, Ya
APPLICANT: Hasmain, Seyde E.
APPLICANT: Hasmain, Seyde E.
APPLICANT: Bandin, Seyde E.
APPLICANT: Bandin, Seyde E.
APPLICANT: Bandin, Seyde E.
APPLICANT: Ping Shi, Ya
APPLICANT: Bandin, Seyde E.
APPLICANT: Bandin, Seyde E.
APPLICANT: Bandin, Seyde E.
APPLICANT: Bandin, Seyde E.
APPLICANTON: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falci
FILE REFERENCE: 5395-57049

CURRENT APPLICATION NUMBER: US 60/097,703
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Version 3.1
SEQ ID NO 2
BANDIN ADMINISTRATION NUMBER: PATENT APPLICATION NUMBER OF SEQ ID NO 2
BANDIN ADMINISTRATION NUMBER OF SEQ ID NO 2
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 Gaps
 Gaps
 Sequence 59, Application PC/TUS9926796

GENERAL INFORMATION:
APPLICANT: United States Government as Represented by the APPLICANT: United States Government as Represented by the APPLICANT: Secretary of the Navy Sequence of Human Malaria Parasite TITLE OF INVENTION: Chromosome 2 Sequence of Human Malaria Parasite TITLE OF INVENTION: Plasmodium Falciparum and Proteins of Said TITLE OF INVENTION: Chromosome Useful in Anti-malarial Vaccines and TITLE OF INVENTION: Diagnostic Reagents
FILE REFERENCE: CURRENT APPLICATION NUMBER: PCT/US99/26796
CURRENT PILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 420
SOFTWARE: Patentin Ver. 2.1
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 ;
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 Length 350;
 DB 1; Length 272;
 Indels
 Indels
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0
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0
 100.0%; Score 52; DB 21;
100.0%; Pred. No. 6.9;
iive 0; Mismatches 0;
 0; Mismatches
 GTHER INFORMATION: Recombinant DNA/Protein US-09-763-397A-2
 100.0%; Score 52;
100.0%; Pred. No.
 ; ORGANISM: Plasmodium falciparum PCT-US99-26796-59
 TYPE: PRT ORGANISM: Artificial Sequence
 Ouery Match
Best Local Similarity 100...
Si Conservative
 Query Match 100.
Best Local Similarity 100.
Matches 8; Conservative
 GQHGHMHG 222
 206 GQHGHMHG 213
 1 СОНСИМИС 8
 1 СОНСИМИС 8
1 GQHGHMHG 8
 ULT 2
--US99-26796-59
 RESULT 3
US-09-763-397A-2
 LENGTH: 272
 SOFTWARE: F
SEQ ID NO 59
 TYPE: PRT
 FEATURE:
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Gaps

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TESOL 173-464-228
Sequence 228, Application US/60173464
Sequence 228, Application US/60173464
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO00173
CURRENT APPLICATION NUMBER: US/60/173,464
CURRENT PILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 30269
SOFTWARE: FastSEQ for Windows Version 4.0
 Sequence 1944, Application US/60167324
GENERAL INFORMATION:
APPLICANT: Li, PELE W.D.
TITLE OF INVENTION: ACID MOLECULES ENCODING DROSOPHILA PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILLE REFERENCE: CLOO0155
CURRENT APPLICATION NUMBER: US/60/167,324
CURRENT FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 2272
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 449
 ö
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 Length 449;
 Score 41; DB 24; Length 363;
Pred. No. 3.3e+02;
0; Mismatches 2; Indels
 Length 363,
 Sequence 258, Application US/60191637
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
TIPLE OF INVENTION: NUCLEIC ACID DETECTION KITS COMPRISING
 Score 41; DB 24; L
Pred. No. 3.3e+02;
0; Mismatches 2;
 Score 41; DB 24;
Pred. No. 4.1e+02;
1; Mismatches 1
 0; Mismatches
 78.8%;
75.0%;
 78.8%;
75.0%;
 Query Match 78.8%;
Best Local Similarity 75.0%;
Matches 6; Conservative
 Best Local Similarity 75.0
Matches 6; Conservative
 Conservative
 ; ORGANISM: Drosophila
US-60-173-464-228
 ; ORGANISM: Drosophila
US-60-167-324-1944
 Best Local Similarity
Matches 6; Conserv
 123 GHIGHSHG 130
 123 GHHGHSHG 130
 |:||| ||
195 GEHGHDHG 202
 1 GOHGHMHG 8
 1 сонсимис в
 1 СОНСИМИС 8
 RESULT 10
US-60-167-324-1944
 RESULT 11
US-60-191-637-258
 SEQ ID NO 228
LENGTH: 363
 TYPE: PRT
 Query Match
 Query Match
 qq
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 Systems Containin the Nucleic Acid Sequences
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 ö
 APPLICANT: Li, Peter W. D.
TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLEUCLES ENCODING DROSOPHILA PROTEINS, AND USES
FITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO00152
CURRENT APPLICATION NUMBER: US/60/167,217
CURRENT FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 23195
SOTTWARE: FastSEQ for Windows Version 4.0
 Gaps
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 Score 41; DB 24; Length 289;
Pred. No. 2.7e+02;
1; Mismatches 1; Indels
 Score 41; DB 1; Length 269
Pred. No. 2.5e+02;
 Primary Nucleic
 . LOCATION: (1)...(269)

COTHER INFORMATION: Xaa - X or * as defined in Table 2

PCT-US01-08631-41146
 Sequence 1547, Application US/60161932
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
TITLE OF INVENTION: The Drosophila Genome, Pri:
TITLE OF INVENTION: Acid Sequences, Systems CC;
TITLE REFERENCE: CLOO0122
CURRENT APPLICATION NUMBER: US/60/161,932
CURRENT FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 2626
SOFTWARE: FastESC for Windows Version 4.0
SEQ ID NO 1547
 0; Mismatches
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 41146
LENGTH: 269
 ; Sequence 241, Application US/60167217; GENERAL INFORMATION:
 Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
 Query Match 78.8
Best Local Similarity 85.7
Matches 6; Conservative
 ORGANISM: Homo sapiens
 ; ORGANISM: Drosophila
US-60-167-217-241
 ORGANISM: Drosophila
US-60-161-932-1547
 1:111 | 1
35 GEHGHDHG 42
 1 GOHGHMHG 8
 49 QHGHFHG 55
 2 QHGHMHG 8
 RESULT 7
US-60-161-932-1547
 US-60-167-217-241
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75.0%;

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Best Local Similarity 75.0
Matches 6; Conservative
 RESULT 14
US-60-191-681-213
 SOFTWARE: Far
SEQ ID NO 213
LENGTH: 449
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 US-60-191-637-42246

US-60-191-637-42246

Sequence 42246, Application US/60191637

Sequence 42246, Application US/60191637

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENE ESQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: CL000392

CURRENT APPLICATION NUMBER: US/60/191,637

CURRENT FILING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 42660

SOFTWARE: FASISEQ for Windows Version 4.0
 US-60-191-637-26251

Sequence 26251, Application US/60191637

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Venter, J. Craig

TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND

TITLE OF INVENTION: USES THEREOF;

TITLE OF INVENTION: USES THEREOF;

TITLE FEFERENCE: CL000392

CURRENT FILING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 42660

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 26251
TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND TITLE OF INVENTION: USES THEREOF FLLE REFERENCE: CLOO0392 CURRENT APPLICATION NUMBER: US/60/191,637 CURRENT PILING DATE: 2000-03-23 NUMBER OF SEC ID NOS: 42660 SOFTWARE: FeatSEQ for Windows Version 4.0 SEQ ID NO 258 LENGTH: 449
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 Length 449;
 Score 41; DB 24; Length 449;
Pred. No. 4.1e+02;
); Mismatches 2; Indels
 Score 41; DB 24; Length 44. Pred. No. 4.1e+02; 2; Indels
 78.8%;
75.0%;
 78.8%;
75.0%;
 Conservative
 Query Match 78.8
Best Local Similarity 75.0
Matches 6; Conservative
 ; ORGANISM: DROSOPHILA
US-60-191-637-42246
 ; ORGANISM: DROSOPHILA US-60-191-637-26251
 ; ORGANISM: DROSOPHILA US-60-191-637-258
 Query Match
Best Local Similarity
Matches 6; Conserv
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137 GHHGHSHG 144
 137 GHHGHSHG 144
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 1 GQHGHMHG 8
 SEQ ID NO 42246
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78.8%; Score 41; DB 24; Length 449;

Query Match

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APPLICANT: Li, Peter, W.D.
TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING ISOLATED DROSOPHILA PROTEINS AND
TITLE OF INVENTION: USES THEREOF.
TITLE OF INVENTION: USES THEREOF.
CURRENT APPLICATION NUMBER: US/60/191,681
CURRENT APPLICATION NUMBER: US/60/191,681
CURRENT FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 30973
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 200860
 Sequence 213, Application US/60191681

Sequence 213, Application US/60191681

GENERAL INFORMATION:
TYPLE OF INVENTION:
TITLE OF INVENTION: ACID MOLECULES ENCODING ISOLATED DROSOPHILA PROTEINS AND TITLE OF INVENTION: USES THEREOF.
FILE REFERENCE: c1000390
FILE REFERENCE: c1000390
CURRENT APPLICATION UNMERS: US/60/191,681
CURRENT FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 30973
SOFTWARE: FastSEQ for Windows Version 4.0
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 Score 41; DB 24; Length 449;
pred. No. 4.1e+02;
0; Mismatches 2; Indels
 Score 41; DB 24; Length 449;
Pred. No. 4.1e+02;
0; Mismatches 2; Indels
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pred. No. 4.1e+02;
1; Mismatches 1;
 Search completed: January 29, 2002, 10:56:08
Job time: 2404 sec
 78.8%;
75.0%;
 Query Match 78.8
Best Local Similarity 75.0
Matches 6; Conservative
 Conservative
), ORGANISM: DROSOPHILA
US-60-191-681-20860
 ; TYPE: PRT
; ORGANISM: DROSOPHILA
US-60-191-681-213
 Query Match
Best Local Similarity
Matches 6; Conserv
 137 GHHGHSHG 144
 137 GHHGHSHG 144
 195 GEHGHDHG 202
 1 сонсимнс в
 1 GQHGHMHG 8
 1 сонсимис. 8
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Sequence 2909, Ap Sequence 1474, Ap Sequence 1474, Ap Sequence 1472, Ap Sequence 1472, Ap Sequence 29, Appl Sequence 29, Appl Sequence 36336, A Sequence 36336, A Sequence 36334, Ap Sequence 60122, A Sequence 53062, A Sequence 53063, A Sequence 53063, A Sequence 53063, A
 Search time 120.95 Seconds (without alignments)
2.421 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 Pending_Patents_AA_New:*

1: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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US-10-001-137-29
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US-09-708-427-3634
US-09-708-427-53062
 Total number of hits satisfying chosen parameters:
 173191 seqs, 36597120 residues
 January 29, 2002, 10:58:14;
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 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
 US-09-763-397A-15
52
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length: 2000000000
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Match Length
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 Perfect score:
Sequence:
 Score
 Scoring table:
 Minimum DB s
Maximum DB s
 Searched:
 Database
 Run on:
 Result
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Indels 0; Gaps 0;                                  | AND CORRESPONDING POLYPEPTID                                                                                                                                                                                                                                       |
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| 27 35 67.3 28 35 67.3 39 35 67.3 31 35 67.3 31 35 67.3 31 35 67.3 33 35 67.3 34 35 67.3 34 35 67.3 34 35 67.3 34 35 67.3 34 35 67.3 34 35 67.3 34 35 67.3 34 35 67.3 34 35 67.3 34 35 67.3 34 35 67.3 34 35 67.3 34 35 67.3 34 35 67.3 34 35 67.3 34 35 67.3 36 67.3 37 85 67.3 38 85 67.3 39 85 67.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 39 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 86 7.3 30 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ALIGNMENTS | ation US/09620111B DROV et al. Sequence-Determined DNA Fragments Thereby 1070P 2000-07-21 : 9298 is thaliana ure Xaa is any amino acid ure Ceres Seq. ID 1326309                                                                                                                                                                                                                                                                                                                                              | 80.8%; Score 42; DB 5; 75.0%; Pred. No. 1.9; vative 1; Mismatches 1 | Cation US/09708427  DROV et al. THEREBY -1243P NUMBER: US/09/708,427 0000-11-09 ES500-11-09 ersion 3.1                                                                                                                                                             |
| ₩Ď ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 35 67.<br>36 67.<br>37 67.<br>38 67.<br>38 67.<br>39 67.<br>30 67. |            | SEGULT 1 S. 09-620-111B-2909 Sequence 2909, Applic GENERAL INFORMATION: TITLE OF INVENTION: TITLE OF INVENTION: FILE REFERENCE: 275G CURRENT FILING DATE: WUMBER OF SEQ ID NOS SEQ ID NO 2909 LENGTH: 137 LENGTH: 137 CRGANISM: ARABIGOPS FEATURE: NAME/KEY: misc_feat LOCATION: 1137 OTHER INFORMATION: NAME/KEY: misc_feat LOCATION: 1137 | imi<br>;<br>HMH<br>  †                                              | RESULT 2 US-09-708-427-50273 US-09-708-427-50273 SEQUENCE 50273, Applis GENERAL INFORMATION: TITLE OF INVENTION: TITLE OF INVENTION: FILE REFERENCE: 2750 CURRENT APPLICATION CURRENT FILING DATE: NUMBER OF SEQ ID NOS SOFTWARE: PATENTIN V LENGTH: 406 TYPE: PRT |

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 APPLICANT: Bower. Stanley G.
APPLICANT: Bower. Stanley G.
APPLICANT: Bower. Steven C.
TITLE OF INVENTION: Sphingomonas elodea genome sequences and uses thereof
FILE REFERENCE: 38-10(15806)B
CURRENT APPLICATION NUMBER: US/10/015,127
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: US 60/252,455
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 14357
SEQ ID NO 13379
 Gaps
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 Length 408;
 Length 374;
 Indels
 0; Indels
 DB 5;
8.8;
 DB 5;
8;
 78.8%; Scor.
100.0%; Pred. No. c.
0; Mismatches
 Score 41; DB; Pred. No. 8; 0; Mismatches
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COTHER INFORMATION: Ceres Seq. ID 1807880 US-09-708-427-1473
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Substitution US/10015127
Sequence 13079, Application US/10015127
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 ; TYPE: PRT
; ORGANISM: Sphingomonas elodea
US-10-015-127-13079
 78.8%; ; 100.0%;
 Conservative
 Query Match 78.8
Best Local Similarity 100.
Matches 6; Conservative
 Query Match
Best Local Similarity
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 111111
237 HGHMHG 242
 203 HGHMHG 208
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 US-09-708-427-1472
 3 НСНМНС 8
 RESULT 5
US-09-708-427-1472
 з ненмне
 LENGTH: 408
 TYPE: PRT
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 APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE PATENTIAL DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE PATENT OF SECOND NOS: 85364
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SOFTWARE PATENT OF SECOND NOS: 85364
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SOFTWARE PATENT NOS: 85364
SOFTWARE PATENT NOS: 85364
 Squence 14.4, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: THEREBY
FILE REPERBENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT PILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 1474
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 78.8%; Score 41; DB 5; Length 294; 100.0%; Pred. No. 6.2; tive 0; Mismatches 0; Indels
 DB 5; Length 406;
 1; Mismatches
 CRGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..406
CHER INFORMATION: Xaa is any amino acid
NAME/KEX: misc_feature
LOCATION: 1..406
COTHER INFORMATION: Ceres Seq. ID 1924393
US-09-708-427-50273
 NAME/KEY: misc_feature
COATION: 1..294
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
COATION: 1..294
OCHER INFORMATION: Ceres Seq. ID 1807881
US-09-708-427-1474
 Score 42;
 Pred. No
 US-09-708-427-1473; Sequence 1473, Application US/09708427; GENERAL INFORMATION:
 TYPE: PRT
ORGANISM: Arabidopsis thaliana
 ORGANISM: Arabidopsis thaliana
 80.8%;
 6; Conservative
 Query Match 80.8
Best Local Similarity 75.0
Matches 6; Conservative
 NAME/KEY: misc_feature
 Query Match
Best Local Similarity
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 123 HGHMHG 128
 1 сонсимис 8
 3 НСНМНС 8
 Matches
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162 GGHGHSHG 169
 1 СОНСИМИС 8
 US-09-708-427-71051
 1 GQHGHMHG
 FEATURE:
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 GENERAL INFORMATION:
Sequence 29, Application US/10001137
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel A.
APPLICANT: Gutts, Rory A. J.
APPLICANT: Gutts, Rory A. J.
APPLICANT: Glucksmann, Maria Alexandra
TITLE OF INVENTION: 44746, 67210, 48875, 46842, 33201,
TITLE OF INVENTION: 44746, 67210, 48875, 46842, 33201,
TITLE OF INVENTION: HATA, GATOB, B5041, AND 84234,
TITLE OF INVENTION: BAYER GRASFREASE, DEAD TYPE HELICASE, CENTANRIN,
TITLE OF INVENTION: DEHYDROGENASF/REDUCTASE, AND METAL TRANSPORTER
TITLE OF INVENTION: FAMILY MEMBERS AND USES THEREOF
TITLE OF INVENTION: PAMILY MEMBERS AND USES THEREOF
TITLE OF INVENTION: DEHYDROGENASF/REDUCTASE, AND METAL TRANSPORTER
TITLE OF INVENTION: DAYBER: 05/10/001,137
CURRENT FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: 60/250,077
PRIOR APPLICATION NUMBER: 60/250,077
PRIOR FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 62
SOFTWARE FASTSEQ for Windows Version 4.0
 APPLICANT: CUTLIS, ROY A. J.
APPLICANT: CUTLIS, ROY A. J.
APPLICANT: CUTLIS, ROY A. J.
APPLICANT: CUTLIS, ROY A. J.
APPLICANT: CLUCKSMANN, MARÍA ALEXANDRA
TITLE OF INVENTION: 4476, 67210, 49875, 46842, 33201,
TITLE OF INVENTION: 83738, 84233, 64708, 85041, AND 84234,
TITLE OF INVENTION: GLYCOSYLFRANSFERASE, DEAD TYPE HELICASE, CENTAURIN,
TITLE OF INVENTION: DEHYDROGENASE/REDUCTASE, AND METAL TRANSPORTER
TITLE OF INVENTION: FAMILY MEMBERS AND USES THEREOF
FILE REFERENCE: 10448-119001
CURRENT APPLICATION NUMBER: US/10/001,137
CURRENT FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
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DB 6; Length 366;
17;
 Score 39; DB 6; Length 376;
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 0; Mismatches
 Score 39;
Pred. No.
 ; Sequence 59, Application US/10001137; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
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62.5%;
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75.0%;
 Query Match 75.0
Best Local Similarity 75.0
Matches 6; Conservative
 5; Conservative
 ORGANISM: Homo sapiens US-10-001-137-29
 Best Local Similarity
Matches 5; Conserv
 162 GGHGHSHG 169
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299 GRHGHLYG 306
 1 СОНСИМИС 8
 1 GOHGHMHG 8
 US-10-001-137-59
 Query Match
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Sequence 71051, Application US/09708427
GRAERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REPERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
EBNGTH: 168
 APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-1067P
CURRENT APPLICATION NUMBER: US/09/620,394B
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 DB 6; Length 378;
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 Length 168;
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 Score 39; DB 6
Pred. No. 17;
0; Mismatches
 Score 38; DB 5
Pred. No. 11;
0; Mismatches
PRIOR FILING DATE: 2000-11-14

PRIOR FILING DATE: 2000-11-14

PRIOR FILING DATE: 2000-11-14

PRIOR APPLICATION NUMBER: 60/250,077

PRIOR PILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-30

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2000-11-30

NUMBER OF SEQ ID NOS: 62

SOFTWARE: FESTESQ for Windows Version 4.0

SEQ ID NO 59

LENGTH: 378
 NAME/KEY: misc_feature
LOCATION: 1..168
OTHER INFORMATION: Xaa is any amino acid
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; LCCATION: 1..168
US-09-708-427-71051
 US-09-620-394B-8225
Sequence 8225, Application US/09620394B; GENERAL INFORMATION:
APPLICANT: ALEXANDROV, NICKOLBI
 ORGANISM: Zea mays subsp. mays
 75.0%;
75.0%;
 73.1%;
75.0%;
 Query Match 75.0
Best Local Similarity 75.0
Matches 6; Conservative
 Query Match 73.1
Best Local Similarity 75.0
Matches 6; Conservative
 ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-001-137-59
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Sequence 36334, Application US/09708427

Sequence 36334, Application US/09708427

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: US/09/708,427
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SEQ ID NO 36334
LENGTH: 398
 APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding Polypeptid
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-1067P
CURRENT APPLICATION NUMBER: US/09/620,394B
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9131
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0
 Length 389;
 Length 344;
 Indels
 1; Indels
 DB 5;
34;
 Score 37; DB 5;
Pred. No. 39;
 1; Mismatches
 1; Mismatches
 NAME/KEY: misc_feature
COGATION: 1..389
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
COGATION: 1..389
USCATION: 1..389
USC-09-620-394B-8224
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LOCATION: 1..34
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
 ; LOCATION: 1..344
; OTHER INFORMATION: Ceres Seq. ID 1843031
US-09-708-427-36335
 Sequence 8224, Application US/09620394B
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai
 TYPE: PRT
ORGANISM: Arabidopsis thaliana
 TYPE: PRT ORGANISM: Arabidopsis thaliana
 ORGANISM: Arabidopsis thaliana
 71.2%;
71.4%;
 Conservative
 5; Conservative
 Query Match
Best Local Similarity (
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 Query Match
Best Local Similarity
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163 EHGHSHG 169
 1||:||
218 HGHVHG 223
 RESULT 14
US-09-708-427-36334
 2 онснинс 8
 RESULT 13
US-09-620-394B-8224
 з нснмнс в
 SEQ ID NO 8224
LENGTH: 389
LENGTH: 344
 FEATURE:
 Matches
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 US-09-708-477-36335
Sequence 36335, Application US/09708427
Sequence 36335, Application US/09708427
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES:
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 36335
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 Gaps
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0
 Length 330;
 DB 5; Length 309; 30;
 Indels
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 core 37; DB 5 red. No. 32; Mismatches
 Score 37; DB 9
Pred. No. 30;
1; Mismatches
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LOCATION: 1..330
OTHER INFORMATION: Ceres Seq. ID 1843032
 Score 37;
Pred. No.
 NAME/KEY: misc_feature
LOCATION: 1.309
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1.309
OTHER INFORMATION: Ceres Seq. ID 1411807
US-09-620-394B-8225
 OTHER INFORMATION: Xaa is any amino acid
 Sequence 36336, Application US/09708427 GENERAL INFORMATION:
 CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9131
SEQ ID NO 8225
 ORGANISM: Arabidopsis thaliana
 71.2%;
71.4%;
 ORGANISM: Arabidopsis thaliana
 71.2%;
83.3%;
 Conservative
 Conservative
 NAME/KEY: misc_feature
 Query Match
Best Local Similarity
 Best Local Similarity
Matches 5; Conserv
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149 EHGHSHG 155
 138 HGHVHG 143
 US-09-708-427-36336
 2 QHGHMHG 8
 US-09-708-427-36336
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 TYPE: PRT
 Query Match
 Matches
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Sequence 8223, Application US/09620394B
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ALEXANDROW, Nickolai
APPLICANT: ALEXANDROW, Vacheslav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
TITLE REFERENCE: 2750-1067P
CURRENT PFLICATION NUMBER: US/09/620,394B
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9131
SOD ID NO 8223
LENGTH: 453
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 Score 37; DB 5; Length 453;
Pred. No. 45;
1; Mismatches 0; Indels
 Score 37; DB 5; Length 398; Pred. No. 40; 1; Mismatches 1; Indels
; FEATURE:

NAME/KEY: misc_feature

LOCATION: 1..398

OTHER INFORMATION: Xaa is any amino acid

NAME/KEY: misc_feature

LOCATION: 1..398

COCATION: 1..398

US-09-708-427-36334
 FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..453
OTHER INPORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..453
COTHER INFORMATION: Ceres Seq. ID 1411805
US-09-620-394B-8223
 Search completed: January 29, 2002, 10:58:15 Job time: 2511 sec
 TYPE: PRT
ORGANISM: Arabidopsis thaliana
 Query Match 71.2%;
Best Local Similarity 71.4%;
Matches 5; Conservative
 Query Match 71.2%;
Best Local Similarity 83.3%;
Matches 5; Conservative
 :||| ||
217 EHGHSHG 223
 111:11
282 HGHVHG 287
 2 ОНСНМНС 8
 RESULT 15
US-09-620-394B-8223
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; Search time 1760.55 Seconds
(without alignments)
1.262 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 3148936 seqs, 277657034 residues
 January 29, 2002, 10:56:06
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 Pending_Patents_AA_Main:*
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 US-09-763-397A-14
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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1 SNTFINNA 8
 Title:
Perfect score:
 Scoring table:
 Database :
 Searched:
 Sequence:
 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |        | Description | Sequence 14, Appl | Sequence 59, Appl | Sequence 2, Appli | Sequence 13377, A    | Sequence 2046, Ap  | Sequence 3944, Ap  | Sequence 7203, Ap  | Sequence 75, Appl | Sequence 29418, A   |
|-----------|--------|-------------|-------------------|-------------------|-------------------|----------------------|--------------------|--------------------|--------------------|-------------------|---------------------|
| SUMMARIES |        | ID          |                   | PCT-US99-26796-59 | US-09-763-397A-2  | US-09-489-039A-13377 | US-09-757-028-2046 | US-08-827-356-3944 | US-09-611-529-7203 | PCT-US99-26796-75 | US-09-417-507-29418 |
|           |        | DB          | 21                | _                 | 21                | 18                   |                    | 12                 |                    | П                 | 18                  |
|           | Query  | Length      | 80                | 272               | 350               | 116                  | 118                | 214                | 214                | 2010              | 9/                  |
| ð         | Query  | Match       | 100.0             | 100.0             | 100.0             | 87.8                 | 80.5               | 80.5               | 80.5               | 80.5              | 78.0                |
|           |        | Score       | 41                | 41                | 41                | 36                   | 33                 | 33                 | 33                 | 33                | 32                  |
|           | Result | SO.         |                   | 7                 | e                 | 4                    | 5                  | 9                  | 7                  | 8                 | 6                   |

| Sequence 827, App Sequence 1563, Ap Sequence 1563, Ap Sequence 1563, App Sequence 1977, App Sequence 995, App Sequence 996, App Sequence 996, App Sequence 2850, App Sequence 1187, App Sequence 1187, App Sequence 1187, App Sequence 1187, App Sequence 7755, App Sequence 7755, App Sequence 1187, App Sequence 1187, App Sequence 1187, App Sequence 1187, App Sequence 29473, App Sequence 1205, App Sequence 10602, App Sequence 10002, App Sequence 10003, App Sequenc | erica, as represented by the<br>d Human Services, Centers for<br>Vaccine Against Plasmodium Fa                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| US-60-164-763-827 US-60-194-912-587-1563 US-60-194-911-1522 US-60-194-911-1522 US-60-194-919-977 US-60-194-919-977 US-60-194-919-978 US-60-194-919-978 US-60-194-919-978 US-60-194-919-978 US-60-170-346-1857 US-60-229-515-1187 US-60-229-515-1187 US-60-234-109-29473 US-60-234-109-29473 US-60-324-109-29473 US-60-324-109-29473 US-60-196-713-3281 US-60-196-713-3281 US-60-196-713-3281 US-60-196-713-3281 US-60-196-713-3281 US-60-196-713-3281 US-60-196-713-3281 US-60-196-713-3281                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | RESULT 1  1S-09-763-397A-14  Sequence 114, Application US/09763397A  GENERAL INFORMATION: APPLICANT: The Government of the United States of America, APPLICANT: Secretary of the Department of Health and Hume, APPLICANT: Cal, Altaf A. APPLICANT: Cal, Altaf A. APPLICANT: Ping Shi, Ya APPLICANT: Hasnain, Seyed E. TILE REFERENCE: 6395-57049  CURRENT APPLICATION NUMBER: US 60/097,703  PRIOR FILING DATE: 1999-08-19  PRIOR APPLICATION NUMBER: PCT / US99/18869  PRIOR FILING DATE: 1999-08-19  NUMBER OF SEQ ID NOS: 26  NUMBER OF SEQ ID NOS: 26  SOFTWANET: DATE-11 version 3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| 24444444444444444444444444444444444444                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | of t<br>of t<br>he D<br>even<br>leven<br>inan<br>inan<br>inan<br>inan<br>inan<br>inan<br>inan<br>in                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| 88 88 88 88 88 88 88 88 88 88 88 88 88                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | plication US/09 TION: Government of Cretary of the Introl and Preve I, Altaf A. ng Shi, Ya Sinin, Seyed E. ON E. ON BOATE: 1999-08-19 TON NUMBER: US ATE: 1999-08-19 TON NUMBER: PCT ATE: 1999-08-19                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| 77888888888888888888888888888888888888                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 1 3-397A-14 Cee 14, Application US/05 L INFORMATION: CANT: The Government of CANT: Secretary of the CANT: Control and Preve CANT: Ping Shi, Ya CANT: Hasnain, Seyed E OF INVENTION: Recombine REFERENCE: 6395-57649 RTLING DATE: 1999-08-13 APPLICATION NUMBER: US FILING DATE: 1999-08-13 ROF SEQ ID NOSS: 26 FILING DATE: 1999-08-13 ROF SEQ ID NOSS: 26 REING DATE: 1999-08-13                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 197A-1974, MEORU 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
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Length 8; Query Match
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 8; Conservative 0; Mismatches 0; ORGANISM: Plasmodium falciparum US-09-763-397A-14 SOFTWARE: PatentIn version 3.1 SEQ 10 NO 14 LENGTH: 8 TYPE: PRT

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Indels

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APPLICANT: GATY Breton et. al
APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLETC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLETC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF ES IN NOS: 14342
SEQ ID NO 13377
LENGTH: 116
 ; LOCATION: (62); CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-757-028-2046
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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 Sequence 2046, Application US/09757028

Sequence 2046, Application US/09757028

Sequence 2046, Application US/09757028

TILE REPERENCE:

TILE REFERENCE: PM01

CURRENT APPLICATION NUMBER: US/09/757,028

CURRENT FILING DATE: 2001-01-09

PRIOR APPLICATION NUMBER: 60/179,065

PRIOR APPLICATION NUMBER: 60/180,628

PRIOR APPLICATION NUMBER: 60/180,628

PRIOR APPLICATION NUMBER: 60/180,628

SPROFT FILING DATE: 2000-02-04

NUMBER OF SEQ ID NOS: 2660

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 2046
 Score 33; DB 21; Length 118;
Pred. No. 1.1e+02;
 Length 116;
 Indels
 DB 18;
26;
 1; Mismatches
 Mismatches
 Score 36;
Pred. No.
 Sequence 13377, Application US/09489039A GENERAL INFORMATION:
 Sequence 3944, Application US/08827356 GENERAL INFORMATION:
APPLICANT: George H. Shimer, Jr.
 APPLICANT: George H. Shimer, Jr. APPLICANT: George H. Miller
 ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13377
 80.5%;
 87.8%;
 Query Match 80.5
Best Local Similarity 75.0
Matches 6; Conservative
 6; Conservative
 ORGANISM: Homo sapiens
 Query Match
Best Local Similarity
Matches 6; Conserv
 1111:1 1
25 SNTFLNGA 32
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| 97 NTEVNNA 103
 1 SNTFINNA 8
 US-09-489-039A-13377
 2 NTFINNA 8
 RESULT 6
US-08-827-356-3944
 RESULT 5
US-09-757-028-2046
 NAME/KEY: SITE
 TYPE: PRT
 LOCATION:
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 Sequence 2, Application US/09763397A
; Sequence 2, Application US/09763397A
; Sequence 2, Application US/09763397A
; GENERAL THE GOVERNMENT ON THE GOVERNMENT OF THE GOVERNMENT OF THE GOVERNMENT SECRETARY OF THE DEPARTMENT OF THE GOVERNMENT SECRETARY OF THE DEPARTMENT CONTROL APPLICANT: Lal, Altaf A.

APPLICANT: Lal, Altaf A.

APPLICANT: Hasnain, Seyed E.

APPLICANT: Hasnain Seyed E.

APPLICANT: Hasnain, Seyed E.

APPLICANT: Hasnain, Seyed E.

APPLICANT: Hasnain, Seyed E.

APPLICANT: Hasnain, Seyed E.

APPLICANT: Hasnain ;
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 Sequence 59, Application PC/TUS9926796
GENERAL INFORMATION:
APPLICANT: United States Government as Represented by the
APPLICANT: United States Government as Represented by the
APPLICANT: Secretary of the Navy Squence of Human Malaria Parasite
TITLE OF INVENTION: Chromosome 2 Sequence of Human Malaria Parasite
TITLE OF INVENTION: Chromosome Useful in Anti-malarial Vaccines and
TITLE OF INVENTION: Diagnostic Reagents
FILE REFERENCE:
 0;
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0
 Length 350;
 Score 41; DB 1; Length 272; Pred. No. 6.2;
 Indels
 Query Match 100.0%; Score 41; DB 21; Best Local Similarity 100.0%; Pred. No. 8.1; Matches 8; Conservative 0; Mismatches 0;
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 Query Match 100.0%; Score 41; DE Best Local Similarity 100.0%; Pred. No. 6.2 Matches 8; Conservative 0; Mismatches
 CTHER INFORMATION: Recombinant DNA/Protein US-09-763-397A-2
 CURRENT APPLICATION NUMBER: PCT/US99/26796
CURRENT FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 420
 ; ORGANISM: Plasmodium falciparum PCT-US99-26796-59
 ORGANISM: Artificial Sequence
 PatentIn Ver. 2.1
 1 SNTFINNA 8
 1 SNTFINNA 8
1 SNTFINNA
 NUMBER SOFTWARE: Pate
SOFTWARE: Pate
SEQ ID NO 59
 RESULT 2
PCT-US99-26796-59
 TYPE: PRT
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PUTCH 1899-26796-75

Sequence 75, Application PC/TUS9926796

Sequence 75, Application PC/TUS9926796

Sequence 75, Application PC/TUS9926796

Sequence 75, Application Secretary of the Navy
APPLICANT: United States Government as Represented by the APPLICANT: Secretary of the Navy
TITLE OF INVENTION: Chromosome 2 Sequence of Human Malaria Parasite
TITLE OF INVENTION: Chromosome Useful in Anti-malarial Vaccines and
TITLE OF INVENTION: Diagnostic Reagents
FILE REFERENCE:
CURRENT APPLICATION NUMBER: PCT/US99/26796

CURRENT FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 420

SOFTWARE: PatentIn Ver. 2.1
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 80.5%; Score 33; DB 20; Length 214; llarity 71.4%; Pred. No. 2e+02; Conservative 2; Mismatches 0; Indels
 PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/037,934
PRIOR PLING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-06
PRIOR FILING DATE: 1998-03-06
PRIOR PLING DATE: 1998-03-06
PRIOR FILING DATE: 1998-03-06
PRIOR FILING DATE: 1998-03-06
 PRIOR FILING DATE: 1998-03-06
PRIOR FILING DATE: 1998-03-06
PRIOR FILING DATE: 1998-03-06
PRIOR PILING DATE: 1998-03-06
PRIOR FILING DATE: 1996-03-06
PRIOR FILING DATE: 1996-03-06
PRIOR FILING DATE: 1996-03-06
PRIOR FILING DATE: 1996-04-01
PRIOR FILING DATE: 1997-04-01
PRIOR FILING DATE: 1997-04-01
PRIOR FILING DATE: 1996-05-02
PRIOR FILING DATE: 1996-05-03
PRIOR FILING DATE: 1996-05-05-03
PRIOR PRIOR PRIOR DATE: 1996-05-05-03
 ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-611-529-7203
 ; ORGANISM: Plasmodium falciparum PCT-US99-26796-75
 Query Match
Best Local Similarity
Matches 5; Conserv
 : | | | : | |
93 ANTEVNN 99
 1 SNTFINN 7
 SEQ ID NO 75
LENGTH: 2010
 APPLICANT: Roberta S. Hare,
APPLICANT: Roberta S. Hare,
APPLICANT: Raren J. Shaw
TITLE OF INVENTION: Staphylococcus aureus Related Compositions and Methods
FILE REFERENCE: 1034/AC96JUS1
CURRENT APPLICATION NUMBER: US/09/611,529
CURRENT APPLICATION NUMBER: US 09/417,811
PRIOR FILING DATE: 1999-10-14
PRIOR FILING DATE: 1999-07-14
PRIOR FILING DATE: 1999-07-14
PRIOR FILING DATE: 1999-03-11
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 Gaps
 80.5%; Score 33; DB 12; Length 214;
71.4%; Pred. No. 2e+02;
.ive 2; Mismatches 0; Indels
APPLICANT: Roberta S. Hare
APPLICANT: Karen J. Shaw
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS RELATED
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 5574
CORRESPONDENCE ADDRESS:
 3: Schering-Plough Corporation
2000 Galloping Hill Road
 SOFTWARE: Patentin C-DOS/MS-DOS SOFTWARE: Patentin CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,356 FILING DATE: 01-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/014,477
FILING DATE: 01-APR-1996
APPLICATION NUMBER: 60/016,743
FILING DATE: 02-MAY-1996
INFORMATION FOR SEQ ID NO: 3944:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
 ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 7203, Application US/09611529 GENERAL INFORMATION:
 HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Staphylococcus aureus
 APPLICANT: George H. Shimer, Jr. APPLICANT: George H. Miller
 ; NAME/KEY: misc_feature
; LOCATION: 1...214
US-08-827-356-3944
 Query Match 80.5
Best Local Similarity 71.4
Matches 5; Conservative
 MOLECULE TYPE: protein HYPOTHETICAL: YES
 CITY: Kenilworth
STATE: New Jersey
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93 ANTFVNN 99
 1 SNTFINN 7
 RESULT 7
US-09-611-529-7203
 ADDRESSEE:
STREET: 20
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78.0%;
85.7%;
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Best Local, Similarity 85.7.
 Ouery Match
Best Local Similarity 85.,
 NAME/KEY: VARIANT
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73 SDTFINN 79
 |:|||||
13 SDTFINN 19
 TYPE: PRT
ORGANISM: HUMAN
 1 SNTFINN 7
 ORGANISM: HUMAN
 1 SNTFINN 7
 ; TYPE: PRT
; ORGANISM: Human
US-60-169-842-4538
 RESULT 13
US-60-194-091-1522
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 Sequence 29418, Application US/09417507
GENERAL INFORMATION:
APPLICANT: RITH G. WEINSTOCK ET AL.
APPLICANT: RITHG G. WEINSTOCK ET AL.
TITLE OF INVENTION: FUNICATION FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FUNICATION FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/417,507
CURRENT FILING DATE: 1999-10-14
NUMBER OF SEQ ID NOS: 44312
SEQ ID NO 29418
LENGTH: 76
 Sequence 827, Application US/60164763

General Bromazi, Vivien

TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN GPCR PROTEINS AND USES THEREOF

FILE REFERENCE: CLO00140

CURRENT APPLICATION NUMBER: US/60/164,763

CURRENT FILING DATE: 1999-11-12

NUMBER OF SEQ ID NOS: 1154

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 827

LENGTH: 89
 Sequence 4538, Application US/60169842
GENERAL INFORMATION:
APPLICANT: BOAZZI, VIVVEN
TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN GPCR PROTEINS AND USES THEREOF
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Length 2010;
 Score 32; DB 24; Length 89;
Pred. No. 1.3e+02;
1; Mismatches 0; Indels
 Length 76;
80.5%; Score 33; DB 1; Le
100.0%; Pred. No. 2.1e+03;
:ive 0; Mismatches 0;
 DB 18;
1.1e+02;
 1; Mismatches
 Mismatches
 Score 32;
Pred. No.
 78.0%;
85.7%;
 78.0%;
85.7%;
 Query Match 78.0
Best Local Similarity 85.7
Matches 6; Conservative
 Conservative
 Conservative
 ORGANISM: A.fumigatus US-09-417-507-29418
 Best Local Similarity
Matches 6; Conserv
 Query Match
Best Local Similarity
Matches 6; Conserv
 43 SNNFINN 49
 |:|||||
13 SDTFINN 19
 111111
735 NTFINN 740
 ; ORGANISM: Human
US-60-164-763-827
 1 SNTFINN 7
 1 SNTFINN 7
 RESULT 9
US-09-417-507-29418
 RESULT 11
US-60-169-842-4538
 2 NTFINN 7
 US-60-164-763-827
 Query Match
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 RESULT 14
US-60-192-587-995
Sequence 995, Application US/60192587
Sequence 995, Application US/60192587
Sequence 995, Application US/60192587
Tarric OF INVENTION: SOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
CURRENT APPLICATION NUMBER: US/60/192,587
CURRENT FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 1666
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 995
LENGTH: 127
 RESULT 15
US-60-194-091-977
Sequence 977, Application US/60194091
Sequence 977, Application US/60194091
SENERAL INFORMATION:
TATLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
CURRENT APPLICATION NUMBER: US/60/194,091
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 1598
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 127
TYPE: PRT
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 Score 32; DB 24; Length 127;
Pred. No. 1.9e+02;
1; Mismatches 0; Indels
 Score 32; DB 24; Length 127;
Pred. No. 1.9e+02;
1; Mismatches 0; Indels
 Score 32; DB 24; Length 90;
Pred. No. 1.3e+02;
1; Mismatches 0; Indels
; LOCATION: (1)...(90)
; OTHER INFORMATION: Xaa - Any Amino Acid
US:60-194-091-1522
 78.0%;
85.7%;
 Query Match 78.0%;
Best Local Similarity 85.7%;
Matches 6; Conservative
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Best Local Similarity 85.7%;
Matches 6; Conservative
 Query Match
Best Local Similarity 85.77
Matches 6; Conservative
 1 SNTFINN 7
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73 SDTFINN 79
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112 SDTFINN 118
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 ; ORGANISM: HUMAN
US-60-192-587-995
 1 SNTFINN 7
 1 SNTFINN 7
 ; ORGANISM: HUMAN US-60-194-091-977
 TYPE: PRT
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Sequence 76264, A Sequence 76263, A Sequence 76263, A Sequence 4936, A P Sequence 54646, A Sequence 4934, Ap Sequence 11, Appli Sequence 11, Appli Sequence 19897, A Sequence 18897, A Sequence 284, Appli Seq
 2, Appli
2, Appli
424, App
424, App
 ; Search time 120.95 Seconds
(without alignments)
2.421 Million cell updates/sec
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Sequence
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3: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

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7: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
 US-09-708-427-76264

US-09-708-427-76263

US-09-620-394B-4936

US-09-620-394B-4936

US-09-620-394B-4934

US-09-620-394B-4934

US-09-620-394B-4934

US-09-620-394B-4934

US-09-620-394B-4934

US-09-620-394B-4934

US-09-620-394B-4934

US-09-708-427-1989B

US-09-708-427-1989B

US-09-708-427-1989B

US-09-801-388-284

PCT-USO1-17103-2

US-09-801-368-22

US-09-801-368-424

US-09-801-368-424

US-09-816-028A-19

US-09-816-028A-19

US-09-816-028A-19

US-09-816-028A-19

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US-09-816-028A-19

US-09-708-427-68823

US-09-708-427-68823

US-09-708-427-68823

US-09-708-427-68823
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1 SNTFINNA 8
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 Title:
Perfect score:
 Score
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 Database
 Run on:
 Result
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19, Appl 25, Appl 480, App

Sequence 1

Sequence Sequence Sequence

79046, A 22562, A 68823, A 48, Appl

Sequence Sequence Sequence

us-09-763-397a-14.rapn

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Sequence 54645, Application US/09708427

Sequence 54645, Application US/09708427

GENERAL INFORMATION:

APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID

TITLE OF INVENTION: THEREBY

TITLE OF INVENTION: THEREBY

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SOFTWARE: Patentin version 3.1

LENGTH: 343
 Sequence 54646, Application US/09708427
GENERAL INFORMATION:
APPLICAPT: N. ALEXANDROV et al.
APPLICAPT: N. ALEXANDROV et al.
TITLE OF INVENTION: THEREBY
FILLE REPRENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: US/09/708,427
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 54646
LENGTH: 329
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 Gaps
 .;
0
 ö
 Length 329;
 Length 275;
 0; Indels
 Indels
 DB 5;
64;
 Score 31; DB 5;
Pred. No. 53;
0; Mismatches
 Score 31; DB 5
Pred. No. 64;
3; Mismatches
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LOCATION: 1..343
OTHER INFORMATION: Xaa is any amino acid
 NAME/KEY: misc_feature
| LOCATION: 1..329
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| OTHER INFORMATION: Xaa is any amino acid
| NAME/KEY: misc_feature
| LOCATION: 1..329
| COTHER INFORMATION: Ceres Seq. ID 1933688
US-09-708-427-54646
 ID 1393687
; NAME/KEY: misc_feature
; LOCATION: 1..275
; OTHER INFORMATION: Xaa is any am;
; NAME/KEY: misc_feature
; LOCATION: 1..275
; COTHER INFORMATION: Ceres Seq. IL
US-09-620-394B-4936
 TYPE: PRT ORGANISM: Zea mays subsp. mays
 75.6%;
 75.6%;
85.7%;
 ORGANISM: Zea mays subsp.
 Query Match
Best Local Similarity 62.5
Matches 5; Conservative
 Query Match 75.6
Best Local Similarity 85.7
Matches 6; Conservative
 311 SSSFVNNA 318
 1 SNTFINNA 8
 || || || || || || 72 SNDFINN 78
 1 SNTFINN 7
 US-09-708-427-54646
 TYPE: PRT
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 q
 QQ
 Sequence 4936. Application US/09620394B
Sequence 4936. Application:
Sequence 4936. App
 APPLICANT: N. ALEXANDROV et al.

APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRACMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 75262
LENGTH: 190
 0;
 ö
 ó;
 0;
 Length 190;
 Score 31; DB 5; Length 152;
Pred. No. 27;
 1; Indels
 Score 31; DB 5;
Pred. No. 35;
0; Mismatches
 0; Mismatches
 OTHER INFORMATION: Ceres Seq. ID 1959857
US-09-708-427-76262
 NAME/KEY: misc_feature
COCATION: 1..152
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
COCATION: 1..152
OTHER INFORMATION: Ceres Seq. ID 1959858
195-09-708-427-76263
 Sequence 76262, Application US/09708427 GENERAL INFORMATION:
 TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
 ORGANISM: Arabidopsis thaliana
 NAME/KEY: misc_feature
LOCATION: 1..190
OTHER INFORMATION: Xaa is any
 ORGANISM: Arabidopsis thaliana
 75.6%;
85.7%;
 75.6%;
85.7%;
 Query Match 75.6
Best Local Similarity 85.7
Matches 6; Conservative
 6; Conservative
 NAME/KEY: misc_feature
LOCATION: 1..190
 Query Match
Best Local Similarity
 104 NLFINNA 110
 | |||||
66 NLFINNA 72
 2 NTFINNA 8
 RESULT 4
US-09-620-394B-4936
 2 NTFINNA 8
 US-09-708-427-76262
 LENGTH: 275
 FEATURE:
 Matches
 qq
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TITLE OF INVENTION: SHRIMPRY NUCLEOTIDE SEQUENCE OF THE
TITLE OF INVENTION: SYSTEMS CONTAINING THIS SEQUENCE AND DETECTION KITS AND
TITLE OF INVENTION: SYSTEMS CONTAINING THIS SEQUENCE AND DETECTION KITS AND
TITLE OF INVENTION: OUTBREAK AND SPREAD
FILE REFERENCE: CL000895
CURRENT APPLICATION NUMBER: US/0/005,368
CURRENT APPLICATION NUMBER: 99124717.5
PRIOR FILING DATE: 1999-11.24
PRIOR FILING DATE: 1999-11.24
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 293
SSOFTARE: FastSEQ for Windows Version 4.0

LENGTH: 621
 Sequence 2, Application US/09881165
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HOOD, ELIZABETH
APPLICANT: GASTEL, FRANS
APPLICANT: GASTEL, FRANS
APPLICANT: WARG, HUAMING
APPLICANT: WARD, MICHAEL
APPLICANT: WANG, HUAMING
APPLICANT: WANG, HUAMING
APPLICANT: WANDOARD, SUSAN
TITLE OF INVENTION: BELYMES PRODUCED IN PLANTS
FILE REFERENCE: 1003AR
CURRENT APPLICATION NUMBER: US/09/881,165
CURRENT APPLICATION NUMBER: 60/211,732
PRIOR FILING DATE: 2001-06-14
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 5
SOSTWARE: PATENTIN VET. 2.1
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 Length 374;
 Score 31; DB 5;
Pred. No. 74;
 Score 31; DB 5;
Pred. No. 1e+02;
 1; Mismatches
 0; Mismatches
 US-10-005-368-41; Sequence 41, Application US/10005368; Sequence 41, Application US/10005368; APPLICANT: Xun XU et al.
 75.6%;
75.0%;
 Query Match 75.6
Best Local Similarity 85.7
Matches 6; Conservative
 Conservative
 ORGANISM: Trametes sp
US-09-881-165-2
 Query Match
Best Local Similarity
 :| ||||||
335 TNFFINNA 342
 171 SNDFINN 177
 1 SNTFINNA 8
 ; ORGANISM: SHRIMP
US-10-005-368-41
 1 SNTFINN 7
 US-09-620-394B-4934
 9
 RESULT 9
US-09-881-165-2
 LENGTH: 499
 SEQ ID NO 2
 Matches
 Dp
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 δ
 Sequence 4935, Application US/09620394B
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE OF INVENTION: Thereby
FILE REPERENCE: 2750-1067P
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9131
SEQ ID NO 4935
 Sequence 4934, Application US/09620394B
GENERAL INFORMATION:
APPLICANT: ALEXANDROW, Nickolai
APPLICANT: ALEXANDROW, Nickolai
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-1067P
CURRENT APPLICATION NUMBER: US/09/620,394B
CURRENT FILING DATE: 2000-07-21
SEQ ID NO 4934
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 Gaps
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0
 ö
 Length 343;
 Score 31; DB 5; Length 366;
Pred. No. 72;
0; Mismatches 1; Indels
 0; Indels
 Score 31; DB 5;
Pred. No. 67;
 3; Mismatches
 NAME/KEY: misc_feature

// CCATION: 1.366

// OTHER INFORMATION: Ceres Seq. ID 1393686

US-09-620-394B-4935
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LOCATION: 1..374
OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: 1..343
; OTHER INFORMATION: Ceres Seq. ID 1933687
US-09-708-427-54645
 LOCATION: 1.366
OTHER INFORMATION: Xaa is any amino acid
 OTHER INFORMATION: Ceres Seq. ID 1393685
 TYPE: PRT ORGANISM: Arabidopsis thallana
 TYPE: PRT
ORGANISM: Arabidopsis thallana
 75.6%;
62.5%;
 Query Match
Best Local Similarity 62...
Best Conservative
 Query Match
Best Local Similarity 85.7
Matches 6; Conservative
 NAME/KEY: misc_feature
LOCATION: 1..374
 NAME/KEY: misc_feature
 1::|:||
325 SSSEVNNA 332
 || ||||
163 SNDFINN 169
 1 SNTFINNA 8
 RESULT 7
US-09-620-394B-4935
 RESULT 8
US-09-620-394B-4934
 FEATURE:
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
 Sequence 19896, Application US/09708427
Sequence 19896, Application US/09708427
GENERAL INFORMATION:
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 83364
SOFTWARE: PATENTIN VERSION 3.1
ö
 Gaps
 .;
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 Length 518;
 Indels
 Indels
 .;
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 Score 30; DB 5; I
Pred. No. 1.7e+02;
1; Mismatches 0;
 Mismatches
 CURRENT APPLICATION NUMBER: US/09/801,368 CURRENT FILING DATE: 2001-03-07
 NAME/KEY: misc_feature
LOCATION: 1..518
OTHER INFORMATION: Xaa is any amino acid
 NAME/KEY: misc_feature
CCATTON: 1..518
COTHER INFORMATION: Ceres Seq. ID 1836874
03-09-708-427-19896
 CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
 PRIOR APPLICATION NUMBER: US 60/160,587 PRIOR FILING DATE: 1999-10-20
 Sequence 284, Application US/09801368 GENERAL INFORMATION:
 TYPE: PRT ORGANISM: Saccharomyces cerevisiae
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 TYPE: PRT
ORGANISM: Arabidopsis thaliana
 NUMBER OF SEQ ID NOS: 440
SOFTWARE: PatentIn version 3.0
 73.2%;
 APPLICANT: Busby, Robert
APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Hothzman, Doug
APPLICANT: Madden, Kevin
 Norman, Thea
Royer, John
Salama, Sofie
 Best Local Similarity 83.3
Matches 5; Conservative
 Conservative
 Sherman, Amir
Silva, Jeff
 Summers, Eric
 Maxon, Mary
Milne, Todd
 ||:|||
292 TFVNNA 297
 3 TFINNA 8
 3 TFINNA 8
 US-09-801-368-284
 SEQ ID NO 19896
LENGTH: 518
 5,
 Query Match
 APPLICANT
 FEATURE:
 RESULT 13
 Matches
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 Sequence 19897, Application US/09708427

GENERAL INFORMATION:
APPLICANT: N. ALEXANDROW et al.
TITLE OF INVENTION:
THEREBY
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 19897
LENGTH: 502
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THERBY TITLE OF INVENTION: THERBY CURRENT APPLICATION NUMBER: US/09/708,427 CURRENT PPLICATION NUMBER: US/09/708,427 CURRENT FILING DATE: 2000-11-09 NUMBER OF SEQ ID NOS: 85364 SOFFWARE: PALENTIN VERSION 3.1 SEQ ID NO 19898
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0
 Length 502;
 Length 449;
 DB 6; Length 621;
 0; Indels
 Score 31; DB 6; Length 621
Pred. No. 1.3e+02;
2; Mismatches 0; Indels
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Pred. No. 1.6e+02;
 Score 30; DB 5;]
Pred. No. 1.4e+02;
1; Mismatches 0
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LOCATION: 1..502
OTHER INFORMATION: Xaa is any amino acid
 NAME/KEY: misc_feature

! LOCATION: 1..502

! OTHER INFORMATION: Ceres Seq. ID 1836875

US-09-708-427-19897
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; OTHER INFORMATION: Ceres Seq. ID 1836876
US-09-708-427-19898
 Sequence 19898, Application US/09708427 GENERAL INFORMATION:
 ORGANISM: Arabidopsis thaliana
 TYPE: PRT
ORGANISM: Arabidopsis thaliana
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83.3%;
 73.2%;
 75.68;
71.48;
 5; Conservative
 NAME/KEY: misc_feature
 Best Local Similarity
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Matches 5; Conserv
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263 SSTFVNN 269
 11:111
239 TFVNNA 244
 RESULT 12
US-09-708-427-19897
 1 SNTFINN 7
 RESULT 11
US-09-708-427-19898
 3 TFINNA 8
 Query Match
 Query Match
 TYPE: PRT
 FEATURE:
 δ
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US-09-801-368-284

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APPLICANT: Hecht, Peter
APPLICANT: Hecht, Peter
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary
APPLICANT: Mine, Todd
APPLICANT: Mine, Todd
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLIC
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 Gaps
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0
 73.2%; Score 30; DB 5; Length 979; 83.3%; Pred. No. 3.4e+02; tive 1; Mismatches 0; Indels
 Query Match 73.2%; Score 30; DB 5; Length 979; Best Local Similarity 83.3%; Pred. No. 3.4e+02; Matches 5; Conservative 1; Mismatches 0; Indels
 RESULT 15
US-09-487-558-284
Sequence 284, Application US/09487558
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Call, Brian
APPLICANT: Hedrik, Peter
APPLICANT: Hedrik, Peter
APPLICANT: Madden, Kevin
NobilCANT: Madden, Kevin
 ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-487-558-284
Query Match 73.2
Best Local Similarity 83.3
Matches 5; Conservative
 1 SNTFIN 6
 1 SNTFIN 6
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us-09-763-397a-13.rapm

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LENGTH: 17
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Sequence 2, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
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Sequence 3, Appli
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 ; Search time 1760.55 Seconds (without alignments)
2.681 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-763-397A-2
US-09-10-000-8
US-07-867-768A-2
US-07-867-768A-4
US-08-195-705-2
US-08-195-705-2
US-08-195-705-3
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US-08-195-705-4
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Maximum Match 100%
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 OM protein – protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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 US-09-763-397A-13
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 Length
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3350
3350
3344
3394
3394
3394
3394
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1000.0
1000.0
1000.0
 Potal number of
 Score
 8888888888
 Perfect score:
 Scoring table:
 Minimum DB
Maximum DB
 Sequence:
 Searched:
 Database
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ó
 Length 394;
 Indels
 APPLICANT: Chang, Sandra
APPLICANT: Chang, George
APPLICANT: Barr, Philip
APPLICANT: Gibson, Helen
TITLE OF INVENTION: BACULOVIRUS PRODUCED PLASMODIUM
TITLE OF INVENTION: FALCIPARUM VACCINE
NUMBER OF SEQUENCES: 5
 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SORTWARE APPLICATION DATA:
APPLICATION NUMBER: US/07/867,768A
FILING DATE: 19920413
 100.0%; Score 88; DB 3; 100.0%; Pred. No. 1.9e-05; Live 0; Mismatches 0;
 ORGANISM: Plasmodium falciparum
STRAIN: falciparum uganda palo glto (FUP)
US-07-867-768A-2
 ADDRESSEE: Davis Hoxie Faithfull Hapgood STREET: 45 Rockefeller Pl.
 11880A3
 RESULT 5
US-07-867-768A-4
; Sequence 4, Application US/07867768A
; GENERAL INFORMATION:
APPLICANT: Chang, Sandra
appLICANT: Hul, George
 Sequence 2, Application US/07867768A GENERAL INFORMATION:
 NAME: Jacobs, Seth H
REGISTRATION NUMBER: 32140
REFRENCE/POCKET NUMBER: 1186
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-757-2200
TELEPAX: 212-586-1461
 ZIP: 10111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
 TELEFAX: 216-22
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
TRNGTH: 394 amino acids
 118 GISYYEKVLAKYKDDLE 134
 C-terminal
 Barr, Philip
Gibson, Helen
 1 GISYYEKVLAKYKDDLE 17
 119 GISYYEKVLAKYKDDLE 135
 Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
 1 GISYYEKVLAKYKDDLE 17
 STRANDEDNESS: single
 MOLECULE TYPE: peptide HYPOTHETICAL: NO
 CORRESPONDENCE ADDRESS:
 linear
 FRAGMENT TYPE: CORIGINAL SOURCE:
 New York
 S
N
 HYPOTHETICAL:
 APPLICANT:
APPLICANT:
APPLICANT:
 US-07-867-768A-2
 COUNTRY:
 CITY: N
STATE:
 RESULT
 RESULT
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 g
 APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the Department of Health and Human Services, Centers for Dis APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis APPLICANT: Control and Prevention

APPLICANT: Lal, Altaf A.

APPLICANT: Ping Shi, Ya

APPLICANT: Hasnain, Seyed E.

TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falci
FILE REFERENCE: 6395-57049

CURRENT APPLICATION NUMBER: US/09/763,397A

CURRENT APPLICATION NUMBER: US 60/097,703

PRIOR FILING DATE: 1998-08-19

PRIOR APPLICATION NUMBER: PT / US99/18869

PRIOR APPLICATION NUMBER: PT / US99/18869

PRIOR FILING DATE: 1999-08-19

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn Version 3.1
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 Gaps
 Gaps
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 Length 375;
 Length 350;
 Indels
 Indels
 . OTHER INFORMATION: amino acid sequence of PfMSP-142 0S\!-\!09\!-\!710\!-\!000\!-\!8
 Query Match
100.0%; Score 88; DB 21;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 17; Conservative 0; Mismatches 0;
 Query Match 100.0\$; \ \, Score \ 88; \ \, \mathrm{DB} \ 21; Best Local Similarity 100.0\$; \ \, \mathrm{Pred}. No. 1.6e-05; Matches 17; Conservative 0; Mismatches 0;
 APPLICANT: Hui, George, S.N.
APPLICANT: Hui, George, S.N.
APPLICANT: Ho, Walter K.K.
APPLICANT: Lap-Yin, Pang
TITLE OF INVENTION: Malaria Vaccine
FILE REFERENCE: 23461-2001100
CURRENT APPLICATION NUMBER: US/09/710,000
CURRENT FILING DATE: 2000-11-10
PRIOR PELICATION NUMBER: 60/226,861
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/168,327
PRIOR APPLICATION NUMBER: 60/168,327
PRIOR APPLICATION NUMBER: 60/168,327
PRIOR FILING DATE: 1999-11-12
SPRIOR FILING DATE: 1999-12-11
SOUTHARRE: FASTERQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 375
 ; FEATURE:
; OTHER INFORMATION: Recombinant DNA/Protein
05-09-763-997A-2
 ; Sequence 8, Application US/09710000
; GENERAL INFORMATION:
; APPLICANT: Hui, George, S.N.
 Sequence 2, Application US/09763397A GENERAL INFORMATION:
 TYPE: PRT
ORGANISM: Artificial Sequence
 334 GISYYEKVLAKYKDDLE 350
 1 GISYYEKVLAKYKDDLE 17
1 GISYYEKVLAKYKDDLE 17
 TYPE: PRT
ORGANISM: Unknown
 US-09-710-000-8
 δ
 qq
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Gaps
 ö
 Length 394;
 Indels
 Sequence 4. Application US/08195705
GENERAL INFORMATION:
APPLICANT: Chang, Sandra
APPLICANT: Hui, George
APPLICANT: Hui, George
APPLICANT: Gibson, Helen
TITLE OF INVENTION: BACULOVIRUS PRODUCED PLASMODIUM
TITLE OF INVENTION: FALCIPARUM VACCINE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Davis Hoxie Faithfull Hapgood
STREET: 45 Rockefeller Pl.
CITY: New York
STATE: N.Y.
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 14-FEB-1994
CLASSIFICATION: 435
 Query Match 100.0%; Score 88; DB 5; 1
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 17; Conservative 0; Mismatches 0;
 ORGANISM: Plasmodium falciparum
STRAIN: falciparum uganda palo alto (FUP)
 MBER: US/08/195,705
14-FEB-1994
 REFERENCE/DOCKET NUMBER: 1186
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-757-2200
TELEFAX: 212-586-1461
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
 ATTORNEY AGENT INFORMATION:
NAME: Jacobs, Seth H
REGISTRATION NUMBER: 32140
 ATTORNEY/AGENT INFORMATION:
 ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
 118 GISYYEKVLAKYKDDLE 134
 TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO
 COMPUTER READABLE FORM:
 APPLICATION NUMBER:
FILING DATE: 14-FEE
CLASSIFICATION: 435
 ZIP: 10111
 ; STRAIN:
US-08-195-705-2
 COUNTRY:
 US-08-195-705-4
 οy
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 Gaps
 100.0%; Score 88; DB 3; Length 394; 100.0%; Pred. No. 1.9e-05; tive 0; Mismatches 0; Indels
 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/867,768A
FILING DATE: 1992043
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Jacobs, Seth H
RECISTRATION NUMBER: 11880A3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-757-2200
TELEPHONE: 212-757-2200
TELEPAX: 212-586-1461
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
 Sequence 2, Application US/08195705
GENERAL INFORMATION:
APPLICANT: Chang, Sandra
APPLICANT: Barr, Philip
APPLICANT: Barr, Philip
APPLICANT: Gibson, Helen
TITLE OF INVENTION: FALCIPARUM VACCINE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
TITLE OF INVENTION: BACULOVIRUS PRODUCED PLASMODIUM TITLE OF INVENTION: FALCIPARUM VACCINE NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS:
 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
 ADDRESSEE: Davis Hoxie Faithfull Hapgood STREET: 45 Rockefeller Pl. CITY: New York STATE: N.Y.
 ADDRESSEE: Davis Hoxie Faithfull Hapgood
STREET: 45 Rockefeller Pl.
CITY: New York
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
) ORGANISM: Plasmodium falciparum
; STRAIN: MAD
US-07-867-7688-4
 LENGTH: 394 amino acids TYPE: AMINO ACID
 Db 118 GISYYEKVLAKYKDDLE 134
 HYPOTHETICAL: NO FRAGMENT TYPE: C-terminal
 Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
 1 GISYYEKVLAKYKDDLE 17
 TOPOLOGY: linear MOLECULE TYPE: peptide
 single
 ORIGINAL SOURCE:
 STRANDEDNESS:
 STATE: N.Y.
 RESULT 6
US-08-195-705-2
 COUNTRY:
 COUNTRY:
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NAME/KEY: UNSURE
 RESULT 11
US-09-417-507-37685
 RESULT 12
US-09-758-458-380
 RESULT 10
US-09-500-376-16
 SEQ ID NO 16
 TYPE: PRT
 TYPE: PRT
 FEATURE:
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 qq
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 Sequence 3, Application US/09500376
Sequence 3, Application US/09500376
GENERAL INFORMATION:
APPLICANT: University of Hawaii
TITLE OF INVENTION: Baculovirus Produced Plasmodium Falciparum Vaccine
FILE REFERENCE: A-67984
CURRENT APPLICATION NUMBER: US/09/500,376
CURRENT FILING DATE: 2000-02-08
PRIOR FILING DATE: 1994-02-14
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 3.
LENGTH: 394
 Gaps
 APPLICANT: University of Hawaii
APPLICANT: University of Hawaii
TITLE OF INVENTION: Baculovirus Produced Plasmodium Falciparum Vaccine
FILE REFERENCE: A-67984
CURRENT APPLICATION UNMBER: US/09/500,376
CURRENT FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: US 08/195,705
PRIOR FILING DATE: 1994-02-14
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
 Gaps
 Gaps
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0
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0
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 Length 394;
 Length 394;
 Score 88; DB 5; Length 394;
Pred. No. 1.9e-05;
; Mismatches 0; Indels
 Indels
 100.0%; Score 88; DB 19;
100.0%; Pred. No. 1.9e-05;
iive 0; Mismatches 0;
 100.0%; Score 88; DB 19; 100.0%; Pred. No. 1.9e-05;
 Mismatches
 0; Mismatches
 HYPOTHETICAL: NO FRAGMENT TYPE: C-terminal ORIGINAL SOURCE: ORIGINAL SOURCE: ORGANISM: Plasmodium falciparum
 US-09-500-376-2; Sequence 2, Application US/09500376; GENERAL INFORMATION:
 ;
0
 ; TYPE: PRT; ORGANISM: plasmodium falciparum US-09-500-376-2
 , ORGANISM: plasmodium falciparum US-09-500-376-3
 100.0%;
ilarity 100.0%;
Conservative 0
 118 GISYYEKVLAKYKDDLE 134
 118 GISYYEKVLAKYKDDLE 134
 Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
 Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
 1 GISYYEKVLAKYKDDLE 17
 1 GISYYEKVLAKYKDDLE 17
 STRANDEDNESS: single
TOPOLOGY: linear
 MOLECULE TYPE: peptide HYPOTHETICAL: NO
amino acid
 Query Match
Best Local Similarity
Matches 17; Conserv
 MAD
 RESULT 9
US-09-500-376-3
 394
 ; STRAIN:
US-08-195-705-4
 TYPE: PRT
 SEQ ID NO 2
 Matches
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 Dp
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LOCATION: (531)
CTHER INFORMATION: Identity of amino acid sequences at the above locations are un
US-09-417-507-37685
 Sequence 37685, Application US/09417507

Sequence 37685, Application US/09417507

GENERAL INFORMATION:

TITLE OF INVENTION: WOLLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS;

TITLE OF INVENTION: FUNIGATUS FOR DIAGNOSTICS AND THERAPBUTICS

TITLE OF INVENTION: FAMINGS-10

CURRENT APPLICATION NUMBER: US/09/417,507

CURRENT FILING DATE: 1999-10-14

NUMBER OF SEQ ID NOS: 44312

LENGTH: 725
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 Sequence 16, Application US/09500376
Sequence 16, Application US/09500376
Sequence 16, Application
Triving Properties of Hawaii
APPLICANT: University of Hawaii
TITLE OF INVENTION: Baculovirus Produced Plasmodium Falciparum Vaccine
FILE REPERENCE: A-67984
CURRENT APPLICATION NUMBER: US/09/500,376
CURRENT FILING DATE: 200-02-08
PRIOR APPLICATION NUMBER: US/08/195,705
PRIOR FILING DATE: 1994-02-14
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 .;
0
 ;
0
 Length 402;
 54.5%; Score 48; DB 18; Length 725; 75.0%; Pred. No. 1.2e+02; Live 1; Mismatches 2; Indels
 Sequence 380, Application US/09758458; GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVERTION: Nucleic Acids, Proteins, and Antibodies; FILE REFERENCE: PM041
 Indels
 100.0%; Score 88; DB.19;
100.0%; Pred. No. 1.9e-05;
tive 0; Mismatches 0;
 , ORGANISM: plasmodium falciparum
US-09-500-376-16
 NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
 118 GISYYEKVLAKYKDDLE 134
 Query Match
Best Local Similarity 75.0
Matches 9; Conservative
 1 GISYYEKVLAKYKDDLE 17
1 GISYYEKVLAKYKDDLE 17
 Conservative
 ||: |||||||
|170 YEEEFAKYKDDL 181
 5 YEKVLAKYKDDL 16
 ORGANISM: A.fumigatus
 Query Match
Best Local Similarity
Matches 17; Conserv
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Sequence 469, Application US/60141856
 TYPE: PRT
ORGANISM: Drosophila
 ORGANISM: HUMAN
 US-60-230-445-1214
 SEQ ID NO 1214
 LENGTH: 1103
 δ
 qq
 qq
 δy
 RESULT 13
US-09-948-933-336

Sequence 336, Application US/09948933

SEQUENCE 336, Application US/09948933

SERBRAL INFORMATION:
TILLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TILLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
TILLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
TILLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL000787

CURRENT FILING DATE: 2001-09-10

PRIOR FILING DATE: 2001-09-10

PRIOR FILING DATE: 2000-09-08

WUMBER OF SEQ ID NOS: 6404

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 336
 ö
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 CCATION: (28).

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE

CCATION: (60)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE

LOCATION: (96)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE

LOCATION: (113)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
 LOCATION: (114)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-758-458-380
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 Gaps
 ö
 Score 45; DB 21; Length 189;
Pred. No. 69;
 Score 45; DB 23; Length 421;
Pred. No. 1.8e+02;
7; Mismatches 3; Indels
 3; Indels
 7; Mismatches
CURRENT APPLICATION NUMBER: US/09/758,458;
CURRENT FILING DATE: 2001-01-11
SPIGN APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR PILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 520
SOFTWARE: PatentIn Ver: 2.0
SEQ ID NO 380
LENGTH: 189
 51.1%;
41.2%;
 Query Match 51.1%;
Best Local Similarity 41.2%;
Matches 7; Conservative
 92 GIDYYDRNLALFEEELD 108
 1 GISYYEKVLAKYKDDLE 17
 68 GIDYYDRNLALFEEELD 84
 1 GISYYEKVLAKYKDDLE 17
 Ouery Match 51.1
Best Local Similarity 41.2
Matches 7; Conservative
 ORGANISM: Homo sapiens
 TYPE: PRT
ORGANISM: Human
 US-09-948-933-336
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RESULT 14 US-60-141-856-469

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NGS-60-230-445-1214

Sequence 1214, Application US/60230445

Sequence 1214, Application US/60230445

GENERAL INFORMATION:

APPLICANT: Beasley, Ellen

TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: AND USES THEREOF

CURRENT APPLICATION NUMBER: US/60/230,445

CURRENT APPLICATION OFF

CURRENT PILING DATE: 2000-99-06

NUMBER OF SEQ ID NOS: 3051

SOFTWARE: FastSEQ for Windows Version 4.0
 ö
 ö
APPLICANT: KETIAVAGE, Anthony
TITLE OF INVENTION: ISOLATED KINASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: ISOLATED KINASE PROTEINS, AND USES THEREOF
FILE OF INVENTION DUDGEULES ENCODING KINASE PROTEINS, AND USES THEREOF
FILE REFERENCE: CLO00044
CURRENT APPLICATION NUMBER: US/60/141,856
CURRENT FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 617
SEQ ID NO 469
LENGTH: 498
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 Score 45; DB 24; Length 1103;
pred. No. 6e+02;
7; Mismatches 3; Indels
 51.1%; Score 45; DB 24; Length 498;
60.0%; Pred. No. 2.3e+02;
.ive 1; Mismatches 5; Indels
 Search completed: January 29, 2002, 10:56:06 Job time: 2402 sec
 NAME/KEY: VARIANT
COCATION: (1)...(498)
COTHER INFORMATION: Xaa = Any Amino Acid
US-60-141-856-469
 Query Match 51.1%;
Best Local Similarity 41.2%;
Matches 7; Conservative
 1 GISYYEKVLAKYKDDLE 17
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58 GIDYYDRNLALFEEELD 74
 Query Match
Best Local Similarity 60.0
Matches 9; Conservative
 241 SYYRAVLAVHHDDFE 255
 3 SYYEKVLAKYKDDLE 17
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APPLICANT: Anantharamaiah, Gattadahalli
APPLICANT: Navab, Mohamad
TITLE OF INVENTION: Orally Administered Peptides to Ameliorate Atherosclerosis
FILE REFERENCE: 407T-911200US
CURRENT APPLICATION NUMBER: US/09/645,454
 RESULT 1
US-09-978-756-3
 SEQ ID NO 3
LENGTH: 394
 118
 δ
 g
 32, Appl
14, Appl
51280, A
51279, A
51279, A
51278, A
 2018, Ap
5459, Ap
 2, Appli
20, Appl
 Appl
 Appli
Appli
 Appli
 70, Appl
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5.144 Million cell updates/sec
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 Search time 120.95 Seconds
 Sequence 3,
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version 4.5
- 2000 Compugen Ltd.
 US-09-978-756-3

US-09-645-454-32

US-09-645-454-14

US-09-708-427-51280

US-09-708-427-51279

US-09-978-427-51279

US-09-978-427-51279

US-09-978-427-51279

US-09-978-427-51279

US-09-978-427-51279

US-09-117-4158-22

US-09-117-4158-16

US-09-117-4158-16

US-09-117-4158-16

US-09-117-4158-16

US-09-117-4158-16

US-09-269-874A-7

US-09-269-874A-7

US-09-269-874A-7

US-09-620-3948-2020

US-09-66-521-70

US-09-66-521-70

US-09-66-521-70

US-09-966-521-70

US-09-660-3948-2018

US-09-613-481A-20

 US-09-897-516-6447
US-09-897-516-7123
 hits satisfying chosen parameters:
 173191 segs, 36597120 residues
 ٠.
 SUMMARIES
 January 29, 2002, 10:58:13
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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 Pending_Patents_AA_New:*
 Gapop 10.0 , Gapext 0.5
GenCore (c) 1993
 1 GISYYEKVLAKYKDDLE
 US-09-763-397A-13
88
 seq length: 0 seq length: 2000000000
 B
 Length
 Copyright
 BLOSUM62
 Query
Match
 100.0

 Total number of
 Score
 Perfect score:
 4444444444
 Scoring table:
 OM protein
 Minimum DB
Maximum DB
 Database :
 Seguence :
 Searched:
 Run on:
 Result
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ö
5251, Ap
5564, Bp
11298, Ap
11298, Ap
11286, Ap
11286, Ap
11286, Ap
11286, Ap
11286, Ap
11286, Ap
11280, Ap
11534, Ap
 Gaps
 Sequence Seq
 Sequence
Sequence
Sequence
Sequence
 Sequence
 Sequence
 ő
 Length 394;
 Indels
 Score 88; DB 5; L
Pred. No. 4e-06;
Mismatches 0;
 US-09-815-242-12141

US-09-897-516-6564

US-09-815-242-11476

US-09-708-427-10298

US-09-708-427-10440

US-09-708-427-10439

US-09-708-427-10439

US-09-708-427-10439

US-09-708-427-10439

US-09-708-427-12474

US-09-708-427-12474

US-09-108-127-12474

US-09-108-127-12474

US-09-108-127-12474

US-09-108-127-12474

US-09-108-127-12474

US-09-108-127-12474

US-09-108-127-1271

US-09-815-242-11534

US-09-815-242-113392

US-09-815-242-133392
 GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Blidsall, Berry
APPLICANT: Blidsall, Berry
APPLICANT: Feeney, James
APPLICANT: Morgan, William
APPLICANT: Syed, Shabih
TITLE OF INVENTION: Malaria Vaccine
FILE REFERENCE: 18396/1005
CURRENT APPLICATION NUMBER: US/09/978,756
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: OFT/GB00/01558
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN VETSION 3.0
 ALIGNMENTS
 Sequence 32, Application US/09645454 GENERAL INFORMATION:
APPLICANT: Fogelman, Alan
 Query Match 100.0%; S
Best Local Similarity 100.0%; P
Matches 17; Conservative 0;
 ; ORGANISM: Plasmodium falciparum US-09-978-756-3
 GISYYEKVLAKYKDDLE 134
 1 GISYYEKVLAKYKDDLE 17
 US-09-645-454-32
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```
Sequence 51278, Application US/09708427

GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILLE REFERENCE: 2750-12439
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID DATE: 2000-11-09
NUMBER OF SEQ ID DATE: 2000-11-09
 Sequence 51779, Application US/09708427

Sequence 51779, Application US/09708427

GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: THEREBY
FILLE REPERENCE: 2750-1243P

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09

NOWBER OF SEQ ID NOS: 85364

SEQ ID NO 51279

LENGTH: 293
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 Gaps
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 47.7%; Score 42; DB 5; Length 293; 58.3%; Pred. No. 35;
 Length 280;
 1; Indels
 Score 42; DB 5;
Pred. No. 33;
1; Mismatches
 4; Mismatches
 LOCATION: 1..293
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..293
COTHER INFORMATION: Ceres Seq. ID 1926458
US-09-708-427-51279
 NAME/KEY: misc_feature
COGATION: 1..280
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
COGATION: 1..280
UCATION: 1..280
US-09-708-427-51280
2000-11-09
 ORGANISM: Zea mays subsp. mays
 SOFTWARE: PatentIn version 3.1
 47.78;
58.38;
 NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 51280
LENGTH: 280
 Query Match 47.7
Best Local Similarity 58.3
Matches 7; Conservative
 Query Match
Best Local Similarity 58..
7; Conservative
 ORGANISM: Zea mays subsp. FEATURE:
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278 EQIKAKFKDDLD 289
 NAME/KEY: misc_feature LOCATION: 1..293
 1:: ||:|||:
265 EQIKAKFKDDLD 276
 6 EKVLAKYKDDLE 17
 6 EKVLAKYKDDLE 17
 RESULT 6
US-09-708-427-51278
 TYPE: PRT
 g
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 Dp
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 APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
 US-09-645-454-14

Sequence 14, Application US/09645454

GENERAL INFORMATION:
APPLICANT: Fogelman, Alan
APPLICANT: Anantharamaiah, Gattadahalli
APPLICANT: Navab, Mohamad
TITLE OF INVENTION: Orally Administered Peptides to Ameliorate Atherosclerosis
FILE REFERENCE: 407T-911200US
CURRENT APPLICATION WUMBER: US/09/645,454
CURRENT APPLICATION WUMBER: 2000-8-24
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.0
SEQ ID NO 14
LENGTH: 18
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 Gaps
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 ;
 Length 18;
 1; Indels
 Length 14;
 Indels
 Score 42; DB 5;
Pred. No. 1.5;
 CHER INFORMATION: synthetic peptide
NAME/KEY: misc_feature
CATION: (1)...(1)
OTHER INFORMATION: E is blocked with an acetyl
NAME/KEY: misc_feature
LOCATION: (18)...(18)
OTHER INFORMATION: F is blocked with an amide
US-09-645-454-14
 Score 42; DB 5;
Pred. No. 1.1;
3; Mismatches
 CTHER INFORMATION: L is blocked with an acetyl NAME/KEY: misc_feature LOCATION: (14)...(14) CATION: (14)...(14) The RINFORMATION: F is blocked with an amide US-09-645-454-32
 3; Mismatches
 ; Sequence 51280, Application US/09708427; GENERAL INFORMATION:
 OTHER INFORMATION: synthetic peptide NAME/KEY: misc_feature LOCATION: (1)...(1)
 2000-08-24
 47.78;
 TYPE: PRT ORGANISM: Artificial Sequence
 NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.0
SEQ ID NO 32
LENGTH: 14
TYPE: PRT
 47.78;
 ORGANISM: Artificial Sequence FEATURE:
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Best Local Similarity 63.6
Matches 7; Conservative
 Conservative
 4 YYEKVLAKYKD 14
 :||||| |:|:
6 FYEKVLEKFKE 16
 :||||| |:|:
2 FYEKVLEKFKE 12
 4 YYEKVLAKYKD 14
 Query Match
Best Local Similarity
Matches 7; Conserv
 CURRENT FILING DATE:
 US-09-708-427-51280
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Gaps
 APPLICANT: Davidson, Eugene
Yang, Shutong
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition
of a MSAl Peptide
 ö
 NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry D. Coleman, COLEMAN SUDOL SAPONE,
STREET: 714 Colorado Avenue
 Score 41; DB 5; Length 594; Pred. No. 1.1e+02; 4; Mismatches 5; Indels
 COUNTRY: USA
ZIP: 10017
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad (ASCII)
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-Jul-1998
CLASSIFICATION: 435
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad (ASCII)
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-Jul-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
 NAME: COleman, Henry D.
RECISTRATION NUMBER: 32,559
REFERENCE/DOCKET NUMBER: R12-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 679-0090
TELEFA: (212) 679-9121
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
 REFERENCE/DOCKET NUMBER: R12-030 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 679-9121 INFORMATION FOR SEQ ID NO: 22:
 | LENGTH: 594 amino acids | TYPE: amino acids | TYPE: amino acid | TOPOLOGY: linear | MOLECULE TYPE: protein | SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-09-117-415B-2
 STREET: 714 Colorado Avenue
 ATTORNEY/AGENT INFORMATION:
NAME: Coleman, Henry D.
REGISTRATION NUMBER: 32,559
 Sequence 22, Application US/09117415B GENERAL INFORMATION:
 46.68;
 CITY: Bridgeport
STATE: Connecticut
COUNTRY: USA
 CITY: Bridgeport
STATE: Connecticut
 338 LGYYKILSEKYKSDLD 353
 Query Match 46.6
Best Local Similarity 43.8
Matches 7; Conservative
 2 ISYYEKVLAKYKDDLE 17
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 Gaps
 APPLICANT: Davidson, Eugene
APPLICANT: Davidson, Shutong
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition
of a MSAl Peptide
 ;
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry D. Coleman, COLEMAN SUDOL SAPONE, PC
 Score 41; DB 5; Length 376;
Pred. No. 66;
4; Mismatches 5; Indels
 Score 42; DB 5; Length 306;
Pred. No. 37;
 1; Indels
 GENERAL INFORMATION:

APPLICANT: HOLDER, Anthony
APPLICANT: Blidgall, Berry
APPLICANT: Blidgall, Berry
APPLICANT: Breaey, James
APPLICANT: Morgan, William
APPLICANT: Morgan, William
APPLICANT: Morgan, William
APPLICANT: Syed, Shabih
ITTLE OF INVENTION: Walaria Vaccine
FILE REFERENCE: 18396/1065
CURRENT APPLICATION NUMBER: CUT/GB00/01558
FRIOR FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 097/311,817
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN VETSION 3.0
 4; Mismatches
 NAME/KEY: misc_feature
LOCATION: 1..306
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..306
 OTHER INFORMATION: Ceres Seq. ID 1926457
US-09-708-427-51278
 Sequence 2, Application US/09117415B GENERAL INFORMATION:
 ORGANISM: Plasmodium falciparum US-09-978-756-2
 ORGANISM: Zea mays subsp. mays
 Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
 Query Match
Best Local Similarity 43.8%;
Matches 7; Conservative
 : ||: : ||| ||:
120 LGYYKILSEKYKSDLD 135
 NUMBER OF SEQUENCES:
 2 ISYYEKVLAKYKDDLE 17
 |::||:||:|
291 EQIKAKFKDDLD 302
 6 EKVLAKYKDDLE 17
SEQ ID NO 51278
LENGTH: 306
TYPE: PRT
 RESULT 8
US-09-117-415B-2
 LENGTH: 376
 RESULT 7
US-09-978-756-2
 FEATURE
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ATTORNEY/AGENT INFORMATION:
APPLICANT: Davidson, Eugene
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 Gaps
 Sequence 18, Application US/09117415B
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Davidson, Eugene
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition
of a MSAl Peptide
 ;
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0
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry D. Coleman, COLEMAN SUDOL SAPONE,
STREET: 714 Colorado Avenue
 Score 41; DB 5; Length 631;
pred. No. 1.2e+02;
4; Mismatches 5; Indels
 Length 613;
 Score 41; DB 5; Leng. No. 1.1e+02; 5; 7
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/117,415B
TLING DATE: 29-7ul-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 32,559
REPERRENCE/COCKET UNMBER: R12-030
TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad (ASCII)
 SEQUENCE DESCRIPTION: SEQ ID NO: 18: US-09-117-415B-18
 TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-117-4158-22
 Sequence 20, Application US/09117415B GENERAL INFORMATION:
 LENGTH: 631 amino acids
TYPE: amino acid
TOPOLOGY: linear
 679-9121
 INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
 46.6%;
 SEQUENCE CHARACTERISTICS:
 46.68;
43.88;
 ZIP: 10017
COMPUTER READABLE FORM:
 STATE: Connecticut COUNTRY: USA
 NUMBER OF SEQUENCES: 24
 Query Match 46.6
Best Local Similarity 43.8
Matches 7; Conservative
 393 LGYYKILSEKYKSDLD 408
 CITY: Bridgeport
 TYPE: amino acid
 375 LGYYKILSEKYKSDLD 390
 2 ISYYEKVLAKYKDDLE 17
 Conservative
 2 ISYYEKVLAKYKDDLE 17
 'ELEFAX: (212)
 Best Local Similarity
Matches 7; Conserv
 RESULT 11
US-09-117-415B-20
 US-09-117-415B-18
 Query Match
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Gaps
 AAL INFORMATION.
APPLICANT: Addition
Yang, Shutong
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition
of a MSA1 Peptide
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition of a MSA1 Peptide
 ;
0
 Я
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry D. Coleman, COLEMAN SUDOL SAPONE,
STREET: 714 Colorado Avenue
SITREET: Stridgeport
CITY: Bridgeport
STATE: Connecticut
 Coleman, COLEMAN SUDOL SAPONE,
 Indels
 Score 41; DB 5; Le
Pred. No. 1.2e+02;
4; Mismatches 5;
 CURRENT APPLICATION DATA:
REPLICATION UNMERS: US/09/117,415B
FILING DATE: 29-Jul-1998
CLASSIFICATION: 435
 APPLICATION NUMBER: US/09/117,415B FILING DAFE: 29-Jul-1998 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
 REFERENCE/DOCKET NUMBER: R12-030 TELECOMMUNICATION INFORMATION:
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPad (ASCII)
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad (ASCII)
 TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-117-4158-20
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry D. Coleman,
STREET: 714 Colorado Avenue
 NAME: Coleman, Henry D. REGISTRATION NUMBER: 32,559
 RESULT 12
US-09-117-415B-16
; Sequence 16, Application US/09117415B
; GENERAL INFORMATION:
 TELEPHONE: (212) 679-0090
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 LENGTH: 631 amino acids TYPE: amino acid
 679-9121
 CURRENT APPLICATION DATA:
 INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
 46.68;
 CITY: Bridgeport
STATE: Connecticut
COUNTRY: USA
 NUMBER OF SEQUENCES: 24
 Ouery Match
Best Local Similarity 43.5.
..... 7; Conservative
 375 LGYYKILSEKYKSDLD 390
 2 ISYYEKVLAKYKDDLE 17
 NUMBER OF SEQUENCES:
 TELEFAX: (212)
 COUNTRY: USA
 ZIP: 10017
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Gaps

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Score 41; DB 5; Length 1639;
Pred. No. 3.5e+02;
4; Mismatches 5; Indels
 Score 41; DB 5; Length 1621;
Pred. No. 3.5e+02;
4; Mismatches 5; Indels
 TITLE OF INVENTION: Recombinant Process for Preparing a TITLE OF INVENTION: Complete Malaria Antigen, GP190/MSP1. FILE REPERENCE: GROB-003

CURRENT APPLICATION NUMBER: US/09/269,874A

CURRENT FILING DATE: 1999-08-02

PRIOR APPLICATION NUMBER: PCT/EP97/05441

PRIOR PILING DATE: 1995-10-02

PRIOR FILING DATE: 1996-10-02

PRIOR FILING DATE: 1996-10-02

NUMBER: OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 1639
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 Sequence 3, Application US/09269874A GENERAL INFORMATION:
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; ORGANISM: Plasmodium falciparum
US-09-269-874A-5
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 46.6%;
 Query Match
Best Local Similarity 43.8%;
Matches 7; Conservative
 : ||: : ||| ||: 1383 LGYYKILSEKYKSDLD 1398
 : ||: : ||| ||:
1383 LGYYKILSEKYKSDLD 1398
 Query Match
Best Local Similarity 43.8
Matches 7; Conservative
 2 ISYYEKVLAKYKDDLE 17
 2 ISYYEKVLAKYKDDLE 17
 APPLICANT: Bujard, Hermann
 RESULT 15
US-09-269-874A-3
 LENGTH: 1621
 SEQ ID NO 5
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 Sequence 7, Application US/09269874A

Sequence 7, Application US/09269874A

GENERAL INFORMATION:

APPLICANT: BUJACH, Hermann

TITLE OF INVENTION: Recombinant Process for Preparing a

TITLE OF INVENTION: Complete Malaria Antigen, GP190/MSP1

FILE REFERENCE: GRUE-003

CURRENT FILING DATE: 1999-08-02

PRIOR APPLICATION NUMBER: DCT/EP97/05441

PRIOR APPLICATION NUMBER: DE 19640817.2

PRIOR FILING DATE: 1997-10-02

PRIOR FILING DATE: 1996-10-02

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7

LENGTH: 1602

TYPE: PRT
 Sequence 5, Application US/09269874A
GENERAL INFORMATION:
APPLICANT: Buljard, Hermann
TITLE OF INVENTION: Recomblinant Process for Preparing a
TITLE OF INVENTION: Complete Malaria Antigen, GP190/MSP1
FILE REFERENCE: GRUE-003
CURRENT APPLICATION NUMBER: US/09/269,874A
CURRENT FILING DATE: 1999-08-02
PRIOR FILING DATE: 1997-10-02
PRIOR FILING DATE: 1997-10-02
PRIOR FILING DATE: 1996-10-02
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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 Length 649;
 Score 41; DB 5; Length low Pred, No. 3.4e+02;
 Score 41; DB 5; Length 649
Pred. No. 1.2e+02;
4; Mismatches 5; Indels
 4; Mismatches
NAME: COleman, Henry D.
RECISTRATION NUMBER: 32,559
REFERENCE/DOCKET NUMBER: R12-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 679-0090
TELEFA: (212) 679-9121
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
 LENGTH: 649 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-117-4158-16
 ; ORGANISM: Plasmodium falciparum
US-09-269-874A-7
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Best Local Similarity 43.8%;
Matches 7; Conservative
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Best Local Similarity 43.8%;
 393 LGYYKILSEKYKSDLD 408
 7; Conservative
 2 ISYYEKVLAKYKDDLE 17
 2 ISYYEKVLAKYKDDLE 17
 US-09-269-874A-5
 Matches
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Gaps

us-09-763-397a-12.rapm

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 2, Appli
2, Appli
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2, Appli
1, Appli
10, Appli
10, Appl
 Sequence 12, App.
 January 29, 2002, 10:56:05; Search time 1760.55 Seconds (Without alignments) 2:996 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 2, Al
Sequence 2, Al
Sequence 1, Al
Sequence 10, Al
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GenCore version 4.5
(c) 1993 - 2000 Compugen Ltd
 /cgn2_6/ptodata/2/paa/US60_COMB.pep:
 US-09-763-397A-12
US-09-125-031-2
US-09-125-031B-2
US-09-125-031B-2
US-09-134-333-2
US-09-311-817-1
US-09-125-031B-10
US-09-125-031B-10
 Total number of hits satisfying chosen parameters:
 3148936 seqs, 277657034 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

 protein search, using sw model

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1 EDSGSNGKKITCECTKPDS 19
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Gapop 10.0 , Gapext 0.5
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 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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112
113
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 Match
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 Title:
Perfect score:
 Scoring table:
 106
106
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106
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 OM protein
 Searched:
 Sequence:
 Database
 Run on:
 Result
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APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the Department of Health and Human Services, Centers for APPLICANT: Secretary of the Department of Health and Human Services, Centers for APPLICANT: Lal, Altaf A. APPLICANT: Lal, Altaf A. APPLICANT: Ping Shi, Ya APPLICANT: Ping Shi, Ya APPLICANT: Ping Shi, Ya APPLICANT: Ping Shi, Ya APPLICANT: Pologonia Multivalent Malarial Vaccine Against Plasmodium Fa FILE REFERENCE: 6395-57049
CURRENT APPLICATION NUMBER: US 60/097,703
PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR APPLICATION NUMBER: PCT / US99/18869
PRIOR PLICATION NUMBER: PCT / US99/18869
 sequence 8, Appli
Sequence 2, Appli
Sequence 11, Appl
Sequence 12, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 13, Appli
Sequence 2, Appli
Sequence 11, Appli
Sequence 11, Appli
 Sequence 2, Appli
Sequence 2, Appli
Sequence 16, Appli
Sequence 2, Appli
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Sequence 2, Appli
Sequence 22, Appli
 Sequence 2, Appl
Sequence 22, Appl
Sequence 12, Appl
Sequence 18, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 16, Appl
Sequence 16, Appl
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 Gaps
 Sequence 4,
 Sequence 3,
Sequence 3,
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 Length 19;
 Indels
US-09-134-333-10

US-09-125-0311-5

US-09-125-0318-5

US-09-125-0318-8

US-09-175-683-11

US-09-175-683-11

US-09-175-683-13

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US-08-195-176-16

US-08-195-176-16

US-08-195-176-16

US-08-197-176-16

US-08-197-176-16

US-08-177-1615-2

US-08-117-415-2

US-08-593-006-20
 Score 106; DB 21;
Pred. No. 4.3e-08;
Mismatches 0;
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US-09-117-415-20
US-08-593-006-16
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 US-07-867-768A-3
US-08-195-705-3
 US-09-269-874-3
 US-09-500-376-4
 ALIGNMENTS
 Sequence 12, Application US/09763397A GENERAL INFORMATION:
 100.0%; Sc
100.0%; Pr
tive 0;
 ORGANISM: Plasmodium falciparum
US-09-763-397A-12
 NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
 Query Match
Best Local Similarity 100.(
Matches 19; Conservative
 US-09-763-397A-12
 SEQ ID NO 12
LENGTH: 19
 PRT
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Gaps

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Indels

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Mismatches
 US-09-125-031B-2; Sequence 2, Application US/09125031B; GENERAL INFORMATION:
 LONGACRE-ANDRE, SHIRLEY ROTH, CHARLES BARNWELL, JOHN
 .
()
 TYPE: PRT
ORGANISM: Artificial Sequence
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 FDSGSNGKKITCECTKPDS 85
 1 EDSGSNGKKITCECTKPDS 19
 85
 13
 EDSGSNGKKITCECTKPDS
 Conservative
 1 EDSGSNGKKITCECTKPDS
 19;
 SEQ ID NO 2
LENGIH: 95
 TYPE: PRT
 29
 Matches
 67
 δλ
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 g
 GENERAL INFORMATION:

APPLICANT: ROTH, CHARLES

APPLICANT: MENDIS, KAMINI

APPLICANT: MATO, FARIDABANO

TITLE OF INVENTION: RECOMBINING A C-TERMINAL FRAGMENT OF

TITLE OF INVENTION: PLASMODIUM MSP-1

FILE REFERENCE: 0660-0139-0xPCT

CURRENT APPLICATION NUMBER: 05/09/125,031A

CURRENT FILING DATE: 1999-03-10

PRIOR APPLICATION NUMBER: PCT/FR97/00290

PRIOR APPLICATION NUMBER: FP66/01822

PRIOR FILING DATE: 1999-02-14

NUMBER OF SEQ ID NOS: 15

SEQ ID NO 2

LENGTH: 95

LENGTH: 95
 Sequence 2, Application US/09125031

Sequence 2, Application US/09125031

GENERAL INFORMATION:
APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: NOTH, CHARLES
APPLICANT: NOTH, CHARLES
APPLICANT: NOTH, CHARLES
APPLICANT: MENDIS, KAMINI
CURRENT PRINCHO: NOG60-0139-0xPCT
CURRENT PRILING DATE: 1999-03-10
BARLIER APPLICATION NUMBER: PCT/FR97/00290
BARLIER PILING DATE: 1995-02-14
BARLIER FILING DATE: 1996-02-14
NUMBER OF SEQ ID NOS: 14
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 ; FEATURE:
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Pred. No. 2.1e-07;
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Pred. No. 2.1e-07;
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APPLICANT: LONGACRE-ANDRE, SHIRLEY
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 Query Match
Best Local Similarity 100.0%;
Matches 19; Conservative 0.
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 ORGANISM: Artificial Sequence
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 FEATURE:
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Sequence 2, Application US/09134333

Sequence 2, Application US/09134333

GENERAL INFORMATION:

APPLICANT: LOGGACRE-ANDRE, SHIRLEY

APPLICANT: ROTH, CHARLES

APPLICANT: NOTH, CHARLES

APPLICANT: NATIO, FRIDABANO

APPLICANT: MENDIS, KAMINI

TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF

TITLE OF INVENTION: PLASMODIUM MSP-1

FILE REFERENCE: 0660-0135-0XCIP

CURRENT EPLING DATE: 1999-04-18

EARLIER APPLICATION NUMBER: PCT/FR97/00290

EARLIER APPLICATION NUMBER: PCT/FR97/00290

EARLIER FILING DATE: 1999-04-18

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 2

LENGTH: 95

LENGTH: 95
APPLICANT: ROTH, CHARLES
APPLICANT: BARNWELL, JOHN
APPLICANT: BARNWELL, JOHN
APPLICANT: MATO, FARIDABANO
TITLE OF INVENTION: PLASMODIUM MSP-1
TITLE OF INVENTION: PLASMODIUM MSP-1
TITLE OF INVENTION: PLASMODIUM MSP-1
FILE REPERENCE: 0660-0139-0XPCT
CURRENT APPLICATION NUMBER: US/09/125,031B
CURRENT FILING DATE: 1997-02-14
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1996-02-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PALENTIN Ver. 2.1
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US-09-134-333-2
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Matches 19; Conservative 0; Mismatches 0;
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US-09-125-031B-10
Sequence 10, Application US/09125031B
Sequence 10, Application US/09125031B
Sequence 10, Application SHIRLEY
APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: ROTH, CHARLES
APPLICANT: MATO, FARIDABAN
APPLICANT: MATO, FARIDABAN
TITLE OF INVENTION: PLASMODIUM MSP-1
FILE REPRENCE: 0660-0139-0XPCT
CURRENT APPLICATION NUMBER: US/09/125,031B
CURRENT FILING DATE: 1999-03-10
FRIOR APPLICATION NUMBER: PCT/FR97/00290
FRIOR APPLICATION NUMBER: FR96/01822
FRIOR PILING DATE: 1999-02-14
FRIOR PILING DATE: 1996-02-14
SRIOR FILING DATE: 1996-02-14
SRIOR FILING DATE: 1998-02-14
SRIOR FILING DATE: 1998-02-14
SOFTWARE: PATENTING DATE: 1996-02-14
FRIOR FILING DATE: 1996-02-14
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SERVERAL INFORMATION:
APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: ROTH, CHARLES
APPLICANT: ROTH, CHARLES
APPLICANT: ROTH, CHARLES
APPLICANT: MENDIS, KAMINI
APPLICANT: MATO, FARIDABANO
TITLE OF INVENTION: PLASMODIUM MSP-1
FILLE REFRENCE: 0660-0139-0xPCT
FILLE REFRENCE: 0660-0139-0xPCT
CURRENT APPLICANTION NUMBER: US/09/125,031A
CURRENT APPLICATION NUMBER: PCT/FR97/00290
PRIOR APPLICATION NUMBER: FR96/01822
PRIOR FILING DATE: 1996-02-14
PRIOR FILING DATE: 1996-02-14
NUMBER: PSOFTWARE: PALGATION NUMBER: R96/01822
NUMBER OF SEQ ID NOS: 15
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SEQ ID NOS: 15
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Matches 19; Conservative
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Best Local Similarity
Matches 19; Conserv
 US-09-125-031B-10
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 APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: ROTH, CHARLES
APPLICANT: NATO, FARIDABANO
APPLICANT: NATO, FARIDABANO
APPLICANT: NATO, FARIDABANO
APPLICANT: NATO, FARIDABANO
APPLICANT: MENDIS, KAMINI
APPLICANT: MENDIS, KAMINI
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: PLASMODIUM MSP-1
TITLE OF INVENTION: PLASMODIUM MSP-1
FILE REFERENCE: 0660-0139-0xPCT
CURRENT APPLICATION NUMBER: US/09/125,031
CURRENT FILING DATE: 1999-03-10
EARLIER PLLING DATE: 1997-02-14
EARLIER FILING DATE: 1996-02-14
NUMBER OF SEQ ID NOS: 14
SEGUTARE: PALENTING DATE: 1996-02-14
NUMBER OF SEQ ID NOS: 14
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 Length 95;
 Length 96;
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100.0%; Pred. No. 2.4e-07;
iive 0; Mismatches 0;
 Score 106; DB 15;
Pred. No. 2.1e-07;
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TITLE OF INVENTION:
Malaria Vaccine
FILE REFERENCE: 18396-1210
CURRENT APPLICATION NUMBER: US/09/311,817
CURRENT FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
ERNGTH: 96
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 US-09-125-031-10
; Sequence 10, Application US/09125031
; GENERAL INFORMATION:
 US-09-311-817-1; Sequence 1, Application US/09311817; GENERAL INFORMATION:
 ; ORGANISM: Plasmodium falciparum
US-09-311-817-1
 ORGANISM: Plasmodium falciparum
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 1 EDSGSNGKKITCECTKPDS 19
 65 EDSGSNGKKITCECTKPDS 83
 80 EDSGSNGKKITCECTKPDS 98
 1 EDSGSNGKKITCECTKPDS 19
 Ouery Match
Best Local Similarity 100.0
Watches 19; Conservative
 Ouery Match
Best Local Similarity 100.
Matches 19; Conservative
 Query Match 100.0
Best Local Similarity 100.0
Matches 19; Conservative
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SOFTWARE: Pat
SEQ ID NO 5
LENGTH: 116
 TYPE: PRT
 FEATURE:
 FEATURE:
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 SCHEMAL INFORMATION:

APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: NATO, FARIDABANO
APPLICANT: NATO, FARIDABANO
TAPLICANT: BARNWELL, JOHN
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: REASMODIUM MSP-1
FILE REFERENCE: 0660-0139-0XPCT
CURRENT APPLICATION NUMBER: US/09/125,031
CURRENT FILING DATE: 1999-03-10
EARLIER APPLICATION NUMBER: PCT/FR97/00290
EARLIER PILING DATE: 1997-02-14
EARLIER FILING DATE: 1996-02-14
NUMBER OF SEQ 1D NOS: 14

SOCTWARE PARLICATION UNUMBER: PCT/FR97/00290
SARLIER FILING DATE: 1996-02-14
NUMBER OF SEQ 1D NOS: 14
 Sequence 10, Application US/09134333

GENERAL INFORMATION:
APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: ROTH GHARLES
APPLICANT: ROTH CHARLES
APPLICANT: BARNWELL, JOHN
APPLICANT: BERNWELL, JOHN
APPLICANT: PROPERING
FILE OF INVENTION: PLASMODIUM MSP-1
FILE REPRENCE: 0660-0135-0XCIP
CURRENT PLILIG DATE: 1999-04-18
EARLIER APPLICATION NUMBER: PROF/09/194, 333
CURRENT FILING DATE: 1999-02-14
EARLIER APPLICATION NUMBER: FR96/01822
EARLIER PILING DATE: 1996-02-14
SEARLIER PILING DATE: 1996-02-14
SOFTWARD PROPERIOR OF SEQ ID NOS: 14
NUMBER OF SEQ ID NOS: 14
NUMBER OF SEQ ID NOS: 14
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Matches 19; Conservative 0; Mismatches 0;
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 ORGANISM: Plasmodium falciparum US-09-134-333-10
 67 EDSGSNGKKITCECTKPDS 85
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 1 EDSGSNGKKITCECTKPDS 19
 SOFTWARE: PatentIn Ver. 2.1
 Conservative
 Query Match
Best Local Similarity
Matches 19; Conserv
 SEQ ID NO 5
LENGTH: 116
TYPE: PRT
US-09-134-333-10
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```
GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: ROTH, CHARLES

APPLICANT: ROTH, CHARLES

APPLICANT: ROTH, CHARLES

APPLICANT: ROTH, CHARLES

APPLICANT: MENDIS, KAMINI

APPLICANT: MATO, FARIDABANO

TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF

TITLE OF INVENTION: PLASMODIUM MSP-1

FILE REPERENCE: 0660-0139-0xPCT

CURRENT APPLICATION NUMBER: USC/09/125,031A

CURRENT FILING DATE: 1999-03-10

PRIOR APPLICATION NUMBER: PCT/FR97/00290

PRIOR APPLICATION NUMBER: EP96/01822

PRIOR FILING DATE: 1999-02-14

NUMBER OF SEQ ID NOS: 15

SEQ ID NO 5

LENGTH: 116
 Sequence 5, Application US/09125031B

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BARWELL, JOHN
APPLICANT: BARWELL, JOHN
APPLICANT: BARWELL, JOHN
APPLICANT: MENDIS, KAMINI
APPLICANT: MENDIS, KAMINI
APPLICANT: NATO, FARIDABANO
TITLE OF INVENTION: PLASMODIUM MSP-1
FILE REFERENCE: 0660-0139-0XPCT
CURRENT APPLICATION NUMBER: US/09/125,031B
CURRENT FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: PCT/FR97/00290
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100.0%; Pred. No. 2.6e-07;
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 1997-02-14
MBER: FR96/01822
1996-02-14
Sequence 5, Application US/09125031A GENERAL INFORMATION:
APPLICANT: LONGACRE-ANDRE, SHIRLEY
 TYPE: PRT
ORGANISM: Artificial Sequence
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 1 EDSGSNGKKITCECTKPDS 19
 67 EDSGSNGKKITCECTKPDS 85
 PatentIn Ver. 2.1
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Best Local Similarity 100.
Matches 19; Conservative
 PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1996-0:
NUMBER OF SEQ ID NOS: 15
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GENERAL INFORMATION:
APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: ROTH, CHARLES
APPLICANT: ROTH, CHARLES
APPLICANT: BARNWELL, JOHN
CURRENT APPLICATION NUMBER: US/09/134,333
CURRENT APPLICATION NUMBER: PCT/FR97/00290
EARLIER APPLICATION NUMBER: PCT/FR97/00290
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EARLIER PILING DATE: 1996-02-14
NUMBER OF SEQ ID NOS: 14
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 APPLICANT: NATO, FARIDER,
APPLICANT: NATO, FARIDEBANO
APPLICANT: NATO, FARIDEBANO
APPLICANT: NATO, FARIDEBANO
APPLICANT: BARNWELL, JOHN
APPLICANT: MENDIS, KAMINI
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: PLASHODIUM MSP-1
FILE REFERENCE: 0660-0139-0XPCT
CURRENT APPLICATION NUMBER: US/09/125,031
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SOFTWARE PERENCE: PCT/FR97/00290
SOFTWARE PILING DATE: 1996-02-14
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100.0%; Score 106; DB 15;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
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 ; ORGANISM: Plasmodium falciparum US-09-125-031-8
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 67 EDSGSNGKKITCECTKPDS 85
 67 EDSGSNGKKITCECTKPDS 85
 1 EDSGSNGKKITCECTKPDS 19
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US-09-708-427-27613
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GENERAL INFORMATION:
APPLICANT: Holder, Anthony
APPLICANT: Birdsall, Berry
APPLICANT: Feeney, James
APPLICANT: Feeney, James
TITLE OF INVENTION: Malaria Vaccine
FILE REFERENCE: 18396/1005
CURRENT APPLICATION NUMBER: US/09/978,756
CURRENT FILING DATE: 2001-10-16
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 PRIOR PELICATION NUMBER: PCT/GB00/01558
PRIOR PELING DATE: 2000-04-20
PRIOR PELICATION NUMBER: PCT/GB00/01558
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PRIOR PELICATION NUMBER: 2,271,451
PRIOR APPLICATION NUMBER: 9909072.2
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PRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.0
 APPLICANT: Holder, Anthony
APPLICANT: Birdsall, Berry
APPLICANT: Feeney, James
APPLICANT: Morgan, William
APPLICANT: Syed, Shabih
TITLE OF INVENTION: Malaria Vaccine
 ; Sequence 2, Application US/09978756 ; GENERAL INFORMATION:
 ;
 ORGANISM: Plasmodium falciparum
 100.0%;
 1 EDSGSNGKKITCECTKPDS 19
 Query Match
Best Local Similarity 100.
Matches 19; Conservative
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udriririri diriririri
3377778
 RESULT 2
US-09-978-756-2
 US-09-978-756-1
 US-09-978-756-1
 SEQ ID NO 1
LENGTH: 96
 40.5
 0000000000
 65
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Gaps

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Indels

. 0

Mismatches

; 0

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Conservative
 RESULT 4
US-09-117-415B-22
 19;
 545
 Matches
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 QQ
 ;
0
 Sequence 2, Application US/09117415B
Sequence 2, Application:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Davidson, Eugene
Yang, Shutong
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition
of a MSA1 Peptide
 ó
 Length 594;
 Length 376;
 CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry D. Coleman, COLEMAN SUDOL SAPONE,
STREET: 714 Colorado Avenue
CITY: Bridgeport
STATE: Connecticut
 Indels
 100.0%; Score 106; DB 5; 100.0%; Pred. No. 1.3e-08;
 Query Match
100.0%; Score 106; DB 5;
Best Local Similarity 100.0%; Pred. No. 8.5e-09;
Matches 19; Conservative 0; Mismatches 0;
 COMPUTA: COMPECTICAL
COMPUTA: TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: WARTEN PC SYSTEM: PC DOS/MS-DOS
SOFTWARE: WARTEN (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-Jul-1998
CLASSIFICATION: 435
 ATTORNEY STELLINGNATION:
NAME: COleman, Henry D.
REGISTRATION NUMBER: 32,559
REFERENCE/DOCKET NUMBER: R12-030
TELECOMMUNICATION INFORMATION:
TELEPAN: (212) 679-0090
TELEPAN: (212) 679-9121
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
 FILE REFERENCE: 18396/1005
CURRENT APPLICATION NUMBER: US/09/978,756
CURRENT FILING DATE: 2001-10-16
PRIOR PRICATION NUMBER: PCT/GB00/01558
PRIOR PILING DATE: 1000-04-20
PRIOR APPLICATION NUMBER: 09/311,817
PRIOR APPLICATION NUMBER: 2,271,451
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN VETSION 3.0
SEQ ID NO
 ; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-117-415B-2
 LENGTH: 594 amino acids TYPE: amino acid
 ; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-09-978-756-2
 327 EDSGSNGKKITCECTKPDS 345
 NUMBER OF SEQUENCES: 24
 1 EDSGSNGKKITCECTKPDS 19
 Query Match
Best Local Similarity
 RESULT 3
US-09-117-415B-2
 LENGTH:
 Dp
 ó
```

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Gaps
 RESULT 5
US-09-117-415B-18
US-09-117-415B-18
SEQUENCE 18, Application US/09117415B
GENERAL INFORMATION:
APPLICANT: Davidson, Eugene
APPLICANT: Davidson, Eugene
Yang, Shutong
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition
Of a MSAl Peptide
 ö
 Yang, Shutong
TITLE OF INVENTION: malaria Vaccine Based Upon the Addition of a MSA1 Peptide
 NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: Henry D. Coleman, COLEMAN SUDOL SAPONE,
STREET: 714 Colorado Avenue
CITY: Bridgeport
STATE: Connecticut
COUNTRY: USA
 Length 613;
 NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: Henry D. Coleman, COLEMAN SUDOL SAPONE,
STREET: 714 Colorado Avenue
CITY: Bridgeport
STATE: Connecticut
COUNTRY: USA
ZIP: 10017
 Indels
 100.0%; Score 106; DB 5;
100.0%; Pred. No. 1.3e-08;
1ve 0: Mismatches 0;
 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WOAGPAd (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,415B
FILLING DATE: 29-Jul-1998
CLASSIFICATION: 1 INFORMATION:
 Mismatches
 REFERENCE/DOCKET NUMBER: R12-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 679-0090
TELEFAX: (212) 679-9121
 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-117-415B-22
 NAME: Coleman, Henry D. REGISTRATION NUMBER: 32,559
 Sequence 22, Application US/09117415B
GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERESTICS:
LENGTH: 613 amino acida
TYPE: amino acid
 ö
 APPLICANT: Davidson, Eugene
 582 EDSGSNGKKITCECTKPDS 600
 1 EDSGSNGKKITCECTKPDS 19
 HILLHILLHILLHILLH EDSGSNGKKITCECTKPDS 563
1 EDSGSNGKKITCECTKPDS 19
 Query Match 100. Best Local Similarity 100. Matches 19; Conservative
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Gaps
 Gaps
 Yang, Shutong
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition
of a MSAl Peptide
 ö
 ö
 Length 631;
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry D. Coleman, COLEMAN SUDOL SAPONE,
STREET: 714 Colorado Avenue
 Length 649;
 Indels
 Indels
 "Sequence 7, Application US/09269874A
Sequence 7, Application US/09269874A
GENERAL INFORMATION:
APPLICANT: Bujard, Hermann
TITLE OF INVENTION: Recombinant Process for Preparing a
TITLE OF INVENTION: Complete Malaria Antigen, GP190/MSP1
FILE REFERENCE: GRUE-003
 Score 106; DB 5;
Pred. No. 1.4e-08;
Mismatches 0;
 100.0%; Score 106; DB 5;
100.0%; Pred. No. 1.4e-08;
tive 0; Mismatches 0;
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-Jul-1998
CLASSIFICATION: 435
 NAME: Coleman, Henry D.
REGISTRATION NUMBER: 32,559
REFERENCE/DOCKET NUMBER: R12-030
 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-117-415B-16
) MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-117-415B-20
 Sequence 16, Application US/09117415B GENERAL INFORMATION:
 TELECOMMUNICATION INFORMATION
 LENGTH: 649 amino acids TYPE: amino acid
 TELEPHONE: (212) 679-00
TELEFAX: (212) 679-9121
 APPLICANT: Davidson, Eugene
 ATTORNEY/AGENT INFORMATION:
 ö
 100.0%;
100.0%;
 582 EDSGSNGKKITCECTKPDS 600
 INFORMATION FOR SEQ ID NO: 16:
 600 EDSGSNGKKITCECTKPDS 618
 SEQUENCE CHARACTERISTICS
 1 EDSGSNGKKITCECTKPDS 19
 CITY: Bridgeport
STATE: Connecticut
 1 EDSGSNGKKITCECTKPDS 19
 Conservative
 Conservative
 NUMBER OF SEQUENCES:
 COUNTRY: USA
 ZIP: 10017
 Query Match
Best Local Similarity
Matches 19; Conserv
 Query Match
Best Local Similarity
Matches 19; Conserv
 US-09-117-415B-16
 g
 Вb
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 Gaps
 TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition of a MSA1 Peptide
 ö
 ADDRESSEE: Henry D. Coleman, COLEMAN SUDOL SAPONE, PC
 Length 631;
 Indels
 100.0%; Score 106; DB 5;
100.0%; Pred. No. 1.4e-08;
tive 0; Mismatches 0;
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WOLGBAd (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,415B
FLILIG DATE: 29-JU1-1998
ATTORNEY/AGRNY THINCELLES
 COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM FC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPad (ASCII)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/117,415B

FILING DATE: 29-Jul-1998

CLASSIFICATION: 435
 NAME: COLEMAN, Henry D.
REGISTRATION NUMBER: 32,559
REFERENCE/DOCKET WUMBER: R12-030
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 679-090
TELEFAX: (212) 679-9121
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 631 amino acids
TYPE: anino acid
 ATTORNEY/AGENT INFORMATION:
NAME: Coleman, Henry D.
RECISTRATION NUMBER: 32,559
REFERENCE/DOCKET NUMBER: R12-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 679-0921
 TOPOLOGY: 11near

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-117-4158-18
 STREET: 714 Colorado Avenue
 Sequence 20, Application US/09117415B
GENERAL INFORMATION:
APPLICANT: Davidson, Eugene
 SEQUENCE CHARACTERISTICS:
LENGTH: 631 amino acids
TYPE: amino acid
 INFORMATION FOR SEQ ID NO: 20:
 600 EDSGSNGKKITCECTKPDS 618
 CITY: Bridgeport
STATE: Connecticut
 NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
 Query Match
Best Local Similarity 100.(
Matches 19; Conservative
 TOPOLOGY: linear
 COUNTRY: USA
 US-09-117-415B-20
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; LENGTH: 1639
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-09-269-874A-3
 Query Match
Best Local Similarity 89.5'
Matches 17; Conservative
 Query Match 100.0
Best Local Similarity 100.0
Matches 19; Conservative
 NAME/KEY: misc_feature LOCATION: 1..162
 RESULT 12
US-09-708-427-58009
 RESULT 11
US-09-978-756-3
 SEQ ID NO 3
 FEATURE:
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 Gaps
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0
 Length 1621;
 Length 1602;
 JOSEPH 200-209-8044-3

Sequence 3, Application US/09269874A

Sequence 3, Application US/09269874A

Sequence 3, Application US/09269874A

Sequence 3, Application US/09269874A

TITLE OF INVENTION: Recombinant Process for Preparing a

TITLE OF INVENTION: Complete Malaria Antigen, GP190/MSP1

FILE REFERENCE GRUE-003

CURRENT APPLICATION NUMBER: US/09/269,874A

CURRENT FILING DATE: 1997-08-02

PRIOR PAPLICATION NUMBER: DE 19640817.2

PRIOR PILING DATE: 1996-10-02

PRIOR FILING DATE: 1996-10-02

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0
 APPLICANT BUJATO, Hermann

TITLE OF INVENTION: Recombinant Process for Preparing a
TITLE OF INVENTION: Complete Malaria Antigen, GP190/MSP1
TITLE OF THE REPRENCE: GRUE-003
CURRENT FILING DATE: 1999-08-02
PRIOR APPLICATION NUMBER: PCT/FEP97/05441
PRIOR APPLICATION NUMBER: DE 1964-002
PRIOR APPLICATION NUMBER: DE 1964-0817.2
PRIOR APPLICATION NUMBER: DE 1964-002
NUMBER OF SEQ. ID NOS: 8
SOFTWARE: FASELSEQ for Windows Version 4.0
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 100.0%; Score 106; DB 5;
100.0%; Pred. No. 3.3e-08;
Live 0; Mismatches 0;
 100.0%; Score 106; DB 5; 100.0%; Pred. No. 3.3e-08;
 0; Mismatches
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 Sequence 5, Application US/09269874A GENERAL INFORMATION:
 ORGANISM: Plasmodium falciparum
US-09-269-874A-5
) OKGANISM: Plasmodium falciparum US-09-269-874A-7
 Db 1590 EDSGSNGKKITCECTKPDS 1608
 Db 1571 EDSGSNGKKITCECTKPDS 1589
 1 EDSGSNGKKITCECTKPDS 19
 1 EDSGSNGKKITCECTKPDS 19
 Query Match 100.
Best Local Similarity 100.
Matches 19; Conservative
 19; Conservative
 Query Match
Best Local Similarity
 RESULT 9
US-09-269-874A-5
 SEQ ID NO 7
LENGTH: 1602
 TYPE: PRT
 Matches
 δy
```

```
APPLICANT: N. ALEXANDROW et al.
APPLICANT: N. ALEXANDROW et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1249
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 58009
LENGTH: 162
 6
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 Gaps
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 Length 1639;
 87.7%; Score 93; DB 5; Length 394;
89.5%; Pred. No. 8.4e-07;
tive 1; Mismatches 1; Indels
100.0%; Score 106; DB 5;
100.0%; Pred. No. 3.3e-08;
iive 0; Mismatches 0;
 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Holder, Anthony
APPLICANT: Holder, James
APPLICANT: Breeney, James
APPLICANT: Morgan, William
APPLICANT: Syed, Shabih
TITLE OF INVENTION: Malaria Vaccine
FILE REFERENCE: 18396/1065
CURRENT APPLICATION NUMBER: US/09/978,756
CURRENT FILING DATE: 2001-10-16
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 3
SOSTWARRE: PATENTIN VETSION 33.0
 Sequence 58009, Application US/09708427; GENERAL INFORMATION:
 ; Sequence 3, Application US/09978756; GENERAL INFORMATION:
 ORGANISM: Plasmodium falciparum
US-09-978-756-3
 TYPE: PRT
ORGANISM: Zea mays subsp. mays
 DD 1590 EDSGSNGKKITCECTKPDS 1608
 345 EDSGSSRKKITCECTKPDS 363
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 1 EDSGSNGKKITCECTKPDS 19
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Search completed: January 29, 2002, 10:58:13
Job time: 2509 sec
 3 SGSNGKKITCECT 15
 | || || || || || || SNSNHKKLTCAAT 26
 Silva, Jeff
 Query Match
Best Local Similarity
Matches 11; Conserva
 APPLICANT:
APPLICANT:
APPLICANT:
 Query Match
 ò
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 g
 APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
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 Length 162;
 Length 609
 3; Indels
 5; Indels
 Score 45; DB 5;
Pred. No. 7.5;
2; Mismatches
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 1; Mismatches
 : NAME/KEY: misc_feature

: LCCATION: 1..162

: OTHER INFORMATION: Ceres Seq. ID 1941076

US-09-708-427-58009
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 ; ORGANISM: Saccharomyces cerevisiae US-09-801-368-50
 Sequence 50, Application US/09487558 GENERAL INFORMATION:
 42.5%;
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 APPLICANT: Busby, Robert
APPLICANT: Call, Brian
APPLICANT: Hecht, Peter
APPLICANT: Hocker
APPLICANT: Hocker
APPLICANT: Madden, Kevin
 Query Match
Best Local Similarity 50.0 Matches 7; Conservative
 Hecht, Peter
Holzaman, Doug
Madden, Kevin
Maxon, Mary
Milne, Todd
Norman, Thea
Royer, John
Salama, Sofie
 Best Local Similarity 57.9
Matches 11; Conservative
OTHER INFORMATION: Xaa is
 Sherman, Amir
Silva, Jeff
 128 GSRGRRSPCTCTPP 141
 4 GSNGKKITCECTKP 17
 APPLICANT: Busby, Robert APPLICANT: Call, Brian
 Maxon, Mary
Milne, Todd
 Norman, The
Royer, John
 RESULT 14
US-09-487-558-50
 APPLICANT:
APPLICANT:
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 Query Match
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RESULT 15
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Sequence 31899, Application US/09708427
SEQUENCE 31899, Application US/09708427
SEQUENCE 31899, APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
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SEQ ID NO 31899
LENGTH: 230
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production
TITLE OF INVENTION: in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/487,558
CURRENT APPLICATION NUMBER: US/09/801,368
PRIOR APPLICATION NUMBER: US/09/801,368
PRIOR PELING DATE: 2001-03-07
PRIOR PELING DATE: 2001-03-07
PRIOR PELING DATE: 2000-01-19
PRIOR PELING DATE: 1999-10-20
PRIOR PELING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: PATENTIAN VERSION 3.0
SEQ ID NO 50
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 Gaps
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 40.6%; Score 43; DB 5; Length 609; ilarity 57.9%; Pred. No. 51; Conservative 1; Mismatches 3; Indels
 39.6%; Score 42; DB 5; Length 230; 61.5%; Pred. No. 30;
 4; Indels
 1; Mismatches
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CATUTON: 1..230
OTHER INFORMATION: Saa is any amino acid
NAME/KEY: misc_feature
CATUTON: 1..230
COCATION: 1..230
SOTHER INFORMATION: Ceres Seq. ID 1833059
 ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-487-558-50
 ORGANISM: Arabidopsis thaliana
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 Best Local Similarity 61.5
Matches 8; Conservative
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 3148936 seqs, 277657034 residues
 January 29, 2002, 10:56:04
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

 protein search, using sw model

 Pending_Patents_AA_Main:*
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 1 NSGCFRHLDEREECKCLL 18
 US-09-763-397A-11
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 Perfect score:
 Scoring table:
 OM protein
 Database :
 Searched:
 Sequence:
 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Seguence 10, Appl   | Sequence 5, Appli  | Sequence 5, Appli | Sequence 5, Appl1 | 'n                 | æ       | æ                   | Sequence 8, Appli   | ω                  | 7    | Sequence 11, Appl   | 6                   | 12,                 | Sequence 10, Appl    | Sequence 3, Appli  | Sequence 3, Appl1 | Sequence 4, Appli  | 8                  | Sequence 13, Appl   | Sequence 2, Appl1  | 11,                  | 8,                 | Sequence 2, Appli  | Sequence 4, Appli  | Sequence 2, Appl1 | Sequence 4, Appli | ?    | Sequence 3, Appli  | 16,                 | 2, A              | Sequence 2, Appl1  | 22,                | Sequence 22, Appl | Sequence 18, Appl | Sequence 20, Appl  | Sequence 18, Appl   |
|---------------------|--------------------|-------------------|-------------------|--------------------|---------|---------------------|---------------------|--------------------|------|---------------------|---------------------|---------------------|----------------------|--------------------|-------------------|--------------------|--------------------|---------------------|--------------------|----------------------|--------------------|--------------------|--------------------|-------------------|-------------------|------|--------------------|---------------------|-------------------|--------------------|--------------------|-------------------|-------------------|--------------------|---------------------|
| 15 US-09-134-333-10 | 15 US-09-125-031-5 |                   |                   | 15 US-09-134-333-5 | us-09-1 | 15 US-09-125-031A-8 | 15 US-09-125-031B-8 | 15 US-09-134-333-8 | 63   | 15 US-09-175-683-11 | 15 US-09-175-683B-9 | 15 US-09-175-683-12 | 15 US-09-175-683B-10 | 3 US-07-867-768A-3 | 5 US-08-195-705-3 | 19 US-09-500-376-4 | 21 US-09-710-000-8 | 15 US-09-175-683-13 | 17 US-09-311-817-2 | 15 US-09-175-683B-11 | 19 US-09-500-376-8 | 3 US-07-867-768A-2 | 3 US-07-867-768A-4 | 5 US-08-195-705-2 | 5 US-08-195-705-4 |      | 19 US-09-500-376-3 | 19 US-09-500-376-16 | 9 US-08-593-006-2 | 15 US-09-117-415-2 | 9 US-08-593-006-22 | -                 | 3-006             | 9 US-08-593-006-20 | 15 US-09-117-415-18 |
| 108                 | 116                | 116               | 116               | 116                | 127     | 127                 | 127                 | 127                | 350  | 355                 | 355                 | 361                 | 361                  | 375                | 375               | 375                | 375                | 376                 | 376                | 379                  | 384                | 394                | 394                | 394               | 394               | 394  | 394                | 402                 | 594               | 594                | 613                | 613               | 631               | 631                | 631                 |
| 05 100.0            |                    | 05 100.0          |                   |                    |         |                     | 105 100.0           |                    |      |                     |                     |                     |                      |                    |                   |                    |                    |                     |                    |                      |                    | 105 100.0          |                    |                   |                   |      |                    |                     |                   |                    |                    |                   |                   | 7                  | 105 100.0           |
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## ALIGNMENTS

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18-86Quence 11, Application US/09763397A

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18-85Guence 11, Application US/09763397A

18-85ULCANT: The Government of the United States of America, as represented by the APPLICANT: Control and Prevention

18-85ULCANT: Lai, Altaf A.

18-85ULCANT: Lai, Altaf A.

18-85ULCANT: Hasnain, Seyed E.

18-85ULCANT: Laist Dayle: 200-216

18-85ULCANT: Laist Dayle: 1998-08-19

18-85ULCANT: Laist Dayle: 1999-08-19

18-85ULCANT: Hasnain, Seyed E.

18-85ULCANT: Hasnain, Seyed E.

18-85ULCANT: Hasnain, Seyed E.

18-85ULCANT: Laist Dayle: 1999-08-19

18-85ULCANT: Laist Dayle: 1999-08-19

18-85ULCANT: Hasnain, Seyed E.

18-85ULCANT: Hasnai
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1 NSGCFRHLDEREECKCLL 18

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Sequence 2, Application US/09134333
Sequence 2, Application US/09134333
GENERAL INFORMATION:
APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: NATO, FARIDABANO
APPLICANT: NATO, FARIDABANO
APPLICANT: MENDIS, KAMIN
APPLICANT: MENDIS, KAMIN
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: PLASMODIUM MSP-1
FILE REFERENCE: 0660-0135-0XCIP
CURRENT APPLICATION NUMBER: US/09/134,333
CURRENT FILING DATE: 1999-04-14
EARLIER APPLICATION NUMBER: FF86/01822
EARLIER FILING DATE: 1996-02-14
NUMBER OF SED ID NOS: 14
SOFTWARE: PATENTIN VOF: 2.1
SEQ ID NO 2
LENGTH: 95
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 GENERAL INFORMATION:

APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: ROTH, CHARLES
APPLICANT: BARWELL, JOHN
APPLICANT: MENDIS, KAMINA
APPLICANT: MENDIS, KAMINA
APPLICANT: NATO, FARLDABANO
TITLE OF INVENTION: PLEASMODIUM MSP-1
FILE REFERENCE: 0660-0139-02RCT
CURRENT APPLICATION NUMBER: US/09/125,031B
CURRENT FILING DATE: 1999-03-10
PRIOR FILING DATE: 1997-02-14
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NUMBER OF SEQ ID NOS: 15
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100.0%; Pred. No. 1.1e-07;
Live 0; Mismatches 0;
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 Query Match 100.
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Matches 18; Conservative
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 TYPE: PRT
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 17
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 APPLICANT: CHARLES
APPLICANT: BARNWELL, JOHN
APPLICANT: BARNWELL, JOHN
APPLICANT: BARNWELL, JOHN
APPLICANT: MENDIS, KAMINI
APPLICANT: MATO, FALIDABANO
TITLE OF INVENTION: PECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: PLASMODIUM MSP-1
FILE REFERENCE: 0660-0139-0xect
CURRENT APPLICATION NUMBER: US/09/125,031A
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PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1996-02-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VOICE: 2.1
 GENERALI INVORGATION:

GENERALI INVORGANIES

APPLICANT: ROTH, CHARLES

APPLICANT: NOTH, CHARLES

APPLICANT: NOTH, CHARLES

APPLICANT: NATURE CHARLES

APPLICANT: NATURE CHARLES

TAPLICANT: MENDIS, KAMINI

APPLICANT: MENDIS, KAMINI

TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF

TITLE OF INVENTION: PLASMODIUM MSP-1

FILE REFERENCE: 0660-0139-0XPCT

CURRENT PAPLICATION NUMBER: 05709/125,031

CURRENT FILING DATE: 1999-03-10

EARLIER APPLICATION NUMBER: F896/01822

EARLIER FILING DATE: 1997-02-14

EARLIER FILING DATE: 1996-02-14

NUMBER OF SEQ ID NOS: 14

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NUMBER OF SEQ ID NOS: 14

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Pred. No. 1.1e-07;
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Best Local Similarity 100.
Matches 18; Conservative
 17 NSGCFRHLDEREECKCLL
 Query Match
Best Local Similarity
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APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: ROTH, CHARLES
APPLICANT: BARNWELL, JOHN
APPLICANT: BARNWELL, JOHN
APPLICANT: MENDIS, KAMINI
APPLICANT: MENDIS, KAMINI
APPLICANT: NATO, FREIDABANO
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: PRESWOLIDM MSP-1
FILE REFERENCE: 0660-0139-020CT
CURRENT TRIING DATE: 1999-03-10
PRIOR FILING DATE: 1997-02-14
PRIOR PELICATION NUMBER: FR96/01822
PRIOR APPLICATION NUMBER: FR96/01822
PRIOR PELING DATE: 1996-02-14
PRIOR FILING DATE: 1996-02-14
SUMBER OF SEQ ID NOS: 15
 APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: ENTH, CHARLES
APPLICANT: BARNWELL, JOHN
APPLICANT: BARNWELL, JOHN
APPLICANT: BARNWELL, JOHN
APPLICANT: MATO, FARIDABANO
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: PLASHODIUM MSP-1
FILE REFERENCE: 06.60-01.39-0XPCT
CURRENT APPLICATION NUMBER: 1999-03-10
PRIOR APPLICATION NUMBER: PCT/FR97/00290
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PRIOR FILING DATE: 1997-02-14
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; ORGANISM: Plasmodium falciparum
US-09-125-031A-10
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US-09-125-031B-10
 1 NSGCFRHLDEREECKCLL 18
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SOFTWARE: PatentIn Ver. 2.1
 Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
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Best Local Similarity 100.
Matches 18; Conservative
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 Sequence 10 Application US/09125031
Sequence 10 Application US/09125031
Sequence 10 Application:
Sequence 10 Application:
APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: NATO, FARIDABANO
APPLICANT: NATO, FARIDABANO
APPLICANT: MATO, FARIDABANO
APPLICANT: MANUELL, JOHN
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: PLASMODIUM MSP-1
FILE REFERENCE: 0660-0139-0xPCT
CURRENT FILING DATE: 1999-03-10
EARLIER FILING DATE: 1999-03-10
EARLIER FILING DATE: 1996-02-14
EARLIER FILING DATE: 1996-02-14
NUMBER OF SEQ ID NOS: 14
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100.0%; Pred. No. 1.3e-07;
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100.0%; Pred. No. 1.1e-07;
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 GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Medical Research Council
TITLE OF INVENTION: Malaria Vaccine
FILE REFERENCE: 18396-1210
CURRENT APPLICATION WUMBER: US/09/311,817
CURRENT FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: GB 99099072.2
FRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 2
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 1 NSGCFRHLDEREECKCLL 18
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 17 NSGCFRHLDEREECKCLL 34
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Matches 18; Conservative
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Matches 18; Conserv
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Best Local Similarity
Matches 18; Conserv
 US-09-125-031-10
 US-09-311-817-1
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Sequence 5, Application US/09125031
SEQUENCE 5, Application US/09125031
SEQUENCE 5, APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: LONGACRE-ANDRE,
APPLICANT: NATO, FRIDABANO
APPLICANT: BARNWELL, JOHN
APPLICANT: BARNWELL, JOHN
APPLICANT: MECONIANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: PLASMODIUM MSP-1
FILE REFERENCE: 0660-0139-0xC7
CURRENT APPLICATION NUMBER: PCT/FF97/00290
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EARLIER PILING DATE: 1996-02-14
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 116
 GUREACH. INCOGRAFICANT. SHIRLEY
APPLICANT: ROTH, CHARLES
APPLICANT: NOTH, CHARLES
APPLICANT: NATUR. SHIRLEY
APPLICANT: NATUR. SHIRLEY
APPLICANT: NATUR. SHIRLEY
APPLICANT: MANDIS, KAMINI
APPLICANT: MENDIS, KAMINI
APPLICANT: MENDIS, KAMINI
APPLICANT: MENDIS, KAMINI
TITLE OF INVENTION: PLASMODIUM MSP-1
FILE REFERENCE: 0660-0135-0XCIP
CURRENT APPLICATION NUMBER: 207/09/134,333
CURRENT FILING DATE: 1999-04-18
EARLIER APPLICATION NUMBER: PS96/01822
EARLIER FILING DATE: 1997-02-14
EARLIER FILING DATE: 1996-02-14

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PATEUR PLICATION VET. 2.1

SEQ ID NO 10

LENGTH: 108
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100.0%; Pred. No. 1.3e-07;
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 Sequence 10, Application US/09134333 GENERAL INFORMATION:
 ORGANISM: Plasmodium falciparum US-09-134-333-10
 ORGANISM: Artificial Sequence
 1 NSGCFRHLDEREECKCLL 18
 17 NSGCFRHLDEREECKCLL 34
 1 NSGCFRHLDEREECKCLL 18
 30 NSGCFRHLDEREECKCLL 47
 Ouery Match 100.
Best Local Similarity 100.
Matches 18; Conservative
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Best Local Similarity 100.
Matches 18; Conservative
-09-134-333-10
 US-09-125-031-5
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GENERAL INCURRATION:
APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: BOTHO, CHARLES
APPLICANT: BARWHELL, JOHN
APPLICANT: BARWHELL, JOHN
APPLICANT: MENDIS, KAMINI
APPLICANT: MATO, FARIDABANO
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: PLASMODIUM MSP-1
FILE REFERENCE: 0660-0139-OXPCT
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CURRENT FILING DATE: 1999-03-10
PRIOR FILING DATE: 1999-02-14
PRIOR FILING DATE: 1996-02-14
PRIOR FILING DATE: 1996-02-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PLASMODIUM
SED ID NO 5
LENGTH: 116
Sequence 5, Application US/09125031A
; Sequence 5, Application US/09125031A
; Sequence 5, Application SHIRLEY
APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: ROTH, CHARLES
; APPLICANT: ROTH, CHARLES
; APPLICANT: MATO, FALIDABANO
TITLE OF INVENTION: PLASMODIUM MSP-1
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; SOFTWARE: PATENTIN VET. 2.1.
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 ORGANISM: Artificial Sequence
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 17 NSGCFRHLDEREECKCLL 34
 Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
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Matches 18; Conservative
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 Sequence 8 Application US/09125031

GENERAL INFORMATION:
APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: ROTH, CHARLES
APPLICANT: NOTH, CHARLES
APPLICANT: NOTH, CHARLES
APPLICANT: NATO, FARIDABANO
APPLICANT: BARNWELL, JOHN
APPLICANTON: PLASMODIUM MSP-1
CURRENT FILING DATE: 1999-03-10
EARLIER FILING DATE: 1999-03-10
EARLIER FILING DATE: 1996-02-14
NUMBER OF SEQ ID NOS: 14
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LENTH: 127

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 APPLICANT: LONGACRE-NUDRE, SHIRLEY
APPLICANT: ROTH, CHARLES
APPLICANT: NATO, FARIDABANO
APPLICANT: NATO, FARIDABANO
APPLICANT: NATO, FARIDABANO
APPLICANT: MAINI
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
TITLE OF INVENTION: PLASMODIUM MSP-1
TITLE OF INVENTION: PLASMODIUM MSP-1
FILE REFERENCE: 0660-0135-0XCIP
CURRENT FILING DATE: 1999-04-18
EARLIER APPLICATION NUMBER: PCT/FR97/00290
EARLIER FILING DATE: 1997-02-14
EARLIER FILING DATE: 1996-02-14
NUMBER OF SEQ ID NOS: 14
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 SQUENCE 1, Application US/09978756
GENERAL INFORMATION:
APPLICANT: Holder, Anthony
APPLICANT: Birdsall, Berry
APPLICANT: Breney, James
APPLICANT: Morgan, William
APPLICANT: Morgan, William
APPLICANT: Syed, Shabih
TITLE OF INVENTION: Walaria Vaccine
FILE REFERENCE: 18396/1005
CURRENT APPLICATION NUMBER: US/09/978,756
CURRENT FILING DATE: 2001-10-16
PRIOR PILING DATE: 2000-04-20
PRIOR FILING DATE: 1999-05-13
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PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-20
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SPINOR FILING DATE: 1999-06-25
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SPINOR FILING DATE: 1999-06-20
NUMBER OF SEQ ID NOS: 3
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GENERAL INFORMATION:
APPLICANT: Holder, Anthony
APPLICANT: Birdsall, Berry
APPLICANT: Feeney, James
APPLICANT: Syed, Shabih
TITLE OF INVENTION: Malaria Vaccine
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 ORGANISM: Plasmodium falciparum
 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 18; Conservative 0
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Compugen Ltd.
 US-09-978-756-1

US-09-978-756-2

US-09-177-4158-3

US-09-117-4158-2

US-09-117-4158-20

US-09-117-4158-18

US-09-117-4158-18

US-09-269-874A-7

US-09-269-874A-7

US-09-269-874A-7

US-09-269-874A-7

US-09-269-874A-7

US-09-269-874A-7

US-09-269-874A-7

US-09-269-874A-7

US-09-269-874A-7

US-09-708-427-32716

US-09-708-427-32714

US-09-708-427-63903

US-09-708-427-63903

US-09-708-427-82641

US-09-708-427-82641

US-09-908-193-34

US-09-908-193-34

US-09-908-193-38

US-09-908-193-38

US-09-908-193-38
 Total number of hits satisfying chosen parameters:
 173191 seqs, 36597120 residues
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Copyright (c) 1993 - 2000
 January 29, 2002, 10:58:12
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Listing first 45 summaries
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 US-09-763-397A-11
105
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 Minimum DB seq length: 0
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Match Length
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 Title:
Perfect score:
 Score
 Scoring table:
 Database :
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Result

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Gaps

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Length 96; Indels

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AFFILENT Yang, Shutong TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition of a MSA1 Peptide
Yang, Shutong
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry D. Coleman, COLEMAN SUDOL SAPONE, PC
 Length 594;
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry D. Coleman, COLEMAN SUDOL SAPONE,
 Query Match
Best Local Similarity 100.0%; Pred. No. 2.6e-08;
Matches 18; Conservative 0; Mismatches 0;
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-Jul-1998
CLASSIFICATION: 435
 COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDEAG (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-Jul-1998
CLASSIFICATION: 435
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad (ASCII)
 of a MSA1 Peptide
 ; TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-09-117-415B-2
 ATTORNEY/AGENT INFORMATION:
NAME: COLGMEN, HENTY D.
REGISTRATION NUMBER: 32,559
REFERENCE/DOCKET NUMBER: R12-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 679-0030
TELEPRAX: (212) 679-0121
 STREET: 714 Colorado Avenue
 STREET: 714 Colorado Avenue
CITY: Bridgeport
STATE: Connecticut
COUNTRY: USA
 Sequence 22, Application US/09117415B GENERAL INFORMATION:
APPLICANT: Davidson, Eugene
 ZIP: 10017
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 ATTORNEY/AGENT INFORMATION: NAME: Coleman, Henry D
 LENGTH: 594 amino acids TYPE: amino acid
 TELEFAX: (212) 679-9
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
 STATE: Connecticut
COUNTRY: USA
ZIP: 10017
 495 NSGCFRHLDEREECKCLL 512
 NUMBER OF SEQUENCES: 24
 1 NSGCFRHLDEREECKCLL 18
 CITY: Bridgeport
 NUMBER OF SEQUENCES:
 RESULT 5
US-09-117-415B-22
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 ó;
 Length 394;
 Length 376;
 Indels
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 100.0%; Score 105; DB 5; ilarity 100.0%; Pred. No. 1.8e-08; Conservative 0; Mismatches n.
 100.0%; Score 105; DB 5;
ilarity 100.0%; Pred. No. 1.8e-08;
Conservative 0; Mismatches 0;
 US-U9-9/8-/20-3
Sequence 3, Application US/09978756
Sequence 3, Application US/09978756
Sequence 3, Application US/09978756
Sequence 3, Application US/09978756
Sequence 3, Authony
APPLICANT: Birdsall, Berry
APPLICANT: Morgan, William
APPLICANT: Morgan, William
APPLICANT: Syed, Shabih
TTTLE OF INVENTION: Walliam
TTTLE OF INVENTION: 18396/1005
FILE REFERENCE: 18396/1005
FRIOR APPLICATION NUMBER: US/09/978,756
CURRENT FILING DATE: 2001-04-20
FRIOR FILING DATE: 1999-06-25
FRIOR FILING DATE: 1999-05-25
SPRIOR FILING DATE: 1999-05-25
SPRIOR FILING DATE: 1999-05-25
SPRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN VERSION 3.0
 CURRENT APPLICATION NUMBER: US/09/978,756
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: US/109/978,756
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-25
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NUMBER OF SEQ ID NOS: 3
SEQ ID NO
 US-09-117-415B-2
; Sequence 2, Application US/09117415B
; GENERAL INFORMATION:
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 TYPE: PRT ORGANISM: Plasmodium falciparum
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 295 NSGCFRHLDEREECKCLL 312
 1 NSGCFRHLDEREECKCLL 18
 1 NSGCFRHLDEREECKCLL 18
 REFERENCE: 18396/1005
 Best Local Similarity
Matches 18; Conserva
 Query Match
Best Local Similarity
Matches 18; Conserv
 US-09-978-756-3
 RESULT 3
US-09-978-756-3
 Query Match
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Gaps

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Indels

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Sequence 20, Application US/09117415B
GENERAL INFORMATION:
APPLICANT: Davidson, Eugene
APPLICANT: Yang, Shutong
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition
of a MSAl Peptide
 TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition of a MSAl Peptide
 CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE:
ADDRESSE: Henry D. Coleman, COLEMAN SUDOL SAPONE,
STREET: 714 Colorado Avenue
CITY: Bridgeport
STATE: Connecticut
 Length 631;
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry D. Coleman, COLEMAN SUDOL SAPONE,
STREET: 714 Colorado Avenue
 Indels
 Score 105; DB 5;
Pred. No. 2.8e-08;
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-Jul-1998
CLASSIFICATION: 435
ATTORNEY/AGNT INFORMATION:
NAME: COLEMAN. Henry D.
REGISTRATION NUMBER: 32,559
 Mismatches
 REFERENCE/DOCKET NUMBER: R12-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 679-0090
 ZIP: 10017
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 SEQUENCE DESCRIPTION: SEQ ID NO: 20:
 Sequence 16, Application US/09117415B
GENERAL INFORMATION:
APPLICANT: Davidson, Eugene
 LENGTH: 631 amino acids TYPE: amino acid
 679-9121
 ;
0
 100.0%;
1larity 100.0%;
Conservative 0;
 TELEFAX: (212) 679-9
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
 STATE: Connecticut
COUNTRY: USA
 532 NSGCFRHLDEREECKCLL 549
 1 NSGCFRHLDEREECKCLL 18
 CITY: Bridgeport
 NUMBER OF SEQUENCES:
 NUMBER OF SEQUENCES:
 USA
 Query Match
Best Local Similarity
Matches 18; Conserv
 COUNTRY:
 MOLECULE
 US-09-117-415B-16
 US-09-117-415B-20
 RESULT
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 Gaps
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 Yang, Shutong
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition
 ö
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 Length 631;
 Length 613;
 Coleman, COLEMAN SUDOL SAPONE,
 Indels
 Indels
 100.0%; Score 105; DB 5;
100.0%; Pred. No. 2.7e-08;
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 Score 105; DB 5;
Pred. No. 2.8e-08;
 ö
 APPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-Jul-1998
CLASSIFICATION: 435
 Mismatches
 NAME: COleman, Henry D.
REGISTARION NUMBER: 32,559
REFERENCE/DOCKET NUMBER: R12-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 679-0090
TELEFAX: (212) 679-9121
REGISTRATION NUMBER: 32,559
 of a MSA1 Peptide
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad (ASCII)
CURRENT APPLICATION DATA:
 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry D. Coleman.
STREET: 714 Colorado Avenue
CITY: Bridgeport
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 679-0090
TELEFAX: (212) 679-9121
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
 Sequence 18, Application US/09117415B
GENERAL INFORMATION:
APPLICANT: Davidson, Eugene
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 LENGTH: 613 amino acids TYPE: amino acid
 LENGTH: 631 amino acids TYPE: amino acid
 100.0%; Sc
100.0%; Pr
tive 0;
 ATTORNEY/AGENT INFORMATION:
 INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
 532 NSGCFRHLDEREECKCLL 549
 STATE: Connecticut
 550 NSGCFRHLDEREECKCLL 567
 1 NSGCFRHLDEREECKCLL 18
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 Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
 Conservative
 NUMBER OF SEQUENCES:
 COUNTRY: USA
 Query Match
Best Local Similarity
Matches 18; Conserv
 US-09-117-415B-18
 US-09-117-415B-18
 US-09-117-415B-22
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Gaps

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Sequence 1594, Application US/09605703B

Sequence 1594, Application US/09605703B

GENERAL INFORMATION.

GENERAL INFORMATION.

APPLICANT: Scrioder, Hartwig

APPLICANT: Scrioder, Hartwig

APPLICANT: APPLICANT: Gregor

TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL

TITLE OF INVENTION: OFFINEBACTERIUM GLUTAMICUM GENES ENCODING

TITLE OF INVENTION: PROTEING

TITLE OF INVENTION: UMBER: US/09/605,703B

CURRENT FILING DATE: 1999-07-08

PRIOR APPLICATION NUMBER: 60/122,764

PRIOR APPLICATION NUMBER: 60/122,318

PRIOR FILING DATE: 1999-09-03

NUMBER OF SEQ ID NOS: 2934
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 Length 1639;
 Length 1621;
 Sequence 3, Application US/09269874A
; Sequence 3, Application US/09269874A
; GENERAL INFORMATION:
 APPLICANT: Bujard, Hermann
; TITLE OF INVENTION: Recombinant Process for Preparing a
 TITLE OF INVENTION: Recombinant Antigen, GP190/MSP1
; TITLE OF INVENTION: Complete Malaria Antigen, GP190/MSP1
; FILE REPERENCE: GRUE-003
; CURRENT APPLICATION NUMBER: US/09/269,874A
; CURRENT FILING DATE: 1999-08-02
; PRIOR PILING DATE: 1997-10-02
; PRIOR FILING DATE: 1996-10-02
; PRIOR FILING DATE: 1996-10-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Pred. No. 6.3e-08;
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 Score 105; DB 5;
pred. No. 6.2e-08;
0; Mismatches 0;
PRIOR APPLICATION NUMBER: PCT/EP97/05441 PRIOR FILING DATE: 1997-10-02 PRIOR APPLICATION NUMBER: DE 19640817.2 PRIOR FILING DATE: 1996-10-02 NUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5.5
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 1540 NSGCFRHLDEREECKCLL 1557
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 1 NSGCFRHLDEREECKCLL 18
 1 NSGCFRHLDEREECKCLL 18
 Query Match
Best Local Similarity 100.
Matches 18; Conservative
 Query Match 100.C
Best Local Similarity 100.C
Matches 18; Conservative
 RESULT 12
US-09-605-703B-1594
 SEQ ID NO 3
LENGTH: 1639
 RESULT 11
US-09-269-874A-3
 LENGTH: 1621
 Matches
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 0;
 Gaps
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 Score 105; DB 5; Length 1602; Pred. No. 6.1e-08;
 Sequence 7, Application US/09269874A;
Sequence 7, Application US/09269874A;
GENERAL INFORMATION:
APPLICANT: Bujard, Hermann
TITLE OF INVENTION: Complete Malaria Antigen, GP190/MSP1
TITLE OF INVENTION: Complete Malaria Antigen, GP190/MSP1
FILE REFERENCE: GGUE-003
CURRENT APPLICATION NUMBER: US/09/269,874A
CURRENT FILING DATE: 1999-08-02
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PRIOR APPLICATION NUMBER: DE 19640817.2
PRIOR APPLICATION NUMBER: DE 19640817.2
PRIOR FILING DATE: 1996-10-02
NUMBER OF SEQ ID MOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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 Indels
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Best Local Similarity 100.0%; Pred. No. 2.8e-08;
Matches 18; Conservative 0; Mismatches 0;
 SOFTWARE: WordPad (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,415B
FILING DATE: 29-U11-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLOMAN, HENRY D. S.
REFSERUCE/DOCKET NUMBER: 32,559
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 679-0900
TELEPHONE: (212) 679-0900
TELEPHONE: (212) 679-0121
INFORMATION FOR SEQ.ID NO: 16:
SEQUENCE CARRACTERISTICS:
SEQUENCE CARRACTERISTICS:
TYPE: amino acids
 Mismatches
 TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 16:
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), ORGANISM: Plasmodium falciparum US-09-269-874A-7
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 Db 1521 NSGCFRHLDEREECKCLL 1538
 1 NSGCFRHLDEREECKCLL 18
 Query Match
Best Local Similarity 100."
Matches 18; Conservative
 1 NSGCFRHLDEREECKCLL 18
 RESULT 10
US-09-269-874A-5
 LENGTH: 1602
 δλ
 qq
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APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTHARE: PATENTIN VEFSION 3.1
SEQ ID NO 32214
LENGTH: 1444
 ή:
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 Score 44; DB 5; Length 1444;
Pred. No. 69;
 Score 44; DB 5; Length 1342;
Pred. No. 65;
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 CTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
CCATION: 1..1444
US-09-708-427-32714
; OTHER INFORMATION: Ceres Seq. ID 1834859
US-09-708-427-32715
 Search completed: January 29, 2002, 10:58:12 Job time: 2508 sec
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 ORGANISM: Arabidopsis thaliana
 41.9%;
52.9%;
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52.9%;
 1057 GCFSHLKTVFQELEECR 1073
 955 GCFSHLKTVFQELEECR 971
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Best Local Similarity 52.>>
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 Query Match
Best Local Similarity 52.99
Matches 9; Conservative
 3 GCFRHL----DEREECK 15
 3 GCFRHL----DEREECK 15
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US-09-708-427-32714
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 RESULT 13
US-09-708-427-32716
US-09-708-427-32716
SEQUENCE 32716. Application US/09708427
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: US/09/708,427
SOFTWARE: Patentin version 3.1
SEQ ID NO 32716
SEQ ID NO 32716

LINCTH: 1315
 RESULT 14
US-09-708-427-32715
US-09-708-427-32715
US-09-708-427-32715
SEQUENCE 32715, Application US/09708427
GENERAL INFORMATION:
THORMATION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION UNDER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN version 3.1
SEQ ID NO 32715
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 ;
 Score 44; DB 5; Length 1315;
Pred. No. 64;
1; Mismatches 3; Indels
 Length 85;
 5; Indels
 Score 45; DB 5;
Pred. No. 4.3;
4; Mismatches
 OTHER INFORMATION: Xaa is any amino acid;
NAME/KEY: misc_feature
LOCATION: 1.1315
OTHER INFORMATION: Ceres Seq. ID 1834860
US-09-708-427-32716
 NAME/KEY: misc_feature
LOCATION: 1..1342
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NAME/KEY: misc_feature
LOCATION: 1..1342
 ORGANISM: Corynebacterium glutamicum US-09-605-703B-1594
 ORGANISM: Arabidopsis thaliana
 ORGANISM: Arabidopsis thaliana
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 41.9%;
52.9%;
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 2 SGCFRHLDEREECKCLL 18
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 Best Local Similarity 52.9
Matches 9; Conservative
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Sequence 314, App Sequence 318, App Sequence 3037, Ap Sequence 19706, A Sequence 19706, A Sequence 332, App Sequence 332, App

Sequence

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Searched:

Database

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Result Š

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APPLICANT: CHESTNUT, Robert W.
APPLICANT: CHESTNUT, Robert W.
APPLICANT: CHESTNUT, Robert W.
APPLICANT: STTE, Alessandro D.
APPLICANT: GRAY, Howard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: CLL IMMUNITY
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Tower, one Market Plaza
CITY: San Francisco
STREET: Steuart Street Tower, one Market Plaza
COUNTRY: US
STREET: California
COUNTRY: US
STREET: LAND AND ADDRESSEE: PACHOLINE READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/197,484
FILING DATE: 16-FEB-1994
CLASSIFICATION UNMBER: US 07/935,811
FILING DATE: 26-MG-1992
PRIOR APPLICATION DATA:
ALIGNMENTS
 Sequence 19, Application US/08197484 GENERAL INFORMATION:
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US-08-197-484-19
 Sequence 19, Appl
Sequence 2, Appli
Sequence 10, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 7128, Appli
 Sequence 19, Appli
Sequence 2, Appli
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1.262 Million cell updates/sec
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 Search time 1760.55 Seconds
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 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-820-360-19
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 3148936 segs, 277657034 residues
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 January 29, 2002, 10:56:03
 Post-processing: Minimum Match 0%
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Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 US-09-763-397A-10
 Minimum DB seq length: 0
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 1 KPNDKSLY 8
 8
8
8
222
350
67
 Query
 Title:
Perfect score:
 Score
 Scoring table:
 444444460
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Sequence 332, App Sequence 6362, Ap Sequence 6281, Ap Sequence 6281, Ap Sequence 1026, Ap Sequence 1026, Ap Sequence 1106, Ap Sequence 1269, Ap Sequence 5168, Ap Sequence 5168, Ap Sequence 1269, Ap Sequence 1269, Ap Sequence 1269, Ap Sequence 2246, Ap Sequence 435, App Sequence 2246, Ap Sequence 2277, Ap Sequence 2777, Ap Sequence 2777, Ap Sequence 2777, Ap

us-09-763-397a-10.rapm

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ö
 APPLICANT: VITELLO, Maria A.
APPLICANT: VITELLO, Maria A.
APPLICANT: SETTE, Alessandro D.
APPLICANT: SETTE, Alessandro D.
APPLICANT: GRAY, Howard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: CTL IMMUNITY
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,360
FILING DATE: 12-MAR-1997
CLASSIFICATION: 424
 100.0%; Score 44; DB 7; I
100.0%; Pred. No. 2.9e+06;
live 0; Mismatches 0;
 NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,366
FILING DATE: 13 MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,484
FILING DATE: 16-FEB-1994
 FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
 US 07/749,568
 US 07/935,811
 US 07/874,491
 ORGANISM: Plasmodium falciparum US-08-318-856-2
 Sequence 19, Application US/08820360 GENERAL INFORMATION:
 FILING DATE: 16-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
 FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
 FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
TELEFAX: (202) 371-8856 TELEX:
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
 Conservative
 TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
 San Francisco
California
 APPLICATION NUMBER:
 Query Match
Best Local Similarity
Matches 8; Conserv
 1 KPNDKSLY 8
 1 KPNDKSLY 8
 COUNTRY: US
 US-08-820-360-19
 CITY: S
STATE:
 RESULT
 δλ
 Dp
 Peptides of an Antigen, Capable of Recognition by or Induction of Cytotoxic T Lymphocytes, and Method of Identification
 ;;
0
 Gaps
 ;
 Length 8;
 Indels
 100.0%; Score 44; DB 5; I
100.0%; Pred. No. 2.9e+06;
Live 0; Mismatches 0;
 ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
 25,154
ER: 263-PPIR1577US
 NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEPHONE: (206) 629-6793
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
 PADLICATION NUMBER: US/08/318,856
PRIOR DATE: October 3, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 08 068.8
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: GB 92 17 704.7
FILING DATE: AUGUST 20, 1992
PRIOR APPLICATION NUMBER: WO PCT/GB93/00711
FILING DATE: ACTION DATA:
APPLICATION NUMBER: WO PCT/GB93/00711
FILING DATE: ACTION:
APPLICATION NUMBER: WO PCT/GB93/00711
FILING DATE: ACTION:
 WO PCT/GB93/00711
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
 APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 5.1+ CURRENT APPLICATION DATA:
 Sequence 2, Application US/08318856 GENERAL INFORMATION:
APPLICANT:
 REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
 (202)-371-8850
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Best Local Similarity 100.
Matches 8; Conservative
 STRANDEDNESS: unknown TOPOLOGY: unknown
 TITLE OF INVENTION: PEP
TITLE OF INVENTION: REC
TITLE OF INVENTION: MEL
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
 LENGTH: 8 amino acids
 ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-197-484-19
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 NAME: Matthew Jacob REGISTRATION NUMBER:
 CITY: Washington STATE: D.C.
 amino acid
 RY: U.S.A.
20005
 1 KPNDKSLY 8
 1 KPNDKSLY 8
 TELEPHONE:
 COUNTRY:
 US-08-318-856-2
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TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Fa
FILE REFERENCE: 6395-57049
 Sequence 2, Application US/09763397A
GENERAL INFORMATION:
APPLICANT: He Government of the United States of America, as represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for
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 Gaps
 Gaps
 APPLICANT: Hill, Adrian V.S.
APPLICANT: Hill, Adrian V.S.
APPLICANT: Hill, Adrian V.S.
APPLICANT: Gilbert, Sarah C.
APPLICANT: Schneider, Jorg
APPLICANT: Schneider, Jorg
APPLICANT: Plebanski, Magdalena
APPLICANT: Blanchard, Tomas
APPLICANT: Blanchard, Tom
TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response
FILE REPERENCE: 2907.1000-000;
CURRENT APPLICATION NUMBER: US/09/454,204A
CURRENT FILING DATE: 1999-12-09
PRIOR PRILING DATE: 1999-12-09
PRIOR FILING DATE: 1998-06-09
PRIOR FILING DATE: 1997-06-09
 ö
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 100.0%; Score 44; DB 18; Length 229; 100.0%; Pred. No. 1.8;
 Length 8;
 Indels
 ; OTHER INFORMATION: Complete Epitope of Malaria String US-09-454-204A-41
 Score 44; DB 21;
Pred. No. 2.9e+06;
Mismatches 0;
 CURRENT PEPLICATION NUMBER: US/09/763,397A
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR FILING DATE: 1998-08-21
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 10
LENGTH: 8
 0; Mismatches
 NUMBER OF SEQ ID NOS: 78
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41
LENGTH: 229
 US-09-454-204A-41; Sequence 41, Application US/09454204A; GENERAL INFORMATION:
 100.0%; Solitarity 100.0%; Processive 0;
 ORGANISM: Plasmodium falciparum
US-09-763-397A-10
 Query Match 100.

Best Local Similarity 100.
Matches 8; Conservative
 Query Match
Best Local Similarity
Matches 8; Conserv
 1111111
29 KPNDKSLY 36
 ORGANISM: Unknown
 1 KPNDKSLY 8
 1 KPNDKSLY 8
 1 KPNDKSLY 8
 RESULT 7
US-09-763-397A-2
 TYPE: PRT
 .
QQ
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 Sequence 10, Application US/09763397A
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Control and Prevention
APPLICANT: Lal, ALLaf A.
APPLICANT: Lal, ALLaf A.
APPLICANT: Hashain, Seyed E.
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 Gaps
 APPLICANT: MCMIChed, Andrew
APPLICANT: Hill, Adrian V.S.
APPLICANT: Hill, Adrian V.S.
APPLICANT: Hill, Adrian V.S.
APPLICANT: Hill, Adrian V.S.
APPLICANT: Schneider, Jorg
APPLICANT: Schneider, Jorg
APPLICANT: Blanchard, Tomas
APPLICANT: Blanchard, Tom
TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response
TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response
FILE REPERENCE: 2907.1000-000
CURRENT APPLICATION NUMBER: US/09/454,204A
CURRENT FILING DATE: 1999-12-09
PRIOR PAPLICATION NUMBER: GB 97.11957.2
PRIOR PILING DATE: 1999-06-09
PRIOR FILING DATE: 1997-06-09
 ö
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 Length 8;
 Length 8;
 Indels
 Indels
 ; OTHER INFORMATION: CTL Epitope of the Malaria String US-09-454-204A-2
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100.0%; Pred. No. 2.9e+06;
ive 0; Mismatches 0;
 100.0%; Score 44; DB 12;
100.0%; Pred. No. 2.9e+06;
1ve 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 8
 ; Sequence 2, Application US/09454204A; GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 467-9600
TELEFAX: (206) 623-6793
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
 Query Match 100.
Best Local Similarity 100.
Matches 8; Conservative
 Query Match 100.
Best Local Similarity 100.
Matches 8; Conservative
 TOPOLOGY: unknown
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 TYPE: amino acid
STRANDEDNESS: unk
 ORGANISM: Unknown
 1 KPNDKSLY 8
 1 KPNDKSLY 8
 1 KPNDKSLY 8
 US-09-763-397A-10
 RESULT 4
US-09-454-204A-2
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APPLICANT: Hyerdy inc.
APPLICANT: Ford, John E et al
TITLE OF INVENTION: Novel Bone Marrow Nucleic Acids and Polypeptides
TITLE OF INVENTION: Novel Bone Marrow Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-040
CURRENT APPLICATION NUMBER: PCT/USO1/03782A
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR APPLICATION NUMBER: 09/598,075
PRIOR APPLICATION NUMBER: 09/598,075
PRIOR PILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-07-19
PRIOR PLING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
PRIOR PLING DATE: 2000-11-30
NUMBER OF SEC ID NOS: 386
SOFTWARE: Custom
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 Score 36; DB 24; Length 67; Pred. No. 18;
 Score 36; DB 24; Length 67;
Pred. No. 18;
1; Mismatches 1; Indels
 APPLICANT: Tanaka, Hiroaki, Applicant: APPLICANT: Dumas Milne Edwards, Jean Baptiste APPLICANT: Johert, Severin APPLICANT: Glordano, Jean-Yves TITLE OF INVENTION: ESTS and Encoded Human Proteins. FILE REFERENCE: 81.031.PRO CURRENT APPLICATION NUMBER: US/60/197,873
CURRENT FILIG DATE: 2000-04-18
 1; Mismatches
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/60/147,499
CURRENT FILING DATE: 1999-08-05
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
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LENGTH: 67
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PCT-10501-03782A-314
; Sequence 314, Application PC/TUS0103782A
; GENERAL INFORMATION:
 Sequence 22032, Application US/60197873
GENERAL INFORMATION:
APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
 81.8%;
75.0%;
 Query Match
Best Local Similarity 75.0
 Query Match 81.8
Best Local Similarity 75.0
Matches 6; Conservative
 ; ORGANISM: Homo sapiens
US-60-197-873-22032
 ; ORGANISM: Homo sapiens
US-60-147-499-7128
 ||||| :|
58 KPNDKLIY 65
 ||||| :|
58 KPNDKLIY 65
 1 KPNDKSLY 8
 1 KPNDKSLY 8
 g
 ŏ
 APPLICANT: Lal, Altaf A.

APPLICANT: Ping Shi, Ya

APPLICANT: Ping Shi, Ya

APPLICANT: Banalu, Seyed B.

AIPLICANT: Banalu, Seyed B.

AIPLICANT: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falci
FILE REFERENCE: 6395-57049

CURRENT APPLICATION NUMBER: US/09/763,397A

CURRENT APPLICATION NUMBER: US 60/097,703

PRIOR FILING DATE: 1998-08-21

PRIOR FILING DATE: 1999-08-19

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin version 3.1
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 ;
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 Query Match
100.0%; Score 44; DB 21; Length 350;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 0; Indels
 Score 36; DB 22; Length 67;
Pred. No. 18;
1; Mismatches 1; Indels
 APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
 US-09-834-366-22032
Sequence 22032, Application US/09834366
GENERAL INFORMATION: Stephane
APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
APPLICANT: Dunas Milne Edwards, Jean Baptiste
APPLICANT: Jobert, Severin
APPLICANT: Jobert, Severin
APPLICANT: Glordano, Jean-Yves
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: 81.US2.REG
 CURRENT APPLICATION NUMBER: US/09/834,366
CURRENT FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 52153
SOFWWARE: Patent.pm
SEQ ID NO 22032
 ; OTHER INFORMATION: Recombinant DNA/Protein US-09-763-397A-2
 US-60-147-499-7128; Sequence 7128, Application US/60147499; GENERAL INFORMATION:
 Control and Prevention
 81.8%; 75.0%;
 ORGANISM: Artificial Sequence
 Conservative
 ; ORGANISM: Homo sapiens US-09-834-366-22032
 Ouery Match
Best Local Similarity
Matches 6; Conserv
 184 KPNDKSLY 191
 ||||| :|
58 KPNDKLIY 65
 1 KPNDKSLY 8
 1 KPNDKSLY 8
 TYPE: PRT
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APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 810
 CURRENT APPLICATION NUMBER: US/60/324,631
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-25
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PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-5
PRIOR FILING DATE: 2000-01-25
PRIOR PELICATION NUMBER: US 09/491,404
PRIOR PELING DATE: 2000-01-25
PRIOR PELING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR PELING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR APPLICATION NUMBER: PCT/US01/02623
 PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: PCT/USO1/03000
PRIOR FILING DATE: 2001-02-05
PRIOR PLICATION NUMBER: PCT/USO1/03000
PRIOR FILING DATE: 2000-02-28
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 PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR PLICATION NUMBER: US 09/649,167
PRIOR PILING DATE: 2000-08-23
PRIOR PILING DATE: 2000-08-23
PRIOR PILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-04-18
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PRIOR PILING DATE: 2000-04-18
PRIOR PILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: US 09/770,160
PRIOR APPLICATION NUMBER: US 09/770,160
 PILING DATE: 2000-05-19
APPLICATION NUMBER: PCT/US01/04941
FILING DATE: 2001-03-05
APPLICATION NUMBER: US 09/540,217
 FILING DATE: 2000-02-03
APPLICATION NUMBER: US 09/560,875
 Haley-Vicente, Dana
 Zhou, Ping
Ghosh, Malabika
Wang, Dunrui
 Ma, Yunqing
Asundi, Vinod
Wang, Zhiwei
Weng, Gezhi
 ö
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 NAME/KEY: SITE
LOCATION: (50)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 LOCATION: (9)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-758-441-318
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 Gaps
 Gaps
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 APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PM040
CURRENT APPLICATION NUMBER: US/09/758,441
CURRENT PILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 328
SOFTWARE: Patentin Ver. 2.0
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85.7%; Pred. No. 2.5e+02;
iive 1; Mismatches 0; Indels
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 NAME/KEY: misc_feature

| LOCATION: (1)...(514)

| OTHER INFORMATION: Xaa = any amino acid or nothing

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US-60-324-631-3037
Sequence 3037, Application US/60324631
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhang, Jie
APPLICANT: Ren, Felyan
APPLICANT: Xen, Felyan
APPLICANT: Along, Aldong J.
APPLICANT: And, Aldong J.
APPLICANT: Wang, Jian-Rui
 Sequence 318, Application US/09758441 GENERAL INFORMATION:
 Query Match 81.8
Best Local Similarity 85.7
Matches 6; Conservative
 Query Match 81.8
Best Local Similarity 85.7
Matches 6; Conservative
 ORGANISM: Homo sapiens
 ORGANISM: Homo sapiens
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29 PNDRSLY 35
 93 PNDRSLY 99
 2 PNDKSLY 8
 2 PNDKSLY 8
 NAME/KEY: SITE
LOCATION: (115)
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 RESULT 12
US-09-758-441-318
LENGTH: 514
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 Score 36; DB 24; Length 650;
Pred. No. 2.9e+02;
1; Mismatches 0; Indels
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: US 09/577,408
PRIOR FILING DATE: 2000-05-18
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 ORGANISM: HOMO
US-60-324-631-3037
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US-09-733-089-19706

US-09-733-089-19706

Sequence 19706, Application US/09733089

GENERAL INFORMATION:
APPLICANT: Dotson, Stanton B.
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
TITLE OF INVENTION:
APPLICANT: Mu, Wei
APPLICANT: Mu, Wei
APPLICANT: Mu, Wei
TITLE OF INVENTION: Transcription In Plants
FILE REFERENCE: 38-21(15300)D
CURRENT APPLICATION NUMBER: US/09/733,089
CURRENT APPLICATION NUMBER: US 09/474,435
FRIOR FILING DATE: 2000-012-11
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 09/654,617
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 09/620,392

PRIOR FILING DATE: 2000-07-19

NUMBER OF SEQ ID NOS: 24143
SEQ ID NO 19706

LENGTH: 100
TUPLE OF THE Sequence 19706, Application US/09816660

Sequence 19706, Application US/09816660

GENERAL INFORMATION:
APPLICANT: Novalic, David K.
APPLICANT: Lutfiyya, Linda L.
APPLICANT: Lutfiyya, Linda L.
APPLICANT: McIninch, James
APPLICANT: Win Wei
TITLE OF INVENTION: Transcription in Plants
TITLE OF INVENTION: Transcription in Plants
TITLE OF INVENTION: UNBER: US/09/816,660
CURRENT FILING DATE: 2001-03-26
PRIOR PILING DATE: 2001-03-26
PRIOR FILING DATE: 2000-09-05
PRIOR PILING DATE: 2000-09-05
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-10
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 Score 35; DB 21; Length 1100;
Pred. No. 8.7e+02;
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Matches 6; Conservative
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US-09-816-660-19706
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US-09-733-089-19706
 1 KPNDKSLY 8
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93 PNDRSLY 99
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US-09-816-660-19706
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Sequence 5176, Ap
Sequence 21871, A
Sequence 21870, A
Sequence 122, App
 Sequence 4, Appli
Sequence 27, Appl
Sequence 196, App
Sequence 72696, A
Sequence 195, App
 Sequence 12189, A Sequence 4611, Ap Sequence 6876, Ap Sequence 11445, A Sequence 16149, A Sequence 16149, A Sequence 16147, A
 72695, A
194, App
72694, A
54, Appl
56, Appl
 5682, Ap
5330, Ap
 Sequence 6362, Ap
 Search time 120.95 Seconds (without alignments)
2.421 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
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Sequence 5
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2: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
 US-09-897-516-6362

US-09-815-242-11291

US-09-897-516-51872

US-09-987-516-51871

US-09-981-353-12870

US-09-981-353-128

US-09-981-353-128

US-09-637-444-4

US-09-637-7808-196

US-09-637-7808-195

US-09-637-7808-195

US-09-708-427-72695

US-09-708-427-72694

US-09-605-7038-56

US-09-605-7038-56

US-09-815-242-5330

US-09-815-242-5330

US-09-815-242-5330

US-09-815-242-5330

US-09-815-242-5330

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US-09-815-242-12189

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US-09-815-242-13189

US-09-815-242-13189

US-09-815-242-12189

US-09-815-242-11445

US-09-815-242-11445

US-09-708-427-16148
 Total number of hits satisfying chosen parameters:
 173191 seqs, 36597120 residues
 SUMMARIES
 January 29, 2002, 10:58:11
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein – protein search, using sw model
 Gapop 10.0 , Gapext 0.5
 US-09-763-397A-10
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 1 KPNDKSLY 8
 Query
Match Length
 BLOSUM62
 Title:
Perfect score:
 Score
 Scoring table:
 Database :
 Sedneuce:
 Searched:
 Run on:
 Result
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| e 2907, Ap<br>e 6, Applls, A<br>e 12915, A<br>e 394, App<br>e 12469, A<br>e 97, Appl<br>e 96, Appl<br>e 91, Appl<br>e 91, Appl<br>e 11, Appl<br>e 27528, A<br>e 17528, A<br>e 17528, A<br>e 17528, A<br>e 17528, A                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     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| Uses.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  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| US-09-611-526-2907 US-09-991-496-6 US-09-815-242-12915 US-09-817-242-12915 US-09-817-12469 US-09-991-496-97 US-09-991-496-96 US-09-991-496-96 US-09-392-941A-69 US-09-392-941A-69 US-09-392-941A-91                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ALIGNMENTS  5,09897516  5. 10. 10. 11. 11. 12. 13. 14. 16. 18. 18. 18. 18. 18. 18. 18. 18. 18. 18                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | re 34; DB 5; Lengt ismatches 2; In 15.242                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| 4994<br>6565<br>71865<br>80335<br>80335<br>80335<br>16415<br>1005<br>1105<br>1105<br>1105<br>1105<br>1105<br>1105<br>1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | on US  rry S  separate S  con US  con                                                                                                                                                                                                                                                                                                      | 77.3%; Scor<br>75.0%; Prec<br>75.0%; Prec<br>Ication US/09815<br>k, Robert<br>Kari L.<br>Judith W.<br>John D.<br>John D.<br>Fant J.<br>John D.<br>Fant J.<br>Howard                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| 00000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 3362<br>2. Applicati<br>2. Applicati<br>2. Applicati<br>3. Applicati<br>3. Applicati<br>5. Applicati<br>6. Applicati<br>6. Applicati<br>8. Applicati<br>9. Applica | Similarity 6; Conserv NDKSLX 8 1   1   NSKGLX 49 12-11291 1291, Applic FORMATION: 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
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|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        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Sequence 21871, Application US/09708427
Sequence 21871, Application US/09708427
SERBRAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: WIGHER: US/09/708,427
CURRENT APPLICATION UNDERS: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SEQ ID NO 21871
LENGTH: 334
 APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
 ö
 APPLICANT: Goldman, Marian.
APPLICANT: Goldman, Barrian.
APPLICANT: Hosching, Joseph E.
APPLICANT: Hassing, Joseph E.
APPLICANT: Hassing, Joseph E.
APPLICANT: Krasomil-Osterfeld, Karina C.
APPLICANT: Slater, Steven C.
APPLICANT: Spiridonov, Sergei
TILE REFERENCE: 38-21(51847)B
CURRENT APPLICATION NUMBER: US/09/897,516
CURRENT APPLICATION NUMBER: US/09/897,516
CURRENT FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 8409
SEQ ID NO 51/6
LENGTH: 300
 Gaps
 Gaps
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0
 72.7%; Score 32; DB 5; Length 334; 71.4%; Pred. No. 62;
 Length 300;
 0; Indels
 0; Indels
 DB 5;
55;
 72,7%; Score 32; DB 100.0%; Pred. No. 55; ive 0; Mismatches
 2; Mismatches
 COTHER INFORMATION: Xaa is any amino acid OTHER INFORMATION: Xaa is any amino acid NAME/KEY: misc_feature ICCATION: 1.334
COTHER INFORMATION: Ceres Seq. ID 1840163
US-09-708-427-21871
 Sequence 21870, Application US/09708427 GENERAL INFORMATION:
 ORGANISM: Arabidopsis thaliana
 Query Match 72.7
Best Local Similarity 71.4
Matches 5; Conservative
 Query Match 72,7
Best Local Similarity 100.
Matches 6; Conservative
 TYPE: PRT
CRCANISM: Xenorhabdus sp.
US-09-897-516-5176
 NAME/KEY: misc_feature
 307 PHDKSIY 313
 294 PNDKSL 299
 2 PNDKSLY 8
 RESULT 6
US-09-708-427-21870
 RESULT 5
US-09-708-427-21871
 2 PNDKSL 7
 Matches
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 Sequence 21872, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROW et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: US/09/708,427
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATCHIN VEFSION 3.1
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 Gaps
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 Length 290;
 Length 380;
 Indels
 1; Indels
 DB 5;
 Score 34; DB 5;
Pred. No. 28;
1; Mismatches
 2; Mismatches
 72.7%; Score 32; DB
71.4%; Pred. No. 53;
FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

PRIOR APPLICATION NUMBER: 06/191,078

PRIOR FILING DATE: 2001-03-21

PRIOR PLICATION NUMBER: 60/201,078

PRIOR PLICATION NUMBER: 60/207,727

PRIOR PLICATION NUMBER: 60/207,727

PRIOR PLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-05-26

PRIOR PLICATION NUMBER: 60/242,578

PRIOR PLICATION NUMBER: 60/245,578

PRIOR PLICATION NUMBER: 60/253,625

PRIOR PLICATION NUMBER: 60/257,931

PRIOR PLICATION NUMBER: 60/257,931

PRIOR PLICATION NUMBER: 60/269,308

PRIOR PLICATION NUMBER: 60/269,308

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PRICATION NUMBER: 60/269,308

PRIOR PRICATION NUMBER: 60/269,308
 NAME/KEY: misc_feature
LOCATION: 1..290
CTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..290
CTER INFORMATION: Ceres Seq. ID 1840164
US-09-708-427-21872
 NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
 %3-09-897-516-5176
; Sequence 5176, Application US/09897516
 ORGANISM: Arabidopsis thaliana
 ORGANISM: Helicobacter pylori
 77.3%;
75.0%;
 5; Conservative
 Query Match 77.3
Best Local Similarity 75.0
Matches 6; Conservative
 Query Match
Best Local Similarity
Matches 5; Conserv
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132 KPNTKALY 139
 1:111:1
263 PHDKSIY 269
 1 KPNDKSLY 8
 2 PNDKSLY 8
 US-09-708-427-21872
 US-09-815-242-11291
 SEQ ID NO 21872
LENGTH: 290
 SEQ ID NO 11291
 LENGTH: 380
 RESULT
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...Lanand DROV, Nickolai
...Lanand BROVER, Vyacheslav
; TTTLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
; TTTLE OF INVENTION: Thereby
; FILE REFERENCE: 2750-1096P
; CURRENT APPLICATION NUMBER: US/09/637,780B
; CURRENT FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 1401
SEQ ID NO 196
LENGTH: 220
 ö
 Gaps
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 Score 32; DB 7; Length 2115;
pred. No. 4.6e+02;
2; Mismatches 0; Indels
 Length 2150;
 APPLICANT Tarczynski, Mitchell C.
APPLICANT Tarczynski, Mitchell C.
APPLICANT Shan, Bo.
APPLICANT Lid, Stein E.
APPLICANT Lid, Stein E.
APPLICANT Lid, Stein E.
APPLICANT Gruis, Darren B.
APPLICANT Ananiev, Evgueni
APPLICANT Maniev, Evgueni
APPLICANT Maniev, Evgueni
TITLE OF INVENTION: Methods for Improving Seed and Grain
TITLE OF INVENTION: Characteristics
FILE REFERENCE: 1390p2
CURRENT APPLICATION NUMBER: US/60/337,444
CURRENT FILING DATE: 2001-10-25
NUMBER OF SEQ IO NOS: 28
SOCTWARE: FastSEQ for Windows Version 3.0
 Score 32; DB 7; Length 213.
Pred. No. 4.7e+02;
 TITLE OF INVENTION: Methods for Improving Seed and Grain FITLE OF INVENTION: Characteristics FILE REFERENCE: 1390p2 CURRENT APPLICATION NUMBER: US/60/337,444 CURRENT FILING DATE: 2001-10-25 SOFTWARE OF SEQ ID NOS: 28 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 4
 2; Mismatches
 US-60-337-444-27; Sequence 27, Application US/60337444; GENERAL INFORMATION:
 ; SEO ID NO 27

: LENGTH: 2150

: TYPE: PRT

: ORGANISM: Arabidopsis thaliana

US-60-337-444-27
 Query Match 72.7%;
Best Local Similarity 71.4%;
Matches 5; Conservative
 Query Match 72.7%;
Best Local Similarity 71.4%;
Matches 5; Conservative
 ; ORGANISM: arabidopsis
US-60-337-444-4
 |||:||:
| Db | 1703 PNDRSLF 1709
 |||:||:
| Db | 1703 PNDRSLF 1709
 2 PNDKSLY 8
 2 PNDKSLY 8
 LENGTH: 2115
 PRT
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 Gaps
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 Query Match 72.7%; Score 32; DB 5; Length 969; Best Local Similarity 71.4%; Pred. No. 2e+02; Matches 5; Conservative 1; Mismatches 1; Indels
 DB 5; Length 341;
63;
 0; Indels
 APPLICANT: Lasek, Amy W.
APPLICANT: Lasek, Amy W.
APPLICANT: Jones, David A.
TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
FILE REPERENCE: PA-0038 US
CURRENT APPLICATION NUMBER: US/09/981,353
CURRENT FILING DATE: 2001-10-11
SUMMER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
FILE REFERENCE: 2750-1243P; FILE REFERENCE: 2750-1243P; CURRENT APPLICATION NUMBER: US/09/708,427; CURRENT FILING DATE: 2000-11-09; NUMBER OF SEQ ID NOS: 85364; SOFTWARE: Patentin version 3.1; SEQ ID NO 21870
 Score 32; DB
Pred. No. 63;
2; Mismatches
 ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 1344279CD1
US-09-981-353-122
 NAME/KEY: misc_feature
| LOGATION: 1..341
| DOPER INFORMATION: Xaa is any amino acid
| NAME/KEY: misc_feature
| LOCATION: 1..341
| COTHER INFORMATION: Ceres Seq. ID 1840162
| US-09-708-427-21870
 Sequence 4, Application US/60337444
GENERAL INFORMATION:
APPLICANT: Tarczynski, Mitchell C.; APPLICANT: Olsen, Odd-Arne
APPLICANT: Shen, Bo
APPLICANT: Lid, Stein E.; APPLICANT: Lid, Stein E.; APPLICANT: Lid, Stein E.; APPLICANT: Jung, Rudolf S. APPLICANT: Grins, Darren B.
 Sequence 122, Application US/09981353 GENERAL INFORMATION:
 ORGANISM: Arabidopsis thaliana
 72.78;
71.48;
 Ananiev, Evgueni
Nichols, Scott E
 Query Match 72.7
Best Local Similarity 71.4
Matches 5; Conservative
 ORGANISM: Homo sapiens
 1:||:|
314 PHDKSIY 320
 |||: ||
95 PNDRGLY 101
 2 PNDKSLY 8
 2 PNDKSLY 8
 RESULT 7
US-09-981-353-122
 SEQ ID NO 122
LENGTH: 969
 US-60-337-444-4
 APPLICANT:
APPLICANT:
 à
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Sequence 194. Application US/09637780B
SERBRAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
TITLE OF INVENTION: Thereby
FILLE REPRENDE: 275-01969F
CURRENT APPLICATION NUMBER: US/09/637,780B
CURRENT APPLICATION NUMBER: US/09.08-11
NUMBER OF SEQ ID NOS: 1401
SEQ ID NO 194
SED ID NO 194
LENGTH: 291
 APPLICANT: N. ALEXANDROV et al.

APPLICANT: N. ALEXANDROV et al.

ITILE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID

TITLE OF INVENTION: THEREBY

FILE REFERENCE: 2750-1243P

CURRENT PELLING NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SOFTWARE: Patentin version 3.1

SEQ ID NO 72695

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67;
 Score 31; DB 5;
Pred. No. 67;
 Score 31; DB 5
Pred. No. 67;
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LOCATION: 1..236
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) LOCATION: 1..236

) OTHER INFORMATION: Xaa is any amino acid

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): LOCATION: 1..236

) OTHER INFORMATION: Ceres Seq. ID 1481829

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62.5%;
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Best Local Similarity 62.5
Matches 5; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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40 KPADKAIY 47
 1 KPNDKSLY 8
 1 KPNDKSLY 8
 US-09-708-427-72695
 RESULT 14
US-09-637-780B-194
 TYPE: PRT
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 Sequence 7266, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE OF INVENTION: 14688187
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
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2; Mismatches
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LOCATION: 1..220
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US-09-637-7808-196
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62.5%; Pred. No.
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ORGANISM: Arabidopsis thaliana
 TYPE: PRT ORGANISM: Zea mays subsp. mays
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 70.5%;
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Best Local Similarity 62.5
Matches 5; Conservative
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24 KPADKAIY 31
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 FEATURE:
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RESULT 15
US-09-708-427-72694
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Matches 5; Conservative 2; Mismatches 1; Indels
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 1 KPNDKSLY 8
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Sequence 39361, A
Sequence 26, Appl
 Sequence 21, Application US/08197484
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: TITLELO, Maria A.
APPLICANT: SETTE, Alessandro D.
APPLICANT: GRAY, Howard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: CALL IMMUNITY
NUMBER OF SEQUENCES:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, one Market Plaza
CITY: San Francisco
STATE: California
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994
CLASSIFICATION: 424
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
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STATE: Ca
COUNTRY:
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US-08-197-484-21
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US-08-38-856-1
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 January 29, 2002, 10:56:02
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 Length
 Query
Match I
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1000.0
1000.0
1000.0
1000.0
 Perfect score:
Sequence:
 Scoring table:
 Score
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Minimum DB Maximum DB

Database

26456786

Result ş

Searched:

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 Length 9;
 Length 9;
 100.0%; Score 50; DB 7; I
100.0%; Pred. No. 2.9e+06;
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COMPUTER: IBM PC compatible
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SOFTWARE: WordPerfect 5.14
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APPLICATION NUMBER: US/08/318,856
FILING DATE: October 3, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 08 068.8
FILING DATE: APril 3, 1992
PRIOR APPLICATION NUMBER: GB 92 17 704.7
FILING DATE: August 20, 1992
PRIOR APPLICATION NUMBER: WO PCT/GB93/00711
FILING DATE: APRIL 5, 1993
ATTORNEY/AGENT INFORMATION:
 ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
 REGISTRATION NUMBER: 25,154
REFERENCE/DOCKET NUMBER: 263-PPIR1577US
TELECOMMUICATION INFORMATION:
TELEPHONE: (202)-371-8850
 Mismatches
 ORGANISM: Plasmodium falciparum
 Sequence 1, Application US/08318856 GENERAL INFORMATION: APPLICANT:
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 TELEFAX: (202) 371-8856
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 Best Local Similarity 100.
Matches 9; Conservative
 ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Flore:
COMPUTER
 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
 9 amino acids
 TITLE OF INVENTION: Pept
TITLE OF INVENTION: RECO
TITLE OF INVENTION: MELS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
 TYPE: amino acid
STRANDEDNESS: single
 MOLECULE TYPE: peptide ORIGINAL SOURCE:
 NAME: Matthew Jacob REGISTRATION NUMBER:
 lineaı
 Washington
 1 KPIVQYDNF 9
 1 KPIVQYDNF
US-08-278-634-35
 RESULT 3
US-08-318-856-1
 Query Match
 Matches
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 Sequence 35, Application US/08278634
GENERAL INFORMATION:
APPLICANT: SETTE, Alessandro
APPLICANT: SIDNEY, John
TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
NUMBER OF SEQUENCES: 288
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Street Tower, 20th
 Length 9;
 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,634
FILING DATE: 21-JUL-1994
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 PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4
TELEPHONE: (206) 467-9600
TELEPHONE: (206) 623-6793
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
 14137-80
 APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
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FILING DATE: 29-JAN-1992
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
 ATTORNEY/AGENT INFORMATION:
NAME: BASTLAIN, KGVID L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/543-9600
 TELEFAX: 415/543-5043
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Best Local Similarity 100.
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STRANDEDNESS: single
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STATE: California
COUNTRY: USA
 unknown
 linear
 FILING DATE: 21
CLASSIFICATION:
 ZIP: 94105
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 US-08-278-634-35
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Gaps

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Gaps
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100.0%; Score 50; DB 7; Length 9;
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Matches 9; Conservative 0; Mismatches 0; Indels
PatentIn Release #1.0, Version #1.30
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APPLICANT:
TITLE OF INVENTION: MALARIA PEPTIDES
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 805 Fifeenth St., Suite 799,
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/344,824A

CLASSIFICATION: UNOV-1994

CLASSIFICATION: A24

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APPLICATION NUMBER: US 08/159,330

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FRIUNG DATE: 29-NOV-1993

FRIUNG DATE: 06-AUG-1993

PRIOR APPLICATION NUMBER: US 08/103,366

FILING DATE: 05-MAR-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/027,746

FILING DATE: 05-MAR-1993

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APPLICATION NUMBER: US 08/027,746

FILING DATE: 05-MAR-1993

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APPLICATION NUMBER: US 07/926,666

FILING DATE: 07-MG-1993
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SOFTWARE: Wordbad for Windows 95
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APPLICATION NUMBER: US/08/714,175
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GENERAL INFORMATION:
APPLICANT:
 NAME: Alicea, Hector A.
REGISTRATION NUMBER: 40,891
REFERENCE/DOCKET NUMBER: 0118(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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 1 KPIVQYDNF 9
 US-08-344-824A-40
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 Sequence 40, Application US/08344824
GENERAL INFORMATION:
APPLICANT: SETTE, Alessandro
APPLICANT: SIDNEY, John
TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
NUMBER OF SEQUENCES: 399
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Street Tower, 20th
STREET: Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
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GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Stdney, John
TITLE OF INVENTION: HLA Binding Peptides and Their Uses:
NUMBER OF SEQUENCES: 308
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Elghth Floor
CITY: San Francisco
STATE: California
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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FILING DATE: 23-NOV-1994
ATOREX/AGENT INFORMATION:
ATOREX/AGENT INFORMATION:
NAME: Bastian, Kevin 1.
REGISTRATION NUMBER: 34,774
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COMPUTER READABLE FORM:
MEDIUM TYPE: FIDPPY disk
COMPUTER: IBM PC COMPATIBLE
 MOLECULE TYPE: DNA (genomic)
 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 1 KPIVQYDNF 9
 1 KPIVQYDNF 9
 94105
 RESULT 5
US-08-344-824A-40
RESULT 4
US-08-344-824-40
 US-08-344-824-40
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CHESTNUT, Robert W.
APPLICANT: CHESTNUT, Robert W.
APPLICANT: GETTE, ALESSAND D.
APPLICANT: GRAY, HOWATCH
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: CL IMMUNITY
NUMBER OF SEQUENCES: 154
CORRESPONDENCES: 154
CORRESPONDENCES: TOWNSEND and TOWNSEND and Crew LLP
 ;
 Length 9;
 Indels
 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,360
FILING DATE: 12-MAR-1997
CLASSIFICATION NUMBER: US/08/820,366
FILING APPLICATION DATA:
APPLICATION NUMBER: US 60/013,366
FILING DATE: 13-MAR-1996
PRIOR APPLICATION NUMBER: US 60/197,484
FILING DATE: 16-FEB-1994
PRIOR APPLICATION NUMBER: US 08/197,484
FILING DATE: 26-AUG-1992
PRIOR APPLICATION NUMBER: US 07/835,811
FILING DATE: 26-AUG-1992
PRIOR APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
PRIOR APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION NUMBER: US 07/827,682
FILING DATE: 26-AUG-1991
APPLICATION NUMBER: US 07/749,568
FILING APPLICATION NUMBER: US 07/749,568
FILING APPLICATION NUMBER: US 07/749,568
FILING APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
ANAMER: LEAGE STEVEN WARE: LEAGE OF WARDER OF STEVEN WAR
 100.0%; Score 50; DB 11;
100.0%; Pred. No. 2.9e+06;
tive 0; Mismatches 0;
 E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, 8th Floor
 REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)-371-8850
TELEFAX: (202)-371-8856
 Parmelee, Steven W
 STREET: Two Embarcader CITY: San Francisco STATE: California COUNTRY: US 834 COUNTRY READABLE FORM: MEDIUM TYPE: Floppy di
 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
 TELEX:
INFORMATION FOR SEQ ID NO:
 SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
 ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-714-175A-21
 1 KPIVQYDNF 9
 1 KPIVQYDNF
 STRANDEDNESS
 RESULT 8
US-08-820-360-21
 pp
 Gaps
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0
 100.0%; Score 50; DB 11; Length 9; 100.0%; Pred. No. 2.9e+06;
 Indels
 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNDBER: WO PCT/GB95/26982
FILING DATE: 30 -MAR-1995
PRIOR APPLICATION NUMBER: GB 9406492.0
FILING DATE: 31 -MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WATTEN CHEEK, JT.
RECISTATION NUMBER: 33.367
REFERENCE/DOCKET NUMBER: 263/KPIR2867US
 FILING DATE:
CLASSIETCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB95/26982
FILING DATE: 30-MAR-1995
PRIOR APPLICATION NUMBER: GB 9406492.0
FILING DATE: 31-MAR-1994
ATTORNEY/AGENT INFORMATION:
 NAME: Warren M Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER: 263/KPIR2867US
TELECOMMUNICATION INFORMATION:
TELECHONE: (202)-371-8856
TELEFAX: (202)-371-8856
 0; Mismatches
 APPLICANT:
TTTLE OF INVENTION: MALARIA PEPTIDES
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: WENDEROTH, LIND & PONACK
STREET: Washington
STRATE: D.C.
 STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
ZIP: 20005
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS 7
SOFTWARE: WOORDAG for Windows 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,175A
FILING DATE:
 Sequence 21. Application US/08714175A GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
 , MOLECULE TYPE: peptide US-08-714-175-21
 amino acid
 linear
 1 KPIVQYDNF 9
 1 KPIVQYDNF 9
 STRANDEDNESS
 TOPOLOGY:
 TELEX:
```

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TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Fa
 Sequence 2, Application US/09763397A; Sequence 2, Application US/09763397A; GPNERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the APPLICANT: The Government of the Department of Health and Human Services, Centers for
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 Gaps
 Gaps
 APPLICANT: MCMICIDEL, Andrew
APPLICANT: Hill, Adrian V.S.
APPLICANT: Gilbert, Sarah C.
APPLICANT: Gilbert, Sarah C.
APPLICANT: Schneder, Jorg
APPLICANT: Plebanski, Magdalena
APPLICANT: Plebanski, Magdalena
APPLICANT: Banchard, Tomas
APPLICANT: Banchard, Tomas
TITLE OF INVENTION: Methods and Reagents for Vaccination
TITLE OF INVENTION: Mothods and Reagents for Vaccination
TITLE OF INVENTION: Mothods and Reagents
CURRENT APPLICATION NUMBER: 2907,1000-000
FILE REFERENCE: 2907,1000-000
CURRENT FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: PCT/GB98/01681
PRIOR PELING DATE: 1998-06-09
PRIOR PELING DATE: 1999-06-09
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 Query Match
100.0%; Score 50; DB 18; Length 229;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels
 Indels
 ; OTHER INFORMATION: Complete Epitope of Malaria String US-09-454-204A-41
 Query Match 100.0%; Score 50; DB 21; Best Local Similarity 100.0%; Pred. No. 2.9e+06; Matches 9; Conservative 0; Mismatches 0;
 FILE REFERENCE: 6395-57049
CURRENT APPLICATION NUMBER: US/09/763,397A
CURRENT FILING DATE: 2001-02-16
 PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR FILING DATE: 1998-08-21
PRIOR PAPLICATION NUMBER: PCT / US99/18869
PRIOR FILING DATE: 1999-08-19
 NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 4.0
 Sequence 41, Application US/09454204A GENERAL INFORMATION:
 ORGANISM: Plasmodium falciparum
 NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 9
 1 KPIVQYDNF 9
 1 KPIVQYDNF 9
 1 KPIVQYDNF 9
 ORGANISM: Unknown
 US-09-763-397A-2
 US-09-763-397A-9
 PRT
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 Sequence 9, Application US/09763397A
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A.
APPLICANT: Ping Shi, Ya
APPLICANT: Hasnain, Seyed E.
 ö
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 Gaps
 Gaps
 APPLICANT: Schneider, Jorg
APPLICANT: Plebanski, Magdalena
APPLICANT: Plebanski, Magdalena
APPLICANT: Hanke, Tomas
APPLICANT: Blanchard, Tom
TITLE OF INVENTION: Methods and Reagents for Vaccination
TITLE OF INVENTION: Method Generate A CD8 T Cell Immune Response
FILE REFERENCE: 2907.1000-000
CURRENT APPLICATION NUMBER: US/09/454,204A
CURRENT FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1997-06-09
PRIOR FILING DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 9
 ;
0
 ö
 Length 9;
 Length 9;
 Indels
 Indels
 ; OTHER INFORMATION: CTL Epitope of the Malaria String
US-09-454-204A-6
 ö
 100.0%; Score 50; DB 12;
100.0%; Pred. No. 2.9e+06;
Live 0; Mismatches 0;
 100.0%; Score 50; DB 18; 100.0%; Pred. No. 2.9e+06;
 0; Mismatches
 Sequence 6, Application US/09454204A GENERAL INFORMATION:
 APPLICANT: MCMIChael, Andrew
APPLICANT: Hill, Adrian V.S.
APPLICANT: Gilbert, Sarah C.
APPLICANT: Schneider, Jorg
APPLICANT: Plebanski, Magdalena
APPLICANT: Hanke, Tomas
APPLICANT: Smith, Geoffrey L.
TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 467-9600
TELERAX: (206) 623-6793
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
 Query Match
Best Local Similarity 100.
Matches 9; Conservative
 TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
 Ouery Match 100.

Best Local Similarity 100.

Matches 9; Conservative
 ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-820-360-21
 1 KPIVQYDNF 9
 1 KPIVQYDNF 9
 ORGANISM: Unknown
 1 KPIVQYDNF
 US-09-763-397A-9
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Gaps

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RESULT 15

US-09-450-96185

US-09-450-969-6185

Sequence 6185, Application US/09450969

SEQUENCE 6185, Application US/09450969

SERVERAL INFORMATION:
APPLICANT: Lyan Doucette-Stamm et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATH99-09A

CURRENT APPLICATION NUMBER: US/09/450,969

CURRENT FILING DATE: 1999-11-29

NUMBER OF SEQ ID NOS: 7544

SEQ ID NO 6185
 Score 38; DB 18; Length 464;
Pred. No. 81;
1; Mismatches 1; Indels
 DB 15; Length 464;
81;
 Score 38; DB 1
Pred. No. 81;
1; Mismatches
 Search completed: January 29, 2002, 10:56:03 Job time: 2399 sec
 TYPE: PRT; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4701
 76.0%;
75.0%;
 76.0%;
 Query Match 76.0
Best Local Similarity 75.0
Matches 6; Conservative
 Query Match 76.0
Best Local Similarity 75.0
Matches 6; Conservative
 NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4701
LENGTH: 464
 ; ORGANISM: S.epidermidis
US-09-450-969-6185
 ||: ||||
348 PIITYDNF 355
 348 PIITYDNF 355
 2 PIVQYDNF 9
 2 PIVQYDNF 9
 qq
 δλ
 Dp
 δλ
 GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE DE INVENTION: BETDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE DE INVENTION: BETDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE DE INVENTION: BETDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BETDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/054,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A.
APPLICANT: Lal, Altaf A.
APPLICANT: Ping Shi, Ya
APPLICANT: Hasnain, Seeyed E.
TILE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falci
FILE REFERENCE: 6395-57049
CURRENT APPLICATION NUMBER: US/09/763,397A
CURRENT APPLICATION NUMBER: US 60/097,703
PRIOR FILING DATE: 1998-08-21
PRIOR FILING DATE: 1998-08-19
PRIOR FILING DATE: 1999-08-19
RIOR FILING DATE: 1999-08-19
RIOR FILING DATE: 1999-08-19
SEQ ID NOS: 26
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 2
LENGTH: 350
 Sequence 15255, Application US/09248796
GENERAL INFORMATION:
APPLICANT: Kelth Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REPERBENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796
CURRENT FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 28206
SEQ ID NO 15255
LENGTH: 329
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0
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 Gaps
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;
 100.0%; Score 50; DB 21; Length 350; 100.0%; Pred. No. 0.21; ive 0; Mismatches 0; Indels
 Score 39; DB 16; Length 329;
Pred. No. 35;
 1; Mismatches
 ; OTHER INFORMATION: Recombinant DNA/Protein US-09-763-397A-2
 78.0%;
75.0%;
 ORGANISM: Artificial Sequence
 Ouery Match
Best Local Similarity 75.v.
 ; ORGANISM: Candida albicans
US-09-248-796-15255
 Query Match
Best Local Similarity 100..
 119 KPIVQYDNF 127
 |: |||||
118 PLAQYDNF 125
 1 KPIVQYDNF 9
 2 PIVQYDNF 9
 RESULT 14
US-09-134-001C-4701
 US-09-248-796-15255
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Gaps

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Sequence 51401, Application US/09708427
GENERAL INFORMATION:
APPLICAMY: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SSEQ ID NOS: 85361
LENGTH: 239
 Best Local Similarity 75.(
Matches 6; Conservative
 ORGANISM: Zea mays subsp.
 679
9993
11883
1223
2270
2270
2270
3310
3310
410
410
427
 ||:|:|||
82 KPLVKYDN 89
 1 KPIVQYDN 8
 RESULT 1
US-09-708-427-51402
 RESULT 2
US-09-708-427-51401
 Query Match
 TYPE: PRT
 FEATURE:
 (without alignments)
2.723 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 January 29, 2002, 10:58:11; Search time 120.95 Seconds
 Pending_Patents_AA_New:*

1: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/USO7_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
 US-09-708-427-51400
US-09-708-427-49931
US-09-708-427-49931
US-09-708-427-49343
US-06-333-726-1306
US-60-333-726-1306
US-60-333-726-1306
US-60-333-726-1306
US-09-509-234A-47
US-09-509-234A-47
US-09-509-234C-47
US-09-509-234C-41
US-09-509-234C-41
US-09-708-427-3135
US-09-708-427-48137
US-09-708-427-48137
 US-09-708-427-65942
US-09-897-516-5513
US-09-976-800-83
 Total number of hits satisfying chosen parameters:
 173191 seqs, 36597120 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 US-09-763-397A-9
50
 seq length: 0
seq length: 200000000
 Query
Match Length DB
 1 KPIVQYDNF 9
 215
239
267
115
139
355
1328
1328
1328
 4111
420
420
844
11157
11194
1152
302
326
326
344
344
344
346
367
967
967
 \begin{smallmatrix} 777 \\ 788 \\ 89
 Score
 Perfect score:
 Scoring table:
 Minimum DB s
Maximum DB s
 OM protein
 Searched:
 sedneuce:
 Run on:
 Result
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
AP
 ö
 Sequence 117, App
Sequence 118, App
Sequence 14, Appl
Sequence 16, Appl
Sequence 31790, A
Sequence 3139, Ap
Sequence 15, Appl
Sequence 3789, A
 Sequence 36, Appl
Sequence 2171, Ap
Sequence 7302, Ap
Sequence 2170, Ap
Sequence 625, App
Sequence 625, App
 Sequence 625, App
Sequence 51, Appl
Sequence 51, Appl
Sequence 7448, Ap
 Gaps
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 Score 38; DB 5; Length 215;
Pred. No. 2.5;
 US-09-976-800-117
US-09-976-800-118
US-09-635-949-16
US-09-635-949-16
US-09-708-427-31790
US-09-708-427-31790
US-09-708-427-31789
US-09-708-427-31789
US-09-708-427-31789
US-09-626-585C-36
US-09-620-3948-2171
US-09-620-3948-2170
 PCT-US01-27760-625
PCT-US01-27760A-625
 US-09-509-234A-51
US-09-509-234C-51
US-09-708-427-7448
 2; Mismatches
 NAME/KEY: misc_feature
LOCATION: 1..215
OTHER INFORMATION: Xaa is any amino acid
 NAME/KEY: misc_feature

CACATION: 1..215

SOTHER INFORMATION: Ceres Seq. ID 1926741

US-09-708-427-51402
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75.0%;
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Sequence 49343, Application US/09708427

SEQUENCE 49343, Application US/09708427

GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P

FILE REFERENCE: 2750-1243P

CURRENT FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SOGTWARE: Patentin version 3.1

SEQ ID NO 49343

LENGTH: 139
 US-09-708-427-54153

Sequence 54153, Application US/09708427

Sequence 54153, Application US/09708427

GENERAL INFORMATION:

APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID

TITLE OF INVENTION: THEREBY

TITLE OF INVENTION: THEREBY

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT APPLICATION NUMBER: US/09/708,427

SOFTWARE: PALENTING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SEQ ID NO 54153

LENGTH: 355
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 ..
 Length 139;
 Length 115;
 1; Indels
 Score 34; DB 5;
Pred. No. 9.6;
3; Mismatches
 Score 34; DB 5;
Pred. No. 7.7;
3; Mismatches
 NAME/KEY: misc_feature
LOCATION: 1..355
OTHER INFORMATION: Xaa is any amino acid
 LOCATION: 1..115
CTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..115
COTHER INFORMATION: Ceres Seq. ID 1923418
US-09-708-427-49931
 NAME/KEY: misc_feature

// LOCATION: 1.139

US-09-7088-427-49343
 OTHER INFORMATION: Xaa is any amino acid
 ORGANISM: Zea mays subsp. mays
 ORGANISM: Zea mays subsp. mays
 68.0%;
55.6%;
 68.0%;
55.6%;
 Query Match
Best Local Similarity 55.v
Local 5; Conservative
 Query Match 68.0
Best Local Similarity 55.6
Matches 5; Conservative
 NAME/KEY: misc_feature
LOCATION: 1..139
NAME/KEY: misc_feature
 ||:: ||:|
94 KPVLGYDDF 102
 ||::||:|
48 KPVLGYDDF 56
 1 KPIVQYDNF 9
 1 KPIVQYDNF 9
 RESULT 5 ... US-09-708-427-49343
 FEATURE
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 qq
 qq
 δy
 Sequence 49931
Sequence 49931
Sequence 49931, Application US/09708427
GENERAL TIPE PROMATION:
TIPE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
TITLE REPRENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: 2000-11-09
NUMBER OF SEQ ID NOS: 85564
SOFTWARE: PATENTIN version 3.1
 Sequence 11400, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: US/09/708,427
SOFTWARE: PETCHING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
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0
 ;
0
 Gaps
 ;
0
 .;
0
 Length 267;
 Length 239;
 0; Indels
 Indels
 Score 38; DB 5;
Pred. No. 3.2;
 DB 5;
 Score 38; DB Pred. No. 2.8; 2; Mismatches
 2; Mismatches
 CTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
COTATION: 1..267
COTHER INFORMATION: Ceres Seq. ID 1926739
US-09-708-427-51400
 NAME/KEY: misc_feature
LOCATION: 1..239
COTHER THORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..239
. OTHER INFORMATION: Ceres Seq. ID 1926740
US-09-708-427-51401
 TYPE: PRT ORGANISM: Zea mays subsp. mays
 TYPE: PRT ORGANISM: Zea mays subsp. mays
 ORGANISM: Zea mays subsp. mays FEATURE:
 76.0%;
75.0%;
 76.0%;
75.0%;
 Query Match 76.0
Best Local Similarity 75.0
Matches 6; Conservative
 Query Match
Best Local Similarity 75...
6; Conservative
 NAME/KEY: misc_feature LOCATION: 1..267
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|134 KPLVKYDN 141
 106 KPLVKYDN 113
 1 KPIVQYDN 8
 1 KPIVQYDN 8
 US-09-708-427-51400
 SEQ ID NO 49931
LENGTH: 115
 SEQ ID NO 51400
LENGTH: 267
 LOCATION: 1
 FEATURE:
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Gaps

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 GENERAL INFORMATION US/09509234A

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: Vannuffel, Pascal

APPLICANT: Vannuffel, Pascal

APPLICANT: Vannuffel, Pascal

TITLE OF INVENTION: GENETIC SEQS....METHODS & DEVICES FOR TITLE OF INVENTION: GENETIC SEQS....METHODS & DEVICES FOR TITLE OF INVENTION: GENETIC SEQS....METHODS & DEVICES FOR TITLE OF INVENTION: LD. OF STAPHYLOCOCCI STRAINS

FILE REFERENCE: DECLEZ7. 001APC

CURRENT APPLICATION NUMBER: US/09/509,234A

CURRENT FILING DATE: 2000-09-25

PRIOR APPLICATION NUMBER: EP 97870146.4

PRIOR FILING DATE: 1997-09-26

NUMBER OF SEQ ID NOS: 64

SOFTWARE: FastSEQ for Windows Version 4.0
 Length 1328;
 Length 1328;
 Length 411;
 Sequence 1345, Application US/60333726
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Qiandong Zeng et al.
TITLE OF INVENTION: Systemic Discovery of New Genes
FILE REFERENCE: 032796-090
CURRENT APPLICATION NUMBER: US/60/333,726
CURRENT FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 1346
SEQ ID NO 1345
LENGTH: 1328
 Score 33; DB 7; I
Pred. No. 2.1e+02;
 Score 33; DB 7; 1
Pred. No. 2.1e+02;
1; Mismatches 1,
 Score 32; DB 5;
Pred. No. 85;
2; Mismatches
 1; Mismatches
FILE REFERENCE: 032796-090
CURRENT APPLICATION NUMBER: US/60/333,726
CURRENT FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 1346
SEQ ID NO 1323
LENGTH: 1328
 Staphylococcus capitis femA
 ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-60-333-726-1323
 ORGANISM: Saccharomyces cerevisiae
 66.0%;
75.0%;
 66.0%;
ilarity 75.0%;
Conservative
 Query Match 64.0%;
Best Local Similarity 57.1%;
Matches 4; Conservative
 Conservative
 Query Match
Best Local Similarity
'-hog 6; Conserve
 Query Match
Best Local Similarity
Matches 6; Conserv
 |||||| :|
129 PIVQYGDF 136
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|129 PIVQYGDF 136
 2 PIVQYDNF 9
 2 PIVQYDNF 9
 US-60-333-726-1345
 US-60-333-726-1345
 US-09-509-234A-47
 SEQ ID NO 47
LENGTH: 411
 ORGANISM:
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 Length 1328;
 Length 1328;
 Length 355;
 Score 33; DB 7; Length 13; Pred. No. 2.1e+02; 1; Mismatches 1; Indels
 1; Indels
 Sequence 1306, Application US/60333726
GENERAL INFORMATION:
APPLICANT: Qlandong Zeng et al.
TITLE OF INVENTION: Systemic Discovery of New Genes
FILE REFERENCE: 032796-090
CURRENT APPLICATION NUMBER: US/60/333,726
CURRENT FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 1346
SEQ ID NO 1306
LENGTH: 1328
 Sequence 1295, Application US/60333726
GENERAL INFORMATION:
APPLICANT: Qiandong Zeng et al.
TITLE OF INVENTION: Systemic Discovery of New Genes FILE REFERENCE: 032796-090
CURRENT APPLICATION NUMBER: US/60/333,726
CURRENT FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 1346
LENGTH: 1328
 Sequence 1322, Application US/60333726
GENERAL INFORMATION:
APPLICANT: Qiandong Zeng et al.
TITLE OF INVENTION: Systemic Discovery of New Genes
 66.0%; Score 33; DB 7; illarity 75.0%; Pred. No. 2.1e+02; Conservative 1; Mismatches 1
 ς,
.,
 Score 33; DB E
Pred. No. 45;
2; Mismatches
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; LOCATION: 1..355
; OTHER INFORMATION: Ceres Seq. ID 1932726
US-09-708-427-54153
 ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-60-333-726-1295
 ORCANISM: Saccharomyces cerevisiae US-60-333-726-1306
 66.0%;
75.0%;
 66.0%;
62.5%;
 Ouery Match
Best Local Similarity 62.5
These 5; Conservative
 Best Local Similarity 75.0
Matches 6; Conservative
 Query Match
Best Local Similarity
Matches 6; Conserv
 101 KPLLYYDN 108
 129 PIVQYGDF 136
 |||||| :|
129 PIVQYGDF 136
 1 KPIVQYDN 8
 2 PIVQYDNF 9
 2 PIVQYDNF 9
 US-60-333-726-1323
 RESULT 7
US-60-333-726-1295
 US-60-333-726-1306
 Query Match
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Conservative
 Query Match
Best Local Similarity
Matches 4; Conserv
 ||:::||
239 KPVIRYD 245
 76 PVIDYDN 82
 1 KPIVQYD 7
 2 PIVQYDN 8
 LENGTH: 420
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 Sequence 47, Application US/09509234C

Sequence 47, Application US/09509234C

Sequence 47, Application US/09509234C

APPLICANT: Vannuffel, Pascal

APPLICANT: Vannuffel, Pascal

TITLE OF INVENTION: ID. OF STAPHYLOCCOCI STRAINS

TITLE OF INVENTION: ID. OF STAPHYLOCCOCI STRAINS

FILE REFERENCE: DECLE27: 001APC

CURRENT APPLICATION NUMBER: US/09/509,234C

CURRENT FILING DATE: 1997-09-25

NUMBER OF SEO ID NOS: 64

SOFTWARE: FASELSEQ for Windows Version 4.0

SEO ID NO 47
 Length 420;
 DB 5; Length 411;
85;
 APPLICANT: Vannuffel, Pascal
APPLICANT: Gala, Jean-Luc
TITLE OF INVENTION: GENETIC SEQS.,...METHODS & DEVICES FOR
 APPLICANT: Gala, Jean-Luc
TITLE OF INVENTION: GENETIC SEQS.,...METHODS & DEVICES FOR
TITLE OF INVENTION: DENETIC SEQS.,...METHODS & DEVICES FOR
TITLE OF INVENTION: DO STAPHYLOCOCCI STRAINS
FILE REFERENCE: DECLEZ?.001APC
CURRENT APPLICATION NUMBER: US/09/509,234A
CURRENT FILING DATE: 2000-09-25
PRIOR FILING DATE: 1997-09-26
NUMBER OS SQE ID NOS: 64
SOFTWARE: FASTEQ for Windows Version 4.0
 1; Indels
 DB 5;
87;
 Mismatches
 Mismatches
 TYPE: PRT ORGANISM: Staphylococcus haemolyticus femA
 Score 32;
Pred. No.
 Score 32;
Pred. No. 8
 ORGANISM: Staphylococcus capitis fema
US-09-509-234C-47
 RESULT 14
US-09-509-234C-41
Sequence 41, Application US/09509234C;
GENERAL INFORMATION:
 Sequence 41, Application US/09509234A GENERAL INFORMATION:
APPLICANT: Vannuffel, Pascal
 64.0%;
57.1%;
 64.0%;
57.1%;
 Query Match
Best Local Similarity 57.1.
 Ouery Match 64.0
Best Local Similarity 57.1
Matches 4; Conservative
 |:: |||
76 PVIDYDN 82
 |:: |||
70 PVIDYDN 76
 2 PIVQYDN 8
1:: |||
70 PVIDYDN 76
 2 PIVQYDN 8
 RESULT 13
US-09-509-234A-41
 US-09-509-234A-41
 US-09-509-234C-47
 SEQ ID NO 41
LENGTH: 420
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 q
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Gaps
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 Ouery Match
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels
 APPLICANT: Xu, Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
NUMBER OF SSC ID NOS: 14110
SSCPTWARE: FBELSQ for Windows Version 4.0
 Length 420;
 1; Indels
TITLE OF INVENTION: ID. OF STAPHYLOCOCCI STRAINS FILE REFERENCE: DECLE27.001APC
CURRENT APPLICATION NUMBER: US/09/509,234C
CURRENT FILING DATE: 2000-09-25
PRIOR FILING DATE: 1997-09-26
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4.0
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 DB
87;
 Mismatches
 TYPE: PRT; ORGANISM: Staphylococcus haemolyticus femA
US-09-509-234C-41
 Score 32;
Pred. No.
 RESULT 15
US-09-815-242-13515
GENUENCE 13515, Application US/09815242
GENUENAL INFORMATION:
 ORGANISM: Streptococcus pneumoniae US-09-815-242-13515
 Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
 64.0%;
57.1%;
 Ohlsen, Kari L.
Zyskind, Judith W.
 APPLICANT: Haselbeck, Robert
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Search completed: January 29, 2002, 10:58:11 Job time: 2507 sec

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 Result
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 Minimum DB
Maximum DB
 Total number of hits satisfying chosen parameters:
 Title:
Perfect score:
 Database
 Searched:
 Scoring table:
 Sequence:
 OM protein -
 ŏ
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Score
 ••
 seq length: 0 seq length: 2000000000
 599559559559559559
 protein search, using sw model
 Query
Match
 100.0
100.0
100.0
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100.0
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 US-09-763-397A-8
59
 Pending_Patents_AA_Main:*
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 Length
 18
18
18
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 DΒ
 5 US-09-197-770-2

11 US-09-763-397A-8

12 US-07-947-33-1

US-07-947-033-9

US-07-947-033-9

US-07-947-033-9

US-07-947-033-10

US-07-947-033-10

US-08-119-694-7
 IJ
 SUMMARIES
 Search time 1760.55 Seconds (without alignments)
1.419 Million cell updates/sec
Sequence 2, Appli
Sequence 8, Appli
Sequence 1, Appli
Sequence 7, Appli
Sequence 8, Appli
Sequence 9, Appli
Sequence 10, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 7, Appli
 Description
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|                   |                   |      |               |               |               | 9             | 8            | 7          |              | 35 5              | 4            | ω            | 2            | 1         | 0               |                 | œ               |                  | σ          | σ.         | 4          | ω          | 2           | 1            |            | 9               |               |               |          |               |               |                |             |              |                   |
|-------------------|-------------------|------|---------------|---------------|---------------|---------------|--------------|------------|--------------|-------------------|--------------|--------------|--------------|-----------|-----------------|-----------------|-----------------|------------------|------------|------------|------------|------------|-------------|--------------|------------|-----------------|---------------|---------------|----------|---------------|---------------|----------------|-------------|--------------|-------------------|
| 9                 | 9                 | 9    | 9             | 9             | 9             | 9             | 9            | 9          | 9            | 59 100            | 9            | 9            | 9            | 9         | 9               | 9               | 9               | 9                | 9          | 9          | 9          | 9          | 9           | 9            | 9          | 9               | 9             | 9             | 9        | 9             | 9             | 59 100         | 9           | 9            | 9                 |
| 0.0               |                   |      |               |               |               | •             |              |            | •            | 0.0               |              |              |              |           | ٠               |                 | •               | •                |            |            |            |            |             | •            |            |                 |               |               |          |               |               |                |             |              |                   |
|                   |                   |      |               |               |               |               |              |            |              | 55                |              |              |              |           |                 |                 |                 |                  |            |            |            |            |             |              |            |                 |               |               |          |               |               |                |             |              |                   |
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| 63-3972           | 9-454-2042        | -992 | -08-119-694B- | -08-119-694B- | -08-119-694B- | -08-119-694B- | -08-119-694- | 8-119-694- | -08-119-694- | -08-119-694       | -07-947-033- | -07-947-033- | -07-947-033- | 07-947-03 | -60-297-86      | 258-37          | -09-782-99      | US-09-471-179-46 | -US99-310; | -US98-2597 | -60-138-68 | 08-395-602 | -US98-25922 | US98-25922-9 | 60-143-992 | S-09-454-204A-2 | -08-395-602-1 | -08-119-694B- | -08-119- | -08-119-694B- | -08-119-694B- | S-08-119-694B- | 8-119-694-  | S-08-119-69  | 94 -              |
| Sequence 2, Appli | Sequence 41, Appl | Сe   | о<br>5        | 4, App        | ω             | ຸນ            | 5            | 4          | ω            | Sequence 2, Appli | s,           | 4, Appl      | Ψ            | 2, Appl   | equence 6, Appl | equence 6, Appl | equence 5, Appl | ce 46, App       | 46,        | 34, App    | 1035,      | , Appl     | 33, App     | 9, A         |            | же 28,          | -             | 10,           | φ,       | œ             | e 7,          | equence 1      | equence 10, | equence 9, A | Sequence 8, Appli |

## ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/197,770A
CURRENT FILING DATE: 1998-11-23
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PATENTIN VEr. 2.0
SEQ ID NO 2
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: fragment/ analog of thrombospondin
US-09-197-770-2
 В
 Qy
 US-09-197-770-2
 ; Sequence 2, Application US/09197770A
; GENERAL INFORMATION:
 Matches
 Query Match
Best Local
 TITLE OF INVENTION: RETROINVERSO POLYPEPTIDES THAT MIMIC OR INHIBIT TITLE OF INVENTION: THROMBOSPONDIN ACTIVITY FILE REFERENCE: 07206-0021
 APPLICANT: Tuszynski, George
APPLICANT: Williams, Taffy
APPLICANT: Actor, Paul
 Local Similarity
hes 9; Conserv
 1 WSPCSVTCG
WSPCSVTCG
 Conservative
 9
 100.0%;
 0
 Score 59; DB 15;
Pred. No. 2.9e+06;
; Mismatches 0;
 Length 9;
 Indels
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RESULT 3
US-07-947-033-1
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 Query Match
Best Local Similarity
"htches 9; Conserva
 US-09-763-397A-8
 US-09-763-397A-8
 SEQ ID NO 8
LENGTH: 9
 Sequence 1, Applicati
GENERAL INFORMATION:
 Sequence 8, Application US/09763397A
 CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR FILING DATE: 1998-08-21
PRIOR APPLICATION NUMBER: PCT / US99/18869
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
 APPLICANT: Ping Shi, Ya
APPLICANT: Hasnain, Seyed E.
APPLICONI: Hasnain, Seyed E.
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falc:
FILE REFERENCE: 6395-57049
CURRENT APPLICATION NUMBER: US/09/763,397A
CURRENT FILING DATE: 2001-02-16
 APPLICANT: The Government of the United APPLICANT: Secretary of the Department APPLICANT: Control and Prevention
 APPLICANT:
INFORMATION FOR SEQ ID NO:
 ORGANISM: Plasmodium falciparum
 ATTORNEY/AGENT INFORMATION:
NAME: Adda C. Gogoris, Esq.
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986/07607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
 SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
 CORRESPONDENCE ADDRESS:
 APPLICANT: Sinnis, Photini
APPLICANT: Nussenzweig, Victor
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING
TITLE OF INVENTION: HEPATOCYTE INVASION BY MALARIAL SPOROZOITES
 APPLICANT: Cerami, Carla
 NUMBER OF SEQUENCES:
 APPLICATION NUMBER: FILING DATE: 199209 CLASSIFICATION: 530
 MEDIUM TYPE: Diskette, 5, inch, 1.2 MB storage COMPUTER: AST Premium II 386/33 OPERATING SYSTEM: DOS 3.3
 STREET:
 TELEFAX:
 COUNTRY:
 TELEX:
 ADDRESSEE:
 1 WSPCSVTCG 9
 1 WSPCSVTCG 9
 INFORMATION:
 New York
: New York
 10022
 Application US/07947033
 Lal, Altaf A.
 236687
 100.0%;
nilarity 100.0%;
Conservative (
 E: Darby & Darby, P.C. 805 Third Avenue
 Frevert, Ute
Sinnis, Photini
 (212) 753-6237
 United States of America
 19920917
 US/07/947,033
 0;
 Score 59; DB 21;
Pred. No. 2.9e+06;
); Mismatches 0;
 States of America, as represented by the of Health and Human Services, Centers fo
 Length 9;
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 RESULT 5
US-07-947-033-8
; Sequence 8, Application US/07947033
; GENERAL INFORMATION:
 밁
 US-07-947-033-7
 Sequence 7
 Matches
 Query Match
Best Local
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 INFORMATION FOR SEQ ID NO:
 SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: AMINO ACID
 SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/9
 REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986/07607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEPAX: (212) 753-6237
 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
 FILING DATE: 19920917
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Adda C. Gogoris, E
 COMPUTER READABLE FORM:
 APPLICANT: Nussenzweig, Victor
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING
TITLE OF INVENTION: HEPATOCYTE INVASION BY MALARIAL SPOROZOITES
 APPLICANT:
 APPLICANT: Cerami, Carla APPLICANT: Frevert, Ute
 SEQUENCE CHARACTERISTICS:
APPLICANT: Cerami, Carla
 LENGTH: Ib u....
 COMPUTER: AST Properties operating system:
 MEDIUM TYPE:
 COUNTRY: UZIP: 10022
 STREET:
 TELEFAX: (212
TELEX: 236687
 ADDRESSEE:
 2 WSPCSVTCG 10
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 TOPOLOGY:
 2 WSPCSVTCG 10
 1 WSPCSVTCG 9
 New York
 Similarity 9; Conserv
 Application US/07947033
 New York
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 Frevert, Ute
Sinnis, Photini
 United States of America
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 Conservative
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 Darby & Darby, P.C
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 US/07/947,033
 Esq
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 Gaps
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밁
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INFORMATION FOR SEQ ID NO: 8:
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LENCTH: 18 amino acids
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UNKNOWN
 US-07-947-033-9
 Sequence 9, Application:
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Best Local Similarity
Matches 9; Conserv
 APPLICANT: Cerami, Carla
APPLICANT: Frevert, Ute
APPLICANT: Sinnis, Photini
APPLICANT: Nussenzweig, Victor
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING
TITLE OF INVENTION: HEPATOCYTE INVASION BY MALARIAL SPOROZOITES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
 MEDIUM TYPE: Diskette, 5, inch, 1.2 MB storage COMPUTER: AST Premium II 386/33
OPERATING SYSTEM: DOS 3.3
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/947,033
 ATTORNEY/AGENT INFORMATION:
NAME: Adda C. Gogoris, Esq.
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986/07607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELLERAX: (212) 753-6237
 STREET: OUT NEW YORK CITY: New York 'TATE: New York 'Inited
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
 SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5, inch, 1.2 MB storage
COMPUTER: AST Premium II 386/33
OPERATING SYSTEM: DOS 3.3
 NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby, P.C.
 APPLICANT: NUSSENZWEIG, VICTOR
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING
TITLE OF INVENTION: HEPATOCYTE INVASION BY MALARIAL SPOROZOITES
NUMBER OF SEQUENCES: 27
 APPLICANT: Frevert, Ute
APPLICANT: Sinnis, Photini
APPLICANT: Nussenzweig, Vi
 APPLICATION NUMBER: U: FILING DATE: 19920917 CLASSIFICATION: 530
 ZIP: 10022
 COUNTRY:
 STREET:
 ADDRESSEE:
 1 WSPCSVTCG 9
 N
 WSPCSVTCG 10
 New York
 10022
 Application US/07947033
 New York
 E: Darby & Darby, P.C.
805 Third Avenue
 805 Third Avenue
 United States of America
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יאבא: US/07/947,033
19920917
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 밁
 US-07-947-033-10
 US-07-947-033-9
 ATTORNEY/AGENT INFORMATION:
NAME: Adda C. Gogoris, Esq.
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEPAX: (212) 537-6237
TELEEX: 236687
INFORMATION FOR SEQ ID NO: 10:
 Sequence 10, Application US/07947033 GENERAL INFORMATION:
 Query Match
Best Local Similarity
Matches 9; Conserv
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: AMINO ACID
 ATTORNEY/AGENT INFORMATION:
NAME: Adda C. Gogoris, Esq.
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986/07607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEPAX: (212) 753-6237
 COMPUTER: AST Premium II 386/33
OPERATING SYSTEM: DOS 3.3
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
 APPLICANT: Cerami, Carla
APPLICANT: Frevert, Ute
APPLICANT: Sinnis, Photini
APPLICANT: Nussenzweig, Victor
 SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: AMINO ACID
 COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
 CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING TITLE OF INVENTION: HEPATOCYTE INVASION BY MALARIAL SPOROZOITES NUMBER OF SEQUENCES: 27
 NUMBER OF SEQUENCES:
 TELEFAX: (212,
 ADDRESSEE: Darby & Darby, P.C. STREET: 805 Third Avenue CITY: New York STATE: New York
 APPLICATION NUMBER: FILING DATE: 1992091 CLASSIFICATION: 530
 COUNTRY: Ut
ZIP: 10022
 CLASSIFICATION:
 TOPOLOGY:
 2 WSPCSVTCG 10
 1 WSPCSVTCG 9
 United States of America
 100.0%; ilarity 100.0%; Conservative 0
 unknown
 unknown
 Diskette,
 19920917
 US/07/947,033
 5, inch,
 0;
 Score 59; DB 3
Pred. No. 0.16;
 Mismatches
 1.2 MB storage
 <u>س</u>
 0;
 Length 18;
 Indels
 0
 Gaps
 0
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100.0%; Score 59; DB 3; Length 18; llarity 100.0%; Pred. No. 0.16; Conservative 0; Mismatches 0; Indels

<u>,,</u>

Gaps

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1 WSPCSVTCG 9

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Query Match
Best Local Similarity
""" 9; Conservi
 RESULT 8
US-08-119-694-1
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 ; TOPOLOGY: unknown US-08-119-694-1
 US-08-119-694-7
 Sequence 1, Applicat:
GENERAL INFORMATION
 Sequence 7, Application GENERAL INFORMATION:
APPLICANT: Cerami
 TELEFAX: (212) 753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
TELEFAX: (212) 753-6237
 TITLE OF INVENTION:
TITLE OF INVENTION:
 APPLICATION NUMBER: US/08/119,694
FILING DATE: 10-Sept-1993
ATTORNEY/AGENT INFORMATION:
NAME: Adda C. Gogoris, Esq.
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
 APPLICANT: Frevert, Ute
APPLICANT: Sinnis, Photini
APPLICANT: Nussenzweig, Victor
 SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
 CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 APPLICANT: Frevert, Ute
APPLICANT: Sinnis, Photini
APPLICANT: Nussenzweig, Victor
APPLICANT: Nussenzweig, Victor
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING
TITLE OF INVENTION: HEPATOCYTE INVASION BY MALARIAL
TITLE OF INVENTION: SPOROZOITES
NUMBER OF SEQUENCES: 28
 NUMBER OF SEQUENCES:
 CORRESPONDENCE ADDRESS:
 OPERATING SYSTEM: DOS 3.3 SOFTWARE: Word Perfect 5.1
 STREET:
CITY:
 REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986/17607-US1
 COMPUTER:
 COUNTRY:
 CITY: New York
 STREET:
 TYPE: amino acid
 ADDRESSEE:
 ADDRESSEE:
 1 WSPCSVTCG 9
 φ
 10022
 Application US/08119694
SEE: Darby & Darby, P.C : 805 Third Avenue New York
 Application US/08119694
 New York
 805 Third Avenue
 18 amino acids
 United States of America
 Cerami, Carla
 Conservative
 Cerami, Carla
 E: Diskette, 5, inch, 1.2 MB storage AST Premium II 386/33 SYSTEM: DOS 3.3
 Darby & Darby, P.C
 HEPATOCYTE INVASION BY MALARIAL SPOROZOITES
 100.0%;
 COMPOSITIONS AND METHODS FOR INHIBITING
 0;
 Score 59; DB 5; Length 18; Pred. No. 0.16;
 Mismatches
 0
 0;
 Gaps
 0;
```

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В
 QΥ
 TOPOLOGY: unknown US-08-119-694-7
 US-08-119-694-8
 TELEFAX: (414,
TELEX: 236687
TELEX: 236687
INFORMATION FOR SEO ID NO: 7:
SEQUENCE CHARACTERISTICS:
FENGTH: 18 amino acids
 ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
AMME: Adda C. Gogoris, Esq.
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986/17607-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 753-6237
TELEFAX: (212) 753-6237
 Sequence 8, Applicati
GENERAL INFORMATION:
 Best Local Similarity Matches 9; Conserv
 Query Match
 COMPUTER: AST FLOOR
COMPUTER: AST FLOOR
OPERATING SYSTEM: DOS 3.3
OPERATING SYSTEM: DOS 3.3
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/119,694
APPLICATION INCOME: 10-Sept-1993
 TELEFAX: (212) 753-623
TELEX: 236687
INFORMATION FOR SEQ ID NO:
 2IP: 10042
COMPUTER READABLE FORM:
COMPUTER: Diskette, 5, inch, 1.2 MB storage
COMPUTER: AST Premium II 386/33
COMPUTER: AST Premium II 386/33
 APPLICANT:
 ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
 CURRENT APPLICATION DATA
 STREET: DOUGHTY: New York
TRATE: New York
TRATE: New York
 FILING DATE: 10-Sept-199
ATTORNEY/AGENT INFORMATION:
NAME: Adda C. Gogoris, E
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby, P.C.
 TITLE OF INVENTION: COMPOSITION: TITLE OF INVENTION: HEPATOCYTE TITLE OF INVENTION: SPOROZOITES
 REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 59
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEPAX: (212) 753-6237
 APPLICANT:
SEQUENCE CHARACTERISTICS
 NUMBER OF SEQUENCES:
 APPLICANT:
 STATE: N
 MEDIUM TYPE: Diskette, 5, inch, 1.2 MB storage COMPUTER: AST Premium II 386/33 OPERATING SYSTEM: DOS 3.3 SOFTWARE: Word Perfect 5.1
 APPLICATION NUMBER: US/08/119,694 FILING DATE: 10-Sept-1993
 COUNTRY:
 2 WSPCSVTCG 10
 1 WSPCSVTCG 9
 10022
 New York
 Application US/08119694
 . United States of America
 805 Third Avenue
 Frevert, Ute
Sinnis, Photini
Nussenzweig, Victor
 United States of America
 Conservative
 Cerami, Carla
 COMPOSITIONS AND METHODS FOR INHIBITING HEPATOCYTE INVASION BY MALARIAL
 100.0%; Score 59; DB 5
100.0%; Pred. No. 0.16;
tive 0; Mismatches
 28
 7:
 Esq
 5986/17607-US1
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 0;
 Length 18;
 Indels
 0,
 Gaps
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US-08-119-694-10; Sequence 10, Application US/08119694; GENERAL INFORMATION: APPLICANT: Cerami, Carla; APPLICANT: Frevert, Ute
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 Query Match
Best Local Similarity
""" 6 9; Conserva
 RESULT 12
 TOPOLOGY: US-08-119-694-9
 В
 ; TOPOLOGY: unknown US-08-119-694-8
 Sequence 9, Applicati
GENERAL INFORMATION:
 Query Match
Best Local :
 SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/119,694
FILING DATE: 10-Sept-1993
ATTORNEY/AGENT INFORMATION:
NAME: Adda C. Gogoris, Esq.
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986/17607-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
 Matches
 INFORMATION FOR SEQ ID NO:
 APPLICANT: Frevert, Ute
APPLICANT: Sinnis, Photini
APPLICANT: Sinnis, Photini
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING
TITLE OF INVENTION: HEPATOCYTE INVASION BY MALARIAL
TITLE OF INVENTION: SPOROZOITES
 SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
 APPLICANT:
 COMPUTER: AST Premium II 386/33
OPERATING SYSTEM: DOS 3.3
SOFTWARE: Word Perfect 5 1
 STREET: 805 This
CITY: New York
STATE: New York
 Match 100.0%;
Local Similarity 100.0%;
ses 9; Conservative 0;
 COUNTRY:
 LENGTH: 18 amino acids TYPE: amino acid
 ADDRESSEE:
 2 WSPCSVTCG
 1 WSPCSVTCG 9
 1 WSPCSVTCG 9
 TRY: United States of America
10022
 Application US/08119694
 236687
 E: Darby & Darby, P.C.
805 Third Avenue
 Conservative
 Cerami, Carla
 unknown
 10
 100.0%; Score 59; DB 5; 100.0%; Pred. No. 0.16;
 0
 Score 59; DB
Pred. No. 0.1
); Mismatches
 Mismatches
 0.16;
 DB 5; Length 18;
 0;
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 Indels
 0;
 0,:
 Gaps
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 US-08-119-694B-1
 US-08-119-694-10
 TELEX: 236687

INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
 Sequence 1, Applicati
GENERAL INFORMATION:
 Query Match
Best Local Similarity
Matches 9; Conserv
 REGISTRATION NUMBER: 29,714
REFERENCE/OOCKET NUMBER: 5986/17607-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEPAX: (212) 753-6237
 COMPUTER READABLE FORM:
MEDIUM TYPE: DISKELLE, 5, inch, 360 KB storage
COMPUTER: COMPAQ PROLINEA MT 4/66
OPERATING SYSTEM: DOS 3.3
SOFTWARE: WOR'D PERCEL 5.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/119,694B
 APPLICANT: NUSSENZWEIG, VICTOR
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: INHIBITING HEPATOCYTE INVASION
TITLE OF INVENTION: BY MALARIAL SPOROZOITES
 APPLICATION NUMBER: US/08/119,694
FILING DATE: 10-Sept-1993
ATTORNEY/ACENT INFORMATION:
NAME: Adda C. Gogoris, Eq.
 COMPUTER: AST Premium II 38
OPERATING SYSTEM: DOS 3.3
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
 TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
 CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES:
 APPLICANT:
 APPLICANT:
 APPLICANT:
 APPLICANT:
 TELLEFAX: 122
TELEFAX: 236687
 APPLICANT:
 STREET: 805 Th
CITY: New York
STATE: New Yor
 CITY: New York
STATE: New York
 COUNTRY:
 TOPOLOGY:
 COUNTRY:
 STREET:
 ADDRESSEE:
 ADDRESSEE:
 2 WSPCSVTCG 10
 1 WSPCSVTCG 9
 TRY: United States
 10022
 1: 18 amino acids
amino acid
 Application US/08119694B
 New York
 805 Third Avenue
 E: Darby & Darby, P.C.
805 Third Avenue
 100.0%; Score 59; DB 5 ilarity 100.0%; Pred. No. 0.16; Conservative 0; Mismatches
 Frevert, Ute
Sinnis, Photini
 Cerami, Carla
 United States of America
 Sinnis, Photini
Nussenzweig, Victor
 unknown
 Darby & Darby, P.C
10-Sept-1993
 COMPOSITIONS AND METHODS FOR INHIBITING HEPATOCYTE INVASION BY MALARIAL SPOROZOITES
 10:
 of Ameri8ca
 5, inch, 1.2 MB storage
II 386/33
 DB 5; Length 18;
 Indels
 0;
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ATTORNEY/AGENT INFORMATION:

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 US-08-119-694B-1
Qy
 US-08-119-694B-7
 US-08-119-694B-7
 Query Match
 Sequence 7, Application US/08119694B GENERAL INFORMATION:
 Best Local Similarity
Matches 9; Conserv
 Best
 Query Match
 TELEX: 236687
INFORMATION FOR SEQ ID NO:
 TELEX: 236687
INFORMATION FOR SEQ ID NO:
 SEQUENCE CHARACTERISTICS: LENGTH: 18 amino acids
 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 527-7700
 REFERENCE/DOCKET NUMBER: 5986/17607-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/119,694B
FILING DATE: 10-Sept-1993
ATTORNEY/AGENT INFORMATION:
NAME: Adda C. Gogoris, Esq.
REGISTRATION NUMBER: 29,714
 APPLICANT: Cerami, Carla APPLICANT: Frevert, Ute APPLICANT: Sinnis, Photir
 SEQUENCE CHARACTERISTICS:
 COMPUTER READABLE FORM:
 NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: INHIBITING HEPATOCYTE INVASION TITLE OF INVENTION: BY MALARIAL SPOROZOITES
 APPLICANT:
 TYPE: amino acid TOPOLOGY: unknow
 TELEFAX:
 REFERENCE/DOCKET NUMBER:
 COMPUTER: COMPAQ PROLINEA MT 4/66
OPERATING SYSTEM: DOS 3.3
SOFTWARE: WORD Perfect 5.2
 REGISTRATION NUMBER:
 Local Similarity
nes 9; Conserv
 MEDIUM TYPE:
 COUNTRY:
 STREET:
 ADDRESSEE:
 ENGTH:
 TOPOLOGY:
 2 WSPCSVTCG 10
 1 WSPCSVTCG 9
 LENGTH:
 1 WSPCSVTCG 9
 10022
 New York
 Adda C. Gogoris,
 : 18 amino acids amino acid
 805 Third Avenue
 Frevert, Ute
Sinnis, Photini
Nussenzweig, Victor
 (212) 753-6237
 100.0%; Score 59; DB 5 ilarity 100.0%; Pred. No. 0.16; Conservative 0; Mismatches
 (212) 753-6237
 United States of Ameri8ca
 Conservative
 unknown
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 Darby & Darby, P.C.
 Diskette, 5,
 100.0%; S
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htive 0;
 29,714
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 7:
 5986/17607-US1
 inch, 360 KB storage
 Score 59; Pred. No.
 Mismatches
 0.16;
 DB 5; Length 18;
 DB 5; Length 18;
 0,
 0;
 Indels
 Indels
 0;
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 Gaps
 Gaps
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B
 US-08-119-694B-8
Search completed: January 29, 2002, 10:56:02 Job time: 2398 sec
 DЪ
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 US-08-119-694B-8
 MEDIUM TYPE: DISKette, 5, inch, 360 KB storage COMPUTER: COMPAO PROLINEA MT 4/66 OPERATING SYSTEM: DOS 3.3 SOCTWARRE: WOO'D PETICATION DATA: APPLICATION UMBER: US/08/119,694B FILING DATE: 10.5ept.1993 ATTORNEY/AGENT INFORMATION: NAME: Adda C. Gogoris, Esq. REGISTRATION NUMBER: 29,714 REFERENCE/DOCKET NUMBER: 5986/17607-US1 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:
 Query Match
Best Local S
Matches 9
 Sequence 8, Application US/08119694B GENERAL INFORMATION:
 TELEFAX: (212) 753-62:
TELEX: 236687
INFORMATION FOR SEQ ID NO:
 APPLICANT:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
 TITLE OF INVENTION:
TITLE OF INVENTION:
 CORRESPONDENCE ADDRESS
 APPLICANT: Cerami, Carla
 SEQUENCE CHARACTERISTICS:
 NUMBER OF SEQUENCES:
 APPLICANT:
 TYPE: am:
TOPOLOGY:
 CITY:
 COUNTRY:
 STREET:
 Local Similarity
nes 9; Conserv
 ADDRESSEE:
 2 WSPCSVTCG 10
 2 WSPCSVTCG 10
 LENGTH:
 1 WSPCSVTCG 9
 10022
 New York
 amino acids
 New York
 805 Third Avenue
 (212) 753-6237
 Nussenzweig, Victor
 Frevert, Ute
Sinnis, Photini
 United States of Ameri8ca
 100.0%;
larity 100.0%;
Conservative 0;
 unknown
 Darby & Darby, P.C.
 BY MALARIAL SPOROZOITES
 COMPOSITIONS AND METHODS FOR INHIBITING HEPATOCYTE INVASION
 0;
 Score 59; DB 5
Pred. No. 0.16;
Mismatches
 Length 18;
 Indels
 0;
 Gaps
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0;

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Result
 Database
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 Run
 Maximum
 Minimum
 Total number
 Searched:
 Scoring table:
 Perfect score:
 Title:
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 ĕ
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 DB DB
 Score
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 protein search, using sw model
 length:
 Match
 Pending_Patents_AA_New:*

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// cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
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 US-09-763-397A-8
59
1 WSPCSVTCG 9
 173191 seqs, 36597120 residues
 January 29, 2002, 10:58:10;
 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
 Lengt
 2000000000
US-09-197-770B-2
US-09-462-909B-2
US-09-468-068-6
US-09-858-068-6
US-09-858-068-6
US-09-978-192-301
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US-09-989-687-10
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 Search time 120.95 Seconds
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 (without alignments)
 Description
Sequence
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 2 Appli
13 Appli
6 Appli
9 Appli
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17 Appl
17 Appli
17 Appli
17 Appli
186 App
207 App
207 Appli
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| RESULT 1 US-09-197-770B-2 ; Sequence 2, Applica : GENERAL INFORMATION | ,          | 45                | 44                | 43                | 42                | 41               | 40              | 39                | 38                | 37                | 36                | 35              | 34              | ယ္              | 32                | 31                | 30                | 29                | . 28             | 27                |  |
|-----------------------------------------------------------------------|------------|-------------------|-------------------|-------------------|-------------------|------------------|-----------------|-------------------|-------------------|-------------------|-------------------|-----------------|-----------------|-----------------|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|--|
| 770B-3                                                                |            | 50                | 51                | 51                | 51                | 51               | 51              | 51                | 51                | 51                | 51                | 51              | 51              | 51              | 51                | 51                | 51                | 51                | 51               | 51                |  |
| 770B-2<br>2, Application US/09197770B                                 |            | 84.7              | 86.4              | 86.4              | 86.4              | 86.4             | 86.4            | 86.4              | 86.4              | 86.4              | 86.4              | 86.4            | 86.4            | 86.4            | 86.4              | 86.4              | 86.4              | 86.4              | 86.4             | 86.4              |  |
| ion US/                                                               |            | 465               | 1203              | 1172              | 1172              | 1170             | 1170            | 1168              | 1152              | 1151              | 1136              | 1093            | 1078            | 1049            | 1034              | 954               | 939               | 926               | 367              | 300               |  |
| 091                                                                   |            | 5                 | Ç,                | 6                 | 6                 | σ                | 6               | տ                 | Ç,                | G,                | თ                 | 5               | Ç               | G               | տ                 | s                 | G.                | ഗ                 | σ                | 5                 |  |
| 97770в .                                                              | ALIGNMENTS | us-09-969-515-12  | US-09-989-687-5   | US-10-020-141-14  | US-10-008-093-4   | US-10-020-141-12 | US-10-008-093-2 | US-09-919-603-2   | US-09-919-603-1   | US-09-854-845-10  | US-09-854-845-12  | US-09-854-845-4 | US-09-854-845-8 | US-09-854-845-2 | US-09-854-845-6   | US-09-854-845-14  | US-09-854-845-16  | US-09-715-417A-28 | US-10-001-054-50 | US-09-919-603-7   |  |
|                                                                       | ÷          | Sequence 12, Appl | Sequence 5, Appli | Sequence 14, Appl | Sequence 4, Appli | 12,              | ,               | Sequence 2, Appli | Sequence 1, Appli | Sequence 10, Appl | Sequence 12, Appl | 4               | 8               | 'n              | Sequence 6, Appli | Sequence 14, Appl | Sequence 16, Appl | Sequence 28, Appl | 50,              | Sequence 7, Appli |  |

```
Sequence 2, Application US/09462909B
GENERAL INFORMATION:
APPLICANT: MEINIEL, Annie
APPLICANT: MONNERIE, Hubert
APPLICANT: GOBRON, Stephane
TITLE OF INVENTION: NOVEL PEPTIDES AND POLYPE
TITLE OF INVENTION: SYSTEM
FILE REFERENCE: 065691/0179
CURRENT APPLICATION NUMBER: US/09/462,909B
CURRENT FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: PCT/FR98/01556
PRIOR APPLICATION NUMBER: FR 97/09016
PRIOR APPLICATION NUMBER: FR 97/09016
PRIOR FILING DATE: 1997-07-16
 FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: fragment/ analog of thrombospondin
US-09-197-770B-2
 RESULT 2
US-09-462-909B-2
 밁
 SEQ ID NO 2
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
 Query Match
Best Local :
 Matches
 APPLICANT: Tuszyński, George
APPLICANT: Williams, Taffy
APPLICANT: Williams, Taffy
APPLICANT: Actor, Paul
TITLE OF INVENTION: THROMBOSPONDIN ACTIVITY
TITLE OF INVENTION: THROMBOSPONDIN ACTIVITY
FILE REFERENCE: 07206-0021
CURRENT FILINGTON NUMBER: US/09/197,770B
CURRENT FILING DATE: 1998-11-23
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.0
 Local Similarity
nes 9; Conserv
 1 WSPCSVTCG
 1 WSPCSVTCG 9
 100.0%; Score 59; DB 5; ilarity 100.0%; Pred. No. 1.6e+05; Conservative 0; Mismatches 0;
 9
 AND POLYPEPTIDES
 Length
 USEFUL FOR REGENERATING
 synthetic
 0
 Gaps
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0

THE

SEQ ID NO

TYPE: PRT

NUMBER OF SOFTWARE:

SEQ

ID NOS: 24

PatentIn version 3.1

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 US-09-462-909B-2
 US-09-980-564-13
 Query Match
Best Local Similarity
---hes 9; Conserv
 ; PAGES: 4375-81
; DATE: 1995
US-09-980-564-13
 RESULT 4
US-09-858-068-6
 Ωy
 Вþ
 Sequence 13, Application US/09980564

Sequence 13, Application US/09980564

GENERAL INFORMATION:

APPLICANT: UNIVERSITY OF WASHINGTON

TITLE OF INVENTION: RECOMBINANT ADENOVIRAL VECTORS FOR CELL SPECIFIC TITLE OF INVENTION: CHYERIC FIBER PROTEINS

TITLE OF INVENTION: CHYERIC FIBER PROTEINS

FILE REFERENCE: 30429.2W001
 Query Match
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Sequence 6, Application US/09858068
GENERAL INFORMATION:
APPLICANT: Kapeller-Liebermann, Rosana
APPLICANT: Cook, William James
APPLICANT: Silos-Santlago, Inmaculada
APPLICANT: Silos-Santlago, Inmaculada
TITLE OF INVENTION: 33428, A NOVEL HUMAN METALLOPROTEASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-057001
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 SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 18
TYPE: PRT
 CURRENT APPLICATION NUMBER: US/09/980,564
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/137,213
PRIOR FILING DATE: 1999-06-01
 AUTHORS: Cerami, C.
JOURNAL: Cell
VOLUME: 70
PAGES: 1021-33
DATE: 1992
 PRIOR APPLICATION NUMBER: 60/161,097 PRIOR FILING DATE: 1999-10-22
 NUMBER OF SEQ ID NOS: 13
 PUBLICATION INFORMATION:
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 ORGANISM: Bovine
 JOURNAL: Infect. Immun. VOLUME: 63
 AUTHORS: Chatterjee, S.
 ORGANISM: Plasmodium falciparum
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 Score 59; DB 5;
Pred. No. 1.6e+05;
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PRIOR FILING DATE: 2000-05-15
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SOFTWARE: FastSEQ for Windows Version 4.0
 APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Cook, William James
APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: 33428, A NOVEL HUMAN METALLOPROTEASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
 NUMBER OF SEQ ID NOS: 8
APPLICANT: Bandaru, Rajasehkar
APPLICANT: Curtis, Rory A.J.
APPLICANT: Spurling, Heidi Lynn
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Millennium Pharmaceuticals, Inc.
TITLE OF INVENTION: 53014, A Human Metalloprotease Family
TITLE OF INVENTION: Member and Uses Therefor
FILE REFERENCE: MPI2000-523PIRCP1(M)
 FILE REFERENCE: 10448-049001
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CURRENT FILING DATE: 2001-05-15
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PRIOR FILING DATE: 2000-05-15
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 US-09-978-189-301
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ORGANISM: Artificial Sequence
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 SOFTWARE: P
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 APPLICANT: Tuszynski, George
APPLICANT: Williams, Taffy
APPLICANT: Actor, Paul
TITLE OF INVENTION: RETROINVERSO POLYPEPTIDES THAT MIMIC OR INHIBIT
TITLE OF INVENTION: THROMBOSPONDIN ACTIVITY
FILE REFERENCE: 07206-0021
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PRIOR FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 11
 APPLICANT: Ashkenazi, Avi
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 APPLICATION NUMBER: US/10/014,070 FILING DATE: 2001-11-13
 PatentIn Ver. 2.0
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
 Filvaroff, Ellen
 Desnoyers, Luc
 Botstein, David
 Baker Kevin P.
 Eaton, Dan
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CURRENT FILING DATE: 2001-10-15
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PRIOR FILING DATE: 1997-11-13
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Shelton, David L.
Stewart, Timothy A.
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 Gurney, Austin I
Hillan, Kenneth
 Godowski, Paul J.
Grimaldi, J. Christopher
 Sophia S.
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GENERAL I
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 APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
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 e 301, Application US/09978192 INFORMATION:
 Similarity
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 Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavín, Ivar J.
Kuo, Sophia S.
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 Goddard, Audrey
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 NUMBER: 60/084598
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Shelton, David L.
Stewart, Timothy A.
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Filvaroff,
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 Desnoyers, Luc
 Napier, Mary A.
 Tumas,
 Paoni,
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 Wei-Qiang
 James;
 1998-05-15
 Sherman
 1998-05-15
 Nicholas F.
Daniel
 , Napoleon
ff, Ellen
 Paul J.
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88.9%;
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 PRIOR APPLIANTE: 1998-03-20
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PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
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 APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
 PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
 PRIOR APPLICATION NUMBER: 09/918585 PRIOR FILING DATE: 2001-07-30
 CURRENT APPLICATION NUMBER: US/09/978,697 CURRENT FILING DATE: 2001-10-16
 PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
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 PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
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FILING DATE: 1998-04-22

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1998-04-22

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APPLICATION NUMBER:

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FILING DATE: 1998-04-29

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NUMBER: NUMBER:

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1998-04-08

1998-04-08

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APPLICANT: KuO, Sophia S.
APPLICANT: Napler, Mary A.
APPLICANT: Pan, James;
APPLICANT: Pani, Micholas F.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Shelton, David L.
APPLICANT: Shelton, David L.
APPLICANT: Williams, Daniel
APPLICANT: Williams, D. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
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TITLE OF INVENTION: Acids Encoding the Same
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 APPLICANT:
 APPLICANT
 APPLICANT:
 APPLICANT: Ashkenazi, Avi
 APPLICANT
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 FILING DATE: 1998-0: APPLICATION NUMBER:
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 Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
 Godowski, Paul J.
Grimaldi, J. Christopher
 Filvaroff, Ellen
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 Gerritsen, Mary
 Gerber, Hanspeter
 Eaton,
 Baker Kevin
 Application US/09978824
 Conservative
 Wei-Qiang
 Sherman
 Dan
 1998-05-1
 Audrey
 Napoleon
 94.9%;
 ۳.
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 60/085700
 60/085339
 60/085580
 60/085582
 Ħ
 Score
Pred.
 Mismatches
 No. 0.
 DB 5;
 Polypeptides and
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 Indels
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 Nucleic
 Gaps
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60/084639

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60/078939

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 APPLICANT: YIING, Steven P.
APPLICANT: YU, JIANGCHUN
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TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C6
CURRENT APPLICATION NUMBER: US/09/970,966
CURRENT FILING DATE: 2001-10-02
 APPLICANT: Stolk, John A. APPLICANT: Molesh, David
 PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
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APPLICANT: TUSZYJNSKI, George
APPLICANT: Williams, Taffy
APPLICANT: Actor, Paul
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 APPLICANT:
APPLICANT:
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 ISHII, SHIZUKO
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## SUMMARIES

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| 412<br>423<br>424<br>424                                                          | 21<br>350<br>396<br>412<br>412                                                                         | Query<br>Match Length DB ID |
| 13                                                                                | 3 3 22 21                                                                                              | DB                          |
| US-08-948-885-18<br>US-08-932-929A-1<br>US-07-842-694-2<br>US-08-760-797-1        | 1 US-09-763-397A-7<br>1 US-09-763-397A-2<br>2 US-09-820-843A-31<br>US-07-677-539B-6<br>US-07-727-636-6 | ID                          |
| Sequence 18, Appli<br>Sequence 1, Appli<br>Sequence 2, Appli<br>Sequence 1, Appli | Sequence 7, Appli<br>Sequence 2, Appli<br>Sequence 31, Appl<br>Sequence 6, Appli<br>Sequence 6, Appli  | Description                 |

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1 DIEKKICKMEKCSSVFNVVNS

21

## ALIGNMENTS

```
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-09-763-397A-7
 US-09-763-397A-7
 Sequence 7, Application US/09763397A GENERAL INFORMATION:
 SOFTWARE: PatentIn version 3.1 SEQ ID NO 7
 Query Match
Best Local Similarity
Matches
 APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for APPLICANT: Control and Prevention APPLICANT: Lal, Altaf A. APPLICANT: Hasnain, Seyed E. TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Fa FILE REFERENCE: 6395-57049
FILE REFERENCE: 6395-57049
FILE REFERENCE: 6395-57049
FILE REFERENCE: 6395-57049
FILE REFERENCE: 6395-57049
FILE REFILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR FILING DATE: 1998-08-21
PRIOR FILING DATE: 1999-08-19
 21;
 Conservative
 100.0%;
 0,
Score 109; DB 21;
Pred. No. 3.2e-09;
); Mismatches 0;
 Indels
 Length
 21;
 0
 Gaps
 0
```

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밁
 В
 Qy
 ; OTHER INFORMATION: Recombinant DNA/Protein US-09-763-397A-2
 Qy
 NAME/KEY: misc_feature;
OTHER INFORMATION: gi|4493889
US-09-820-843A-31
 Вb
 US-09-820-843A-31
 Query Match
Best Local Similarity 100.
 Sequence 31, Application US/09820843A GENERAL INFORMATION:
 SOFTWARE: PatentIn version 3.1 SEQ ID NO 2
 Sequence 2, Application US/09763397A GENERAL INFORMATION:
 SOFTWARE: PatentIn version 3.0 SEQ ID NO 31
 Best Local Similarity 100 Matches 21; Conservative
 CURRENT APPLICATION NUMBER: US/09/763,397A CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR FILING DATE: 1998-08-21
PRIOR APPLICATION NUMBER: PCT / US99/18869
PRIOR APPLICATION NUMBER: PCT / US99/18869
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 26
 -09-763-397A-2
 Query Match
 APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: Q63915
 APPLICANT: Ping Shi, Ya
APPLICANT: Hasnain, Seyed E.
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falc:
FILE REFERENCE: 6395-57049
 APPLICANT:
 APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for DiapplicaNT: Control and Prevention
 CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
 CURRENT APPLICATION NUMBER: US/09/820,843A
 ORGANISM: Artificial Sequence
 FEATURE:
 NAME/KEY: misc_feature OTHER INFORMATION: Circumsporozoite (CS) protein
 FEATURE:
 TYPE: PRT
ORGANISM: Plasmodium falciparum
 ENGTH: 350
 ENGTH: 396
61 DIEKKICKMEKCSSVFNVVNS 81
 1 DIEKKICKMEKCSSVFNVVNS 21
 Lal, Altaf A.
 100.0%;
 100.0%;
 0
 0,
 Score 109; DB 21;
Pred. No. 6.6e-08;
 Score 109; DB 22; Pred. No. 7.5e-08; Mismatches 0;
 Mismatches
 0;
 Length 350;
 Indels
 Length 396;
 0;
 0;
 Gaps
 0,
 0;
 QУ
```

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RESULT 4
US-07-677-539B-6
 ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-07-677-539B-6
 Дb
 RESULT 5
US-07-727-636-6
 Sequence 6, Application US/07677539B GENERAL INFORMATION:
 Query Match
Best Local Similarity 100.
 GENERAL INFORMATION:
 TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
 REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 56
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067
 ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 APPLICANT: LAL, ALTAF A.
APPLICANT: GOLDMAN, IRA F.
TITLE OF INVENTION: CIRCUMSPOROZOITE PROTEIN OF PLASMODIUM
TITLE OF INVENTION: REICHENOWI AND VACCINE FOR HUMAN MALARIA
 CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
 APPLICANT: LAL, ALTAF A.
APPLICANT: GOLDMAN, ITA F.
TITLE OF INVENTION: CIRCUMSPOROZOITE PROTEIN OF PLASMODIUM
TITLE OF INVENTION: REICHENOWI AND VACCINE FOR HUMAN MALARIA
 SEQUENCE CHARACTERISTICS:
 UMBER OF SEQUENCES:
 CORRESPONDENCE ADDRESS
 NUMBER OF SEQUENCES:
 378 DIEKKICKMEKCSSVFNVVNS 398
 COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patentl
 STREET: 1615 L S'
CITY: WASHINGTON
STATE: D.C.
 APPLICATION NUMBER: UPPLICATION NUMBER: UPPLIC
 COUNTRY:
 CLASSIFICATION:
 ADDRESSEE:
 STATE:
 STREET: 1615 L ST
CITY: WASHINGTON
 1 DIEKKICKMEKCSSVFNVVNS 21
 STRANDEDNESS:
 LENGTH:
 COUNTRY:
 ADDRESSEE:
 20036
 20036
 AMINO ACID
 D.C.
Y: USA
 Application US/07727636
 D.C.
 E: CUSHMAN, DARBY & CUSHMAN 1615 L STREET, N.W.
 E: CUSHMAN, DARBY & CUSHMAN 1615 L STREET, N.W.
 412 amino acids
 USA
 Patentin Release #1.0, Version #1.25
 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
 single
 424
 100.0%; Score 109; DB 3;
100.0%; Pred. No. 7.8e-08;
tive 0; Mismatches 0;
 US/07/677,539B
 5683/91540
 Length 412;
 Indels
 0;
 Gaps
```

0

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В
 Ş
 US-08-948-885-18
; Sequence 18, Application US/08948885
; GENERAL INFORMATION:
 STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-727-636-6
 ATTORNEY/AGENT INFORMATION:

NAME: SCOTT, WATSON T.

REGISTRATION NUMBER: 26,581

REFERENCE/DOCKET NUMBER: 5683

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-861-3067

TELEPHONE: 202-822-0944

TELEPAX: 6714627 CUSH

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
 Query Match
Best Local Similarity
Matches 21; Conserv
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/313,288
FILING DATE: January 5, 1995
ATTORNEY_AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
 STATE: New York
COUNTRY: New York
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 19910710
CLASSIFICATION: 424
 APPLICANT: Jessell, Thomas M. and Avihu Klar TITLE OF INVENTION: CLONING, EXPRESSION AND ITTLE OF INVENTION: NOVEL SECRETED PROTEIN, I
 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
 STREET:
 378
 FILING DATE:
CLASSIFICATION:
 TELEFAX: (212) 391-0526
 OPERATING SYSTEM:
STRANDEDNESS:
 APPLICATION NUMBER:
 ADDRESSEE:
 1 DIEKKICKMEKCSSVFNVVNS 21
 LENGTH:
 LENGTH:
 DIEKKICKMEKCSSVFNVVNS 398
 10036
 i: 412 amino acids
AMINO ACID
 amino
 412 amino acids
 3: Cooper & Dunham LLP
1185 Avenue of the Americas
 Conservative
 PatentIn
 100.
 PC-DOS/MS-DOS
 Release #1.0, Version #1.25
 US/07/727,636
 US/08/948,885
 000
 0;
 5683/91540
 Score 109; DB 3;
Pred. No. 7.8e-08;
D; Mismatches 0;
 F-SPONDIN
 USES
 Length 412;
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 Indels
 0
 Gaps
 0;
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Query Match
Best Local Similarity
Thes 21; Conserve
 US-07-842-694-2
 RESULT
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 ; MOLECULE TYPE: US-08-948-885-18
 US-08-932-929A-1
 US-08-932-929A-1
Sequence 2, Application US/07842694
GENERAL INFORMATION:
APPLICANT: Cohen, Joseph
 Sequence 1, Application US/08932929A
GENERAL INFORMATION:
APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
 Matches
 Query Match
Best Local S
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 423 amino acids
 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932,929A
APPLICATION NUMBER: 10497
 FILING DATE: 13-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
 ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
 REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: B4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
 CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
STREET: 709 Swedeland
 TITLE OF INVENTION: Hybrid Protein Between CS TITLE OF INVENTION: from Plasmodium and HBSAG NUMBER OF SEQUENCES: 4
 172 DIEKKICKMEKCSSVFNVVNS 192
 CITY: King of Prussia STATE: PA
 Local Similarity
nes 21; Conserv
 STRANDEDNESS: TOPOLOGY: li
 TELEX:
 TELEFAX:
 COUNTRY:
 TOPOLOGY:
 1 DIEKKICKMEKCSSVFNVVNS 21
 amino acid
 610-270-5090
 USA
 Conservative
 Conservative
 linear
 peptide
 Diskette
 single
 100.0%;
 100.0%; Score 109; DB 13; 100.0%; Pred. No. 8.1e-08; tive 0; Mismatches 0;
 08/663,371
 Beecham Corporation Road
 B45015-1FWC2
 0;
 Score 109; DB 13,
Pred. No. 7.8e-08;
 Indels
 Indels
 Length 423;
 Length 412;
 0;
 0
 Gaps
 Gaps
 0
 0
```

APPLICANT: De Wilde TITLE OF INVENTION: NUMBER OF SEQUENCES:

De Wilde,

Michel

Malaria Vaccine Antigen

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δÃ
 ; ANTI-SENSE: NO US-07-842-694-2
 NAME: CARTOR CAROL G.
REGISTRATION NUMBER: 31151
REFERENCE/DOCKET NUMBER: B4
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino
 р
 US-08-760-797-1
 Sequence 1, Application US/08760797 GENERAL INFORMATION:
 Matches
 Query Match
 TOPOLOGY: linear MOLECULE TYPE: pro
 SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/842,694
FILING DATE: 19920227
 CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation STREET: P.O. Box 1539 / Corporate Patents CITY: King of Prussia
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 APPLICANT: De Wilde, Michel APPLICANT: Cohen, Joseph
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
 PRIOR APPLICATION DATA:
 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION: HYBRID PROTEIN TITLE OF INVENTION: PLASMODIUM AND
 173 DIEKKICKMEKCSSVFNVVNS 193
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
 TYPE: AMINO A
 COUNTRY:
 STREET: P.O. CITY: King of Prussia
STATE: Pennsylvania
 Local Similarity
 ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: P.O. Box 1539 - UW2220
 CLASSIFICATION:
 APPLICATION NUMBER:
FILING DATE: 04-DEC
 COUNTRY:
 1 DIEKKICKMEKCSSVFNVVNS 21
APPLICATION NUMBER: 08/4 FILING DATE: 17-MAY-1995
 19406-0939
 19406-0939
 PA
 USA
 Conservative
 linear
 protein
 04-DEC-1996
 single
 100.0%;
 us/08/760,797
 08/442,612
 0;
 B45015
 Score 109; DB 3;
Pred. No. 8.1e-08;
0; Mismatches 0;
 BETWEEN CS FROM
HBSAG
 Length 424;
 Indels
 0
 0;
```

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밁
 RESULT 10
US-08-760-797-3
 Sequence 3, Applicati
GENERAL INFORMATION:
 Query Match
Best Local
 Matches
 TELEPHONE: 610 270-509
TELEFAX: 610 270-5090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5096
TELEFAX: 610 270-5090
 ATTORNEY/AGENT INFORMATION:
 TELEFAX: 610 270-5090
 MOLECULE TYPE: protein
 SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,79
 TITLE OF INVENTION: HYBRID PROTEIN BETWEEN CS FROM TITLE OF INVENTION: PLASMODIUM AND HBSAG
 ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,1
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
 COMPUTER READABLE FORM:
 CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES:
 APPLICANT:
 169 DIEKKICKMEKCSSVFNVVNS 189
 REFERENCE/DOCKET NUMBER: B4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5096
 NAME: Baumeister, Kirk REGISTRATION NUMBER: 3
 CLASSIFICATION:
 APPLICATION NUMBER: FILING DATE: 21-OCT
 SEQUENCE CHARACTERISTICS:
 Local Similarity
 REFERENCE/DOCKET NUMBER:
 TOPOLOGY:
 ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: P.O. Box 1539 - UW2220 CITY: King of Prussia STATE: Pennsylvania
 STRANDEDNESS:
 APPLICATION NUMBER: 08/442,612
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: US 08/244
FILING DATE: 21-OCT-1994
CLASSIFICATION: 435
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
 1 DIEKKICKMEKCSSVFNVVNS 21
 ENGTH:
 MEDIUM TYPE:
 COUNTRY: USA
 FILING DATE:
LENGTH:
 amino acid
 19406-0939
 Application US/08760797
 424 amino acids
 Conservative
 Cohen, Joseph
424 amino acids
 De Wilde, Michel
 linear
 610
 21-OCT-1994
 Floppy disk
 04-DEC-1996
 single
 100.0%;
 SU
 us/08/760,797
 33,833
 <u>--</u>
 33,833
 08/244,085
 ω..
 B45015C1
 08/244,085
 0;
 B45015C1
 Score 109; DB 11;
Pred. No. 8.1e-08;
 Mismatches
 Version #1
 DB 11;
 Length 424;
 0;
 Gaps
```

0;

single

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S
 ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-760-797-3
밁
 밁
 US-08-903-084-1
 US-08-903-084-1
 Query Match
Best Local :
 Sequence 1, Application US/08903084 GENERAL INFORMATION:
 Matches
 INFORMATION FOR SEQ ID NO:
 CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: 08/741,575
FILING DATE: 30-CCT-1996
APPLICATION NUMBER: 08/303,542
FILING DATE: 09-SEP-1994
 REFERENCE/DOCKET NUMBER: B4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
 ATTORNEY/AGENT INFORMATION:
 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatik
 CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
 APPLICANT: Bruck, Claudine
APPLICANT: Francotte, Myrian
APPLICANT: Kummert, Suzanne
APPLICANT: Slaoui, Moncef
APPLICANT: Wijendale, Frans
 MOLECULE TYPE:
 TITLE OF INVENTION: VACCINE FORMULATIONS CONTAINING
TITLE OF INVENTION: 3-0-DEACYLATED MONOPHOSPHORYL LIPID A AND A CARRIER
 SEQUENCE CHARACTERISTICS:
 NUMBER OF SEQUENCES:
 169 DIEKKICKMEKCSSVFNVVNS 189
169 DIEKKICKMEKCSSVFNVVNS 189
 TELEPHONE: 610-270-5090
 TOPOLOGY:
 STRANDEDNESS:
 TYPE:
 APPLICATION NUMBER: US/0 FILING DATE: 17-JUL-1997
 OPERATING SYSTEM:
 COUNTRY:
 Local
 LENGTH:
 REGISTRATION NUMBER:
 Local Similarity es 21; Conserv
 1 DIEKKICKMEKCSSVFNVVNS 21
 1 DIEKKICKMEKCSSVFNVVNS 21
 19046
 King of Prussia
 Similarity
 : 424 amino acids amino acid
 Kerekes, Zoltan
 PΑ
 U.S.A.
 Francotte, Myriam
 100.0%;
ilarity 100.0%;
Conservative (
 100.0%; Score 109; DB 13; llarity 100.0%; Pred. No. 8.1e-08; Conservative 0; Mismatches 0;
 IBM Compatible
 protein
 single
 US/08/903,084
 38,938
 B45101
 0
 Score 109; DB 11;
Pred. No. 8.1e-08;
D: Mismatches 0;
 2.0
 Length 424;
 Length 424;
 Indels
 Indels
 0,
 0;
 Gaps
 Gaps
 0,
 0;
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Sequence 1, Application US/08932929
GENERAL INFORMATION:
APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: HYBRID PROTEIN BE'
TITLE OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
 US-08-932-929-1
 US-08-903-084-3
 US-08-903-084-3
 밁
 RESULT
 Query Match
Best Local S
Matches 21
 Sequence 3, Application:
 SEQUENCE CHARACTERISTICS:
 APPLICANT:
APPLICANT:
 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/7:
FILING DATE: 30-OCT-1996
APPLICATION NUMBER: 08/7:
 SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
 TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5024
 FILING DATE: 09-SEP-1994
ATTORNEY/AGENT INFORMATION:
 TITLE OF INVENTION: VACCINE FORMULATIONS CONTAINING
TITLE OF INVENTION: 3-0-DEACYLATED MONOPHOSPHORYL LIPID A AND A CARRIER
 APPLICANT:
 APPLICANT: Bruck, Claudine
 169 DIEKKICKMEKCSSVENVVNS 189
 CITY: King of Prussia STATE: PA COUNTRY: U.S.A.
 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
 STRANDEDNESS:
TOPOLOGY: li
 NAME: Kerekes, Zoltan REGISTRATION NUMBER:
 APPLICATION NUMBER: US/08/903,084 FILING DATE: 17-JUL-1997
 LENGTH: 424 amino acids
 TELEFAX: 610-270-5090
 REFERENCE/DOCKET NUMBER:
 1 DIEKKICKMEKCSSVFNVVNS 21
 ADDRESSEE:
 Similarity
 19046
 amino acid
 Application US/08903084
 E: SmithKline Beecham Corporation 709 Swedeland Road
 Wijendale, Frans
 100.0%; Score 109; ilarity 100.0%; Pred. No. 8 Conservative 0; Mismatches
 Francotte, Myriam
 Kummert, Suzanı
Slaoui, Moncef
 linear
SmithKline Beecham Corp./Corporate Intellectual Property
 single
 Suzanne
 for Windows Version
 08/303,542
 08/741,575
 38,938
 B45101
 Mismatches
 BETWEEN CS
 DB 13;
3.1e-08;
s 0;
 Indels
 Length
 424;
 0
 Gaps
```

0

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; TOPOLOGY: li
; MOLECULE TYPE:
US-08-932-929-1
 δÃ
 B
 US-08-932-929-3
 Sequence 3, Application US/08932929 GENERAL INFORMATION:
 Query Match
Best Local Similarity
 Matches
 TELEFAX: 610 270-5090 INFORMATION FOR SEQ ID NO:
 REFERENCE/DOCKET NUMBER: B4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5096
 FILING DATE: US 08/244,085
APPLICATION NUMBER: US 08/244,085
FILING DATE: 21-0CT-1994
ATTORNEY/AGENT INFORMATION:
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
 APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: HYBRID PROTEIN BETWEEN CS FROM
TITLE OF INVENTION: PLASMODIUM AND HBSAG
 SEQUENCE CHARACTERISTICS:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
 169 DIEKKICKMEKCSSVFNVVNS 189
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 COUNTRY: USA
ZIP: 19406-0939
 STREET: P.O. Box 1539 - UW2220 CITY: King of Prussia
 APPLICATION NUMBER: US/08/932,929 FILING DATE: 18-SEP-1997
 STATE: Pennsylvania Beecham Co. CITY: King of Prussia STATE: Pennsylvania
 TYPE: amino acid
STRANDEDNESS: sir
 REGISTRATION NUMBER:
 NAME:
 APPLICATION NUMBER: US/08/663,371
 LENGTH:
 FILING DATE:
 APPLICATION NUMBER: US/08/932,929
 COUNTRY:
 ADDRESSEE: SmithKline Beecham Corp./Corporate
 1 DIEKKICKMEKCSSVFNVVNS 21
APPLICATION NUMBER:
 19406-0939
 Baumeister, Kirk
 Pennsylvania
 424 amino acids
 USA
 Conservative
 linear
 protein
 single
 270-5090
 18-SEP-1997
 100.0%; Score 109; DB 13; 100.0%; Pred. No. 8.1e-08; tive 0; Mismatches 0;
 US/08/663,371
 33,833
 B45015-1
 Version #1.30
 Length 424;
 Indels
 0;
 Gaps
 0;
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-932-929-3
 US-08-932-929A-3
 Db
 δð
TOPOLOGY:
 Sequence 3, Application US/08932929A GENERAL INFORMATION:
 Matches
 Query Match
Best Local Similarity
 APPLICATION NUMBER: US/08/932,929A FILING DATE: 18-SEPT-1997 CLASSIFICATION: 435
PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/663,371
FILING DATE: 13-JUNE-1996
ATTORNEY/AGENT INFORMATION:
 TELEFAX: 610 270-5090
INFORMATION FOR SEQ ID NO:
 INFORMATION FOR SEQ ID NO:
 FILING DATE: 21-OCT-1994
ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: B4
TELECOMMUNICATION INFORMATION:
 SEQUENCE CHARACTERISTICS:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
 CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
 APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: Hybrid Protein Between CS
TITLE OF INVENTION: from Plasmodium and HBsAG
 REFERENCE/DOCKET NUMBER: B4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
 SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
 NUMBER OF SEQUENCES:
 SEQUENCE CHARACTERISTICS:
 169 DIEKKICKMEKCSSVFNVVNS 189
 STREET: 709 STATE: PA
 APPLICATION NUMBER:
 STRANDEDNESS:
 TELEPHONE:
 COMPUTER: IBM CON OPERATING SYSTEM:
 1 DIEKKICKMEKCSSVFNVVNS 21
 LENGTH:
 COUNTRY:
 TYPE: amino acid
STRANDEDNESS: sir
 NAME: Baumeister, Kirk REGISTRATION NUMBER: 3
 TELEFAX: 610-270-5090
 LENGTH:
 19406
 amino acid
 Baumeister, Kirk
 424 amino acids
 610
 424 amino acids
 Conservative
 IBM Compatible
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 610 270-5096
 Diskette
 270-5090
 21-OCT-1994
 single
 single
 100.0%; Score 109; DB 13; 100.0%; Pred. No. 8.1e-08;
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 US 08/244,085
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 B45015-1
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 B45015-1FWC2
 Mismatches
 Length 424;
 Indels
 0;
 Gaps
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0;

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Obery Match

Bast Local Similarity 100.0%; Foca 109; Dail; Length 424;

Bast Local Similarity 00.0%; Pred No. 8.1-06;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DIEKICKNESCSSVEWOWS 11

Db 169 DIEKICKNESCSSVEWOWS 189

Search completed; January 29, 2002, 10:56:02

Job time: 2398 sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Result
No.
 Title:
Perfect score:
 Run
 Database
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 Minimum DB
Maximum DB
 3
 Total number of hits satisfying chosen parameters:
 Searched:
 Scoring table:
 Sequence:
 protein -
 9
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 ..
 Score
 seg length: 0 seg length: 2000000000
 protein search, using sw model
 Pending_Patents_AA_New:*

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 Query
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 January 29, 2002, 10:58:09; Search time 120.95 Seconds (without alignments) 6.354 Million cell updates/sec
 173191 seqs, 36597120 residues
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US-09-708-427-35760
US-09-708-427-35758
US-09-620-111B-3030
US-09-620-111B-3029
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 Description
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| Qy<br>Db                                                | USE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          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| Query<br>Best I<br>Matche                               | SULT O9-611 APPLIC APPL |            | 22222<br>2222<br>2222<br>2321<br>2321<br>2321<br>2321<br>232                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| Match Local Similarity es 7; Conserv 4 KKICKMEKCSSVFN : | 526-3 38.5 38.5 38.7 38.7 38.7 38.7 38.7 38.7 38.7 38.7                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      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| larity<br>Conserva<br>KCSSVFN<br>        <br>KCGEAFN    | pplication: TOSHIC TOSH |            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| 40.<br>50.<br>tive<br>17                                | SHIO SHIO SHIO SHIUKO TAKAO I, KOJI SHIUKO YURI TSU, AI TSU, AI TSU, AI TSU, AI TSU, AI TSU, AI TSUJI I, FETSUJI ILISASHI PRIMERS FOR AND THEIR I PRIMERS FOR I AND THEIR I PRIMERS IUS/0 E 2000-07-07 NUMBER: JP 199 1999-07-08 NUMBER: JP 200 2000-01-11 NUMBER: JP 200 2000-05-02 OS: 4484 Ver. 2.1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |            | 317<br>317<br>317<br>364<br>464<br>51<br>120<br>272<br>272<br>272<br>272<br>334<br>341<br>341<br>379                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             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| 0.4 <u>.</u>                                            | US/0: TSUO O O O O O O O O O O O O O O O O O O                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               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| Score 44; DB:<br>Pred. No. 13;<br>2; Mismatches         | 9611526  R SYNTHESIS OF USES /09/611,526 07 999-194486 000-118774 000-183765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   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                                                                                                                                                         |
| 5; Length 167;<br>5; Indels                             | FULL LENGTH                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |            | 4<br>3000<br>3000<br>2999<br>2999<br>2999<br>1049<br>4032<br>1049<br>1048<br>4404<br>4404<br>4403<br>4403<br>4403<br>4403<br>4403<br>4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           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|                                                         | CDNAs                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        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| Gaps                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |            | 2, Appl<br>116, App<br>116, App<br>330001,<br>32999,<br>32999,<br>223, App<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Appl<br>64932,<br>Ap 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RESULT 2
US-09-708-427-35760
; Sequence 35760, Application US/09708427
; GENERAL INFORMATION:

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US-09-708-427-35758
; Sequence 35758, Appl
; GENERAL INFORMATION:
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 Ş
 US-09-708-427-35760
 RESULT 4
US-09-620-111B-3030
Sequence 3030, Application US/09620111B
GENERAL INFORMATION:
 OTHER INFORMATION: Ceres Seq. US-09-708-427-35758
 밁
 Qy
 Query Match
Best Local S
Matches 6
 APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 35760
LENGTH: 115
 APPLICANT: N. ALEXANDROV et al.

APPLICANT: N. ALEXANDROV et al.

APPLICANT: N. ALEXANDROV et al.

APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: THEREBY

FILE REFERENCE: 2750-1243P

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SOFTWARE: PATENTIA VETSION 3.1

SEQ ID NO 35758

LENGTH: 117
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Best Local Similarity
"Teches 6; Conserv
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Thereby
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 OTHER INFORMATION: Xaa is any
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 FEATURE:
 ORGANISM: Arabidopsis thaliana
 NAME/KEY: misc_feature
LOCATION: 1..117
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..117
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 ORGANISM: Arabidopsis thaliana
 34 RDVLKLSTCSNVLNLIN 50
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 4 KKICKMEKCSSVFNVVN 20
 4 KKICKMEKCSSVFNVVN 20
 RDVLKLSTCSNVLNLIN 52
 Similarity 6; Conserv
 Conservative
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 Application US/09708427
 39.4%;
 39.4%;
 Seq.
 6;
 amino acid
 Score 43; Pred. No.
 Score 43; DB Pred. No. 13;
 ID 1842252
 ID 1842250
 Mismatches
 Mismatches
 DB 5;
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 5.
 5.
 Length 115;
 Length 117;
 Indels
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 0;
 Gaps
 0;
 0
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; LOCATION: 1..68
; OTHER INFORMATION: Xaa is a NAME/KEY: misc_feature; LOCATION: 1..68
; OTHER INFORMATION: Ceres Structure; DOG-620-111B-3029
 ; NAME/KEY: misc_feature; LCATION: 1..58; COTHER INFORMATION: Ceres Seq. US-09-620-111B-3030
 Qy
 Query Match
Best Local Similarity
"-+ches 9; Conserv?
 В
 Db .
 QУ
 US-09-620-111B-3029
 US-09-894-018-273; Sequence 273, Application US/09894018
 RESULT
 CURRENT APPLICATION NUMBER: US/09/620,111B
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9298
SEQ ID NO 3030
LENGTH: 58
 FILE REFERENCE: 2750-1070P
CURRENT APPLICATION NUMBER: US/09/620,111B
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9298
SEQ ID NO 329
 Sequence 3029, Application US/09620111B GENERAL INFORMATION:
 GENERAL INFORMATION
 FILE REFERENCE: 2750-1070P
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 Query Match
Best Local
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 APPLICANT: EPIMMUNE, Inc.
APPLICANT: Sette, Alessa
APPLICANT: Chestnut, Rob
APPLICANT: Livingston, B
 APPLICANT: N. ALEXANDROV et al
 NAME/KEY: misc_feature
LOCATION: 1..58
OTHER INFORMATION: Xaa is
 ORGANISM: Arabidopsis thaliana
APPLICANT: Newman, Mark
APPLICANT: Brown, David
TITLE OF INVENTION: METODS AND SYSTEM FOR OPTIMIZING
 APPLICANT:
 FEATURE:
 FEATURE: misc_feature
 LENGTH: 68
TYPE: PRT
ORGANISM: Arabidopsis thaliana
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 1 DIEKKICKMEK-----CSSVFNVVNS 21
 34
 1 DIEKKICKMEK-----CSSVENVVNS
 DIDRRECKXOKPNNTSTSSYFSVLEN 59
 Similarity
9; Conserv
 Chestnut, Robert
 Baker, Denisw
Newman, Mark
 Livingston, Brian
 Sette, Alessandro
 Conservative
 Conservative
 39.0%;
34.6%;
 39.0%;
 is
 Seq. ID 1326658
 any amino acid
 any amino
 Score 42.5; D. pred. No. 9.1; 7; Mismatches
 Score 42.5; D
Pred. No. 7.9;
 ID 1326659
 Mismatches
 acid
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 DB
 5;
 5
 5
 Length
 Length 68;
 Indels
 <u>ა</u>
 <u>ن</u>
 Gaps
 <u>بر</u>
```

TITLE OF INVENTION:

REFERENCE: 39963-20033.00

MINIGENES AND PEPTIDES THEREBY

```
PRIOR APPLICATION NUMBER: 2001-06-27
PRIOR APPLICATION NUMBER: PCT/US00/35568
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/173,390
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: US 60/284,221
PRIOR APPLICATION NUMBER: US 60/284,221
PRIOR FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 273
ILENCRIP: 1
RESULT 8
US-09-708-427-22442
; Sequence 22442, Application US/09708427
 В
 õ
 В
 Ş
 ; OTHER INFORMATION: PfHTL US-09-894-018-141
 US-09-894-018-141
 ; ORGANISM: P. falciparum US-09-894-018-273
 PRIOR APPLICATION NUMBER: US 60/284,221
PRIOR FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 141
LENGTH: 276
 Query Match
Best Local :
 Matches
 Query Match
 Matches
 APPLICANT: Livingston, Brian
APPLICANT: Baker, Denisw
APPLICANT: Newman, Mark
APPLICANT: Newman, Mark
APPLICANT: Newman, Marid
TITLE OF INVENTION: METODS AND SYSTEM FOR OPTIMIZING
TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
FILE REFERENCE: 39963-20033.00
 PRIOR APPLICATION NUMBER: PCT/US00/35568
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/173,390
PRIOR FILING DATE: 1999-12-28
 CURRENT APPLICATION NUMBER: US/09/894,018
CURRENT FILING DATE: 2001-06-27
 APPLICANT:
 APPLICANT: EPIMMUNE, Inc.
 LENGTH: 15
TYPE: PRT
 CURRENT APPLICATION NUMBER: US/09/894,018
CURRENT FILING DATE: 2001-06-27
 FEATURE:
 ORGANISM: Artificial Sequence
 102
 13 SSVFNVVNS 21
||||||||
102 SSVFNVVNS 110
 Local Similarity
mes 9; Conserv
 13 SSVFNVVNS 21
 Local
 SSVFNVVNS 9
 Similarity 100
9; Conservative
 Chestnut, Robert
 Sette, Alessandro
 Application US/09894018
 Conservative
 38.5%;
 38.5%;
 0;
 0;
 Score 42;
Pred. No.
 Mismatches
 Mismatches
 DB 5;
 DB 5;
 0;
 0;
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 Length 15;
 Indels
 Indels
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 Gaps
 Gaps
 0;
 0;
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; LOCATION: 1..374
; OTHER INFORMATION: Xaa is a
; NAME/KEY: misc_feature
; LOCATION: 1..374
; OTHER INFORMATION: Ceres Se
US-09-620-3948-5663
 Query Match
Best Local Similarity
Thes B; Conserve
 ; OTHER INFORMATION: xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: 1.37
; COTHER INFORMATION: Ceres Seq. ID 1840904
US-09-708-427-22442
US-09-894-018-121
 QΥ
 US-09-620-394B-5663
 Query Match
Best Local Similarity 5/...
Best Conservative
 CURRENT APPLICATION NUMBER: US/09/620,394B
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9131
SEQ ID NO 5663
LENGTH: 374
 Sequence 5663, Application US/09620394B
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-1067P
 CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22442
LENGTH: 372
 GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
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ORGANISM: Arabidopsis thaliana
 NAME/KEY: misc_feature LOCATION: 1..372
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 NAME/KEY: misc_feature
 FEATURE:
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 4 KKICKMEKCSSVFN 17
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 Conservative
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57.1%;
 38.5%;
 Seq.
 any
 Score 42; DB Pred. No. 55;
 ID 1394837
 amino acid
 Score 42; DB
Pred. No. 55;
 Mismatches
 Mismatches
 5.
 <u>ن</u>
 Length 372;
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 Indels
 Indels
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 Gaps
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Sequence 121, Application US/09894018 GENERAL INFORMATION:

APPLICANT: EPIMMUNE, APPLICANT: Sette, A

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; FEATURE:
; OTHER INFORMATION: PfCTL/HTL(N)
US-09-894-018-121
 밁
 Š
 FILE REFERENCE: 39963-20033.00
CURRENT APPLICATION NUMBER: US/09/894,018
CURRENT FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: PCT/US00/35568
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/173,390
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: US 60/284,221
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OTHER INFORMATION: Ceres Seq. ID 1852376
US-09-708-427-39156
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RESULT 12
US-09-708-427-26073
 Dр
 Ωy
 NUMBER OF SEQ ID NOS: 368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 121
 CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 39156
LENGTH: 150
 Sequence 39156, Application US/0 GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
 Query Match
Best Local :
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 APPLICANT: Brown, David
TITLE OF INVENTION: METODS AND SYSTEM FOR OPTIMIZING
TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
FILE REFERENCE: 39963-20033.00
 Query Match
Best Local Similarity
Therefore, 7; Conserv
 PRIOR FILING DATE: 2001-04-16
 APPLICANT:
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
 TYPE: PRT
ORGANISM: Artificial Sequence
 PPLICANT:
 NAME/KEY: misc_feature
LOCATION: 1..150
OTHER INFORMATION: Xaa is any amino acid
 LENGTH:
 ORGANISM: Zea mays subsp.
 FEATURE:
 TYPE: PRT
 Local Similarity
nes 9; Conserv
 111111111
21 SSVFNVVNS 29
 13 SSVFNVVNS 21
 84 DLEKKFCKFGRVTS 97
 1 DIEKKICKMEKCSS 14
 Newman, Mark
Brown, David
 Baker, Denisw
 Livingston,
 Chestnut,
 Conservative
 Application US/09708427
 Conservative
 Robert
 38.5%; Score 42;
100.0%; Pred. No.
 37.6%;
 Brian
 mays
 0
 ω
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 Score 41; DB Pred. No. 32;
 Mismatches
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 DB 5;
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 Indels
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 Gaps
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NAME/KEY: misc_feature
LOCATION: 1..238
OTHER INFORMATION: Ceres
US-09-708-427-26073
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 US-09-605-703B-292
 RESULT
 CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEO ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEO ID NO 26073
LENGTH: 238
 ; ORGANISM: Corynebacterium glutamicum US-09-605-703B-292
 밁
 Sequence 26073, Application US/09708427 GENERAL INFORMATION:
US-09-708-427-4856
 RESULT 14
 Query Match
Best Local Similarity 45.0
Conservative
Cohas
 PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 2934
SEQ ID NO 292
LENGTH: 239
 GENERAL INFORMATION:
 APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
 FILE REFERENCE: 2750-1243P
 Query Match
Best Local Similarity
Matches 5; Conserv
 APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNBBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
TITLE OF INVENTION: PROTEINS
TITLE REFERENCE: BGI-129CP
FILE REFERENCE: BGI-129CP
 APPLICANT:
APPLICANT:
 APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
 PRIOR APPLICATION NUMBER: 60/142,764 PRIOR FILING DATE: 1999-07-08
 CURRENT APPLICATION NUMBER: US/09/605,703B CURRENT FILING DATE: 2000-06-27
 NAME/KEY: misc_feature
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 210 NVETRHCKRERCAAI 224
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 1 DIEKKICKMEKCSSV 15
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 Zelder, Oskar
 Application US/09605703B
 Conservative
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 4.
 Score 41;
Pred. No.
 Score 41; DB
Pred. No. 51;
 Mismatches
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 50;
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 Length 238;
 Length 239;
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 Gaps
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Sequence 4856, Application US/09708427 GENERAL INFORMATION: APPLICANT: N. ALEXANDROV et al.

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: ORGANISM: Arabidopsis thaliana
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: NAME/KEY: misc_feature
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US-09-708-427-4855
 : TYPE: PRT
: ORGANISM: Arabidopsis thaliana
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1..241
: OPHER INFORMATION: xaa is any amino acid
: NAME/KEY: misc_feature
: LOCATION: 1..241
: OPHER INFORMATION: Ceres Seq. ID 1813257
US-09-708-427-4856
 Ş
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Search completed: January 29, 2002, 10:58:10 Job time: 2506 sec
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 밁
 US-09-708-427-4855
 Sequence 4855, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
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 CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4856
LENGTH: 241
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 Query Match
Best Local S
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
 4 KKICKMEKCSSVFNVVNS 21
| :| : | : | :| |
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 Local Similarity 38.9 nes 7; Conservative
 4 KKICKMEKCSSVFNVVNS 21
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38.9%;
 37.6%;
38.9%;
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Pred. No. 54;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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 Perfect score:
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 Run on:
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 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result | Score | Query<br>Match | Query<br>Match Length DB ID | ВВ | ID                  | Description       |
|--------|-------|----------------|-----------------------------|----|---------------------|-------------------|
| _      | 127   | 100.0          | 23                          | 21 | US-09-763-397A-6    | Sequence 6, Appli |
| N      | 127   | 100.0          | 24                          | ω  | US-07-610-222-33    | Sequence 33, Appl |
| ω      | 127   | 100.0          | 24                          | æ  | US-08-480-512-55    | Sequence 55, Appl |
| 4      | 127   | 100.0          | 350                         | 21 | US-09-763-397A-2    | Sequence 2, Appli |
| ۍ.     | 127   | 100.0          | 412                         | w  | US-07-677-539B-6    | Sequence 6, Appli |
| 6      | 127   | 100.0          | 412                         | w  | US-07-727-636-6     | Sequence 6, Appli |
| 7      | 127   | 100.0          | 412                         | 13 | US-08-948-885-18    | Sequence 18, Appl |
| œ      | 127   | 100.0          | 423                         | 13 | US-08-932-929A-1    | Sequence 1, Appli |
| 9      | 127   | 100.0          | 424                         | ω  | 1 3 US-07-842-694-2 | Sequence 2, Appli |
|        |       |                |                             |    |                     |                   |

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1 KPKDELDYENDIEKKICKMEKCS 23

| 45       | 44                                            | 43      | 42                 | 41                | 40                | 39    | 38   | 37    | 36    | 35               | 34              | <b>ω</b>        | 32              | 31              | 30        | 29              | 28                | 27               | 26               | 25       | 24      | 23    | 22      | 21               | 20                | 19           | 18              | 17                                           | 16      | 15              | 14     | 13              | 12                | 11                | F   |
|----------|-----------------------------------------------|---------|--------------------|-------------------|-------------------|-------|------|-------|-------|------------------|-----------------|-----------------|-----------------|-----------------|-----------|-----------------|-------------------|------------------|------------------|----------|---------|-------|---------|------------------|-------------------|--------------|-----------------|----------------------------------------------|---------|-----------------|--------|-----------------|-------------------|-------------------|-----|
|          |                                               |         |                    | 53                |                   |       | 53   | 57    | 57    | 57               | 57              | 57              | 57              | 57              | 57        | 57              | 62                | 62               | 62               | 71       | 75      | 75    | 75      | 96               | 96                | 121          | 121             | 121                                          | 121     | 121             | 121    | 121             | 121               | 122               | 144 |
| 41.7     | 41.7                                          | 41.7    | 41.7               |                   |                   |       | 41.7 | 44.9  | 44.9  | 44.9             | ٠.              |                 | 44.9            |                 |           | 44.9            |                   | 48.8             | 8                | <u>ب</u> | 9       | 9     |         | 5                | 5                 | 5            | ŗ               | 95.3                                         | 5       | 5               | 95.3   | 5               | 5                 | ٥.                | ٠   |
| 21       | 21                                            | 21      | 21                 | 21                | 21                | 21    | 21   | 55    | 55    | 55               | 55              | 55              | 55              | 55              | 55        | 55              | 14                | 14               | 14               | 21       | 20      | 20    | 20      | 19               | 19                | 424          | 424             | 424                                          | 424     | 424             | 424    | 424             | 396               | 388               |     |
| ۍ        | <u>, , , , , , , , , , , , , , , , , , , </u> | _       | <b>–</b>           | _                 | 一                 | _     | -    | ഗ     | u     | ഗ                | ഗ               | ഗ               | ഗ               | w               | ω         | ω               | տ                 | თ                | ω                | 21       | σ       | ഗ     | w       | 13               | 0                 | 13           | ü               | 13                                           | 13      | 13              | 11     | 1               | 22                | ω                 | •   |
| 21-101-1 | US99-1                                        | -13923- | PCT-US94-04832A-48 | PCT-US00-35516-12 | PCT-US00-34318-27 |       | ů    | 694B- | 594B- | US-08-119-694B-3 | US-08-119-694-5 | US-08-119-694-4 | US-08-119-694-3 | US-07-947-033-5 | -947-033- | US-07-947-033-3 | US-08-119-694B-24 | US-08-119-694-24 | US-07-947-033-24 | •        | 9-694B- | -694- | -033-19 | US-08-971-790-42 | US-08-284-439A-42 | -08-932-929A | US-08-932-929-3 | -08-932-929-                                 | - 084 - | US-08-903-084-1 | -08-76 | US-08-760-797-1 | US-09-820-843A-31 | US-07-727-636-5   |     |
| 17,      | 78,                                           | 41,     | 48,                | e 12,             | 27,               | e 68, |      | ٥,    | 4     | e<br>3,          | о<br>5          | 4               | ω               | <u>ب</u>        | 4         | 3, ~            | 24,               | 24,              | 24,              | e 7,     | 19,     | 19,   | 19, ,   | e 42,            | 42,               | Ψ            | ω<br>`          | <u>,                                    </u> | ω       | ۲,              | Ψ      | 1, ,            | e 31,             | Sequence 5, Appli |     |

## ALIGNMENTS

```
US-09-763-397A-6

Sequence 6, Application US/09763397A

GENERAL INFORMATION:

APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for APPLICANT: Control and Prevention

APPLICANT: Lal, Altaf A.

APPLICANT: Lal, Altaf A.

APPLICANT: Ping Shi, Ya

CURRENT FILING DATE: 1059-08-19

CURRENT APPLICATION NUMBER: US/09/763,397A

CURRENT FILING DATE: 1999-08-19

NUMBER: US 60/997,703

PRIOR APPLICATION NUMBER: PCT / US99/18869

PRIOR FILING DATE: 1999-08-19

NUMBER OF SEQ ID NO: 26

SOFTWARE: Patentin version 3.1

SEQ ID NO 6

LEBROTH: 23

TYPE: PRT

ORGANISM: Plasmodium falciparum

US-09-763-397A-6

Query Match

Best Local Similarity 100.0%; Score 127; DB 21; Length 23;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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APPLICANT:

```
망
 RESULT 2
US-07-610-222-33
 Ş
 US-08-480-512-55
; Sequence 55, Applicat
; GENERAL INFORMATION:
 망
 US-07
 Sequence 33, Application US/07610222 GENERAL INFORMATION:
 Matches
 Query Match
Best Local (
 TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 CORRESPONDENCE ADDRESS:
 NAME: Lavin Jr., Lawrence M.
REGISTRATION NUMBER: 30,768
REFERENCE/DOCKET NUMBER: 2481.1003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
 TITLE OF INVENTION: Synthetic Vaccine for t
TITLE OF INVENTION: Induction of Cytotoxic
NUMBER OF SEQUENCES: 36
 APPLICANT:
 TOPOLOGY: linear MOLECULE TYPE: peptide -610-222-33
 PRIOR APPLICATION DATA:
 CURRENT APPLICATION DATA:
 APPLICANT: Deres, Karl
APPLICANT: Wiesmuller, Karl-Heinz
 ATTORNEY/AGENT INFORMATION:
APPLICANT:
 APPLICANT:
 APPLICANT:
 APPLICANT:
 APPLICANT:
 APPLICANT:
 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn_Release #1.0, Version #1.25
 CLASSIFICATION:
 APPLICATION NUMBER: US
FILING DATE: 19901108
 COMPUTER:
 COUNTRY:
 CITY: Washington
 STREET:
 STRANDEDNESS:
 FILING DATE:
 APPLICATION NUMBER: DE P 39 37 412.2
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 KPKDELDYENDIEKKICKMEKCS
 20005-3315
 Similarity
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 D.C
 Application US/08480512
 1300 I Street, N.W. Suite 700
 24 amino acids
 USA
 Jung, Gunther
Rammensee, Hans-Georg
 Schild, Hansjorg
 Conservative
 Jung, Gunther
 Buhring, Hans-Jorg
Becker, Gerhard
Bessler, Wolfgang
 Metzger, Jorg
 Wiesmuller, Karl-Heinz
 IBM PC compatible SYSTEM: PC-DOS/MS-DOS
 Finnegan, Henderson, Farabow,
 10-NOV-1989
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 100.0%; Score 127; DB 3; 100.0%; Pred. No. 2.6e-11;
 us/07/610,222
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 23
 Mismatches
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 T-lymphocytes
 0;
 Length 24;
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 Gaps
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/966,603
APPLICATION NUMBER: 26-OCT-1992
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 APPLICANT: Schild, HansJorg
APPLICANT: Deres, Karl
TITLE OF INVENTION: Conjugate, Its Preparation and its Uses
 CORRESPONDENCE ADDRESS:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/876,479
FILING DATE: 20-JUN-1986
 PRIOR APPLICATION DATA: APPLICATION NUMBER:
 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/340,833
FILING DATE: 20-APR-1989
 NUMBER OF SEQUENCES:
 FILING DATE: 27-DEC-
PRIOR APPLICATION DATA:
 FILING DATE: 08-NOV-PRIOR APPLICATION DATA:
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION DATA:
 SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
 TELECOMMUNICATION INFORMATION:
 FILING DATE: 10-NOV-1989 ATTORNEY/AGENT INFORMATION:
 FILING DATE: 22-APR-
PRIOR APPLICATION DATA:
 FILING DATE: 24-JUN-
PRIOR APPLICATION DATA:
MOLECULE TYPE:
 APPLICATION NUMBER: US 07
APPLICATION NUMBER: US 07
APPLICATION 27-SEP-1990
 APPLICATION NUMBER: FILING DATE: 24-0CT
 STREET: 1300 I St
 FILING DATE:
CLASSIFICATION: 424
 APPLICATION NUMBER: US 0 FILING DATE: 01-AUG-1988
 FILING DATE:
 APPLICATION NUMBER:
 ADDRESSEE:
 TELEPHONE: 202-408-4400
 APPLICATION NUMBER: DE FILING DATE: 27-DEC-1985
 APPLICATION NUMBER: DE P3522512.2 FILING DATE: 24-JUN-1985
 APPLICATION NUMBER:
 APPLICATION NUMBER:
 REGISTRATION NUMBER:
 REFERENCE/DOCKET NUMBER:
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 TOPOLOGY:
 RY: USA
20005-3315
 D.C
 Fleshner, Raz E
 1300 I Street, N.W.
 Rammensee, Hans-Georg
 Dunner
 Finnegan, Henderson, Farabow, Garrett &
 linear
 202-408-4000
peptide
 22-APR-1988
 08-NOV-1990
 US 07/610,222
 US 07/427,914
 US/08/480,512
 US 07/229,770
 US 07/588,794
 US/08/084,091A
 US/08/387,624
 DE P3937412.2
 DE P3813821.2
 DE P3546150.0
 02481.0312-04000
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 RESULT 5
US-07-677-539B-6
 В
 ; FEATURE: ; OTHER INFORMATION: Recombinant DNA/Protein US-09-763-397A-2
 US-09-763-397A-2
 US-08-480-512-55
 Query Match
Best Local Similarity
Matches 23; Conserv
 Sequence 6, Application US/07677539B GENERAL INFORMATION:
 SEQ ID NO 2
 GENERAL INFORMATION:
 Matches
 Query Match
Best Local
 Sequence 2, Application US/09763397A
 PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR FILING DATE: 1998-08-21
PRIOR APPLICATION NUMBER: PCT / US99/18869
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
 APPLICANT: Lal, Altaf A.
APPLICANT: Ping Shi, Ya
APPLICANT: Hasnain, Seyed E.
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falc:
FILE REFERENCE: 6395-57049
 APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis APPLICANT: Control and Prevention APPLICANT: Lal, Altaf A.
 CURRENT APPLICATION NUMBER: US/09/763,397A CURRENT FILING DATE: 2001-02-16
 ORGANISM: Artificial Sequence
 MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1615 L STREET, N.W.
 TITLE OF INVENTION: CIRCUMSPOROZOITE PROTEIN OF PLASMODIUM TITLE OF INVENTION: REICHENOWI AND VACCINE FOR HUMAN MALARIA NUMBER OF SEQUENCES: 54
 ENGTH: 350
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 APPLICANT: LAL, ALTAF A. APPLICANT: GOLDMAN, IRA F.
 51 KPKDELDYENDIEKKICKMEKCS 73
 CITY: WASHINGTON STATE: D.C.
 Local Similarity
 APPLICATION NUMBER:
 COUNTRY:
 1 KPKDELDYENDIEKKICKMEKCS 23
 1 KPKDELDYENDIEKKICKMEKCS 23
 KPKDELDYENDIEKKICKMEKCS 23
 20036
 USA
 Conservative
 Conservative
 100.0%;
 100.0%; Score 127; DB 21; 100.0%; Pred. No. 6.9e-10; tive 0; Mismatches 0;
 US/07/677,539B
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 Mismatches
 Length 24;
 Length 350;
 Indels
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 Gaps
 Gaps
 0;
 0;
 망
 Qy
Query Match
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RESULT 6
US-07-727-636-6
 US-07-677-539B-6
 Sequence 6, Applicati
GENERAL INFORMATION:
 Query Match 100.0%; Score 127; DB 3; Best Local Similarity 100.0%; Pred. No. 8.5e-10; Matches 23; Conservative 0; Mismatches 0;
 TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
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 APPLICATION NUMBER: US/07/
FILING DATE: 19910710
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,58
REFERENCE/DOCKET NUMBER: 5
TOPOLOGY: 1i
MOLECULE TYPE:
17-727-636-6
 SEQUENCE CHARACTERISTICS:
 TELECOMMUNICATION INFORMATION: TELEPHONE: 202-861-3067
 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 APPLICANT: LAL, ALTAF A.
APPLICANT: GOLDMAN.
TITLE OF INVENTION: CIRCUMSPOROZOITE PROTEIN OF PLASMODIUM
TITLE OF INVENTION: REICHENOWI AND VACCINE FOR HUMAN MALARIA
 SEQUENCE CHARACTERISTICS
 TELECOMMUNICATION INFORMATION: TELEPHONE: 202-861-3067
TELEFAX: 202-822-0944
 ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,1
REFERENCE/DOCKET NUMBER:
 CORRESPONDENCE ADDRESS:
 MOLECULE TYPE: peptide
 NUMBER OF SEQUENCES:
 LENGTH:
 368 KPKDELDYENDIEKKICKMEKCS 390
 TELEPHONE: 202-822-0944
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 LENGTH: 412 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
 FILING DATE: 19
CLASSIFICATION:
 COUNTRY:
 CITY: WASHINGTON
 STREET:
 TOPOLOGY:
 STRANDEDNESS:
 ADDRESSEE:
 1 KPKDELDYENDIEKKICKMEKCS 23
 20036
 AMINO ACID
 Application US/07727636
 D.C.
 E: CUSHMAN, DARBY & CUSHMAN 1615 L STREET, N.W.
 412 amino acids
 USA
 linear
 linear
 19911205
 peptide
 single
 US/07/727,636
 26, 581
 26,581
 6.
 5683/91540
 5683/91540
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 Indels
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 Gaps
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0;

100.0%;

Score 127;

DB 3;

Length 412;

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US-08-948-885-18
; Sequence 18, Application US/08948885
; GENERAL INFORMATION:
 RESULT 8
US-08-932-929A-1
 ; STRANDEDNESS: single
; TOPOLOGY: Linear
; MOLECULE TYPE: peptide
US-08-948-885-18
 Matches
 Best Local Similarity 100. Matches 23; Conservative
 Sequence 1, Application US/08932929A GENERAL INFORMATION:
 Matches
 Query Match
 Best Local Similarity
 INFORMATION FOR SEQ ID NO:
 REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
 COMPUTER READABLE FORM:
MEDIJUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
COMPUTER: FLOPPY DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
 APPLICANT: Jessell, TITLE OF INVENTION: TITLE OF INVENTION:
 APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: Hybrid Protein Between CS
TITLE OF INVENTION: from Plasmodium and HBsAG
NUMBER OF SEQUENCES: 4
 FILING DATE: January 5, ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/313,288
 SEQUENCE CHARACTERISTICS:
 CORRESPONDENCE ADDRESS:
 CORRESPONDENCE ADDRESS
 NUMBER OF SEQUENCES:
 368 KPKDELDYENDIEKKICKMEKCS 390
 368 KPKDELDYENDIEKKICKMEKCS 390
 CLASSIFICATION:
 APPLICATION NUMBER: US/08/948,885 FILING DATE:
 CITY: New York
 TYPE: amino acid
 TELEX:
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 COUNTRY:
 STREET:
 ADDRESSEE:
 1 KPKDELDYENDIEKKICKMEKCS 23
 LENGTH:
 ADDRESSEE:
 1 KPKDELDYENDIEKKICKMEKCS 23
 10036
 New York
 412 amino acids
 1185 Avenue of the Americas
 (212) 391-0526
 USA
 Jessell,
 Conservative
 Cooper & Dunham LLP
SmithKline Beecham Corporation
 John P.
, John P.
28,678
400
 Thomas M. and Avihu Klar
CLONING, EXPRESSION AND USES OF A
CTONETTED PROTEIN, F-SPONDIN
 NOVEL
20
 100.0%;
 100.0%; Score 127; DB 13; 100.0%; Pred. No. 8.5e-10;
 18:
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 0;
 0;
 Pred. No. 8.5e-10;
 Mismatches
 Mismatches
 0;
 Indels
 Indels
 Length
 412;
 0;
 0;
 Gaps
 Gaps
 0;
 0;
 QΥ
 RESULT 9
US-07-842-694-2
 Вþ
 US-08-932-929A-1
 Query Match
Best Local S
Matches 23
 Sequence 2, Application US/07842694 GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acid
 REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO:
 ZIP: 1940 COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC DOS/MS-DOS
COMPATING SYSTEM: PC-DOS/MS-DOS
 NAME: Baumeister, Kirk REGISTRATION NUMBER: 33,833 REFERENCE/DOCKET NUMBER: B4: TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5096
 FILING DATE: 13-JUNE-199
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
 SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
 FILING DATE: 19920227
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 APPLICANT: Cohen, Joseph
APPLICANT: De Wilde, Michel
TITLE OF INVENTION: Malaria Vaccine Antigen
 PRIOR APPLICATION DATA:
 SEQUENCE CHARACTERISTICS:
 CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION:
 162 KPKDELDYENDIEKKICKMEKCS 184
 ADDRESSEE: SIII
 APPLICATION NUMBER: FILING DATE: 18-SEF CLASSIFICATION: 435
 STREET: P.O. Box 1539
CITY: King of Prussia
 TOPOLOGY: 11
 TELEFAX:
 APPLICATION NUMBER: 08/663,371 FILING DATE: 13-JUNE-1996.
 COMPUTER: IBM CON OPERATING SYSTEM:
 COUNTRY:
 STATE:
 Local Similarity
les 23; Conserv
 TYPE:
 TELEPHONE:
 STREET:
 NAME: Canter, Carol G
REGISTRATION NUMBER:
 APPLICATION NUMBER:
 COUNTRY: USA
ZIP: 19406-0939
 STATE: PA
 1 KPKDELDYENDIEKKICKMEKCS 23
 19406
 r: 709 Swedeland
King of Prussia
 amino acid
 PA
 423 amino acids
 USA
 610-270-5090
 sss: single
linear
 Conservative
 FastSEQ for Windows Version
 SmithKline Beecham Corporation O. Box 1539 / Corporate Patents
 IBM Compatible
 Diskette
 18-SEPT-1997
 100.0%; Score 127;
100.0%; Pred. No. 8.
tive 0; Mismatches
 SOG
 US/08/932,929A
 US/07/842,694
 Road
 31151
 2:
 B45015-1FWC2
 B45015
 Mismatches
 DB 13;
.7e-10;
 0;
 Indels
 Length
 423;
 0;
 Gaps
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0;

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i: 424 amino acids AMINO ACID

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В
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 ; HYPOTHETICAL: 1
; ANTI-SENSE: NO
US-07-842-694-2
RESULT 11
US-07-727-636-5
 á
 US-07-677-539B-5
 US-07-677-539B-5
 Sequence 5, Application
 Query Match
Best Local :
 Matches
 Query Match
 Matches
 APPLICATION NUMBER: US/07/677
FILING DATE: 19911205
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 5683
 TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
 Type:
STRANDEDNESS: singte
TOPOLOGY: linear
MOLECULE TYPE: protein
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 TELECOMMUNICATION INFORMATION: TELEPHONE: 202-861-3067
TELEFAX: 202-822-0944
 STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide
 SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acid
 NUMBER OF SEQUENCES: 5. CORRESPONDENCE ADDRESS:
 APPLICANT: GOLDMAN, IRA F.
TITLE OF INVENTION: CIRCUMSPOROZOITE PROTEIN OF PLASMODIUM
TITLE OF INVENTION: REICHENOWI AND VACCINE FOR HUMAN MALARIA
 APPLICANT:
 163 KPKDELDYENDIEKKICKMEKCS 185
 TYPE: AMINO ACID
 Local Similarity
nes 23; Conserv
 COUNTRY:
 CITY: WASHINGTON
 STREET:
 ADDRESSEE:
 1 KPKDELDYENDIEKKICKMEKCS 23
 Similarity
 Application US/07677539B
 D.C
 E: CUSHMAN, DARBY & CUSHMAN 1615 L STREET, N.W.
 USA
 LAL, ALTAF A.
 100.0%; ilarity 100.0%; i
Conservative 0;
 Conservative
 ss: single
linear
 96.1%;
91.3%;
 US/07/677,539B
 Score 122; DB 3; ...
Pred. No. 4.3e-09; ...
 5683/91540
 Score 127;
Pred. No. 8
 Mismatches
 8.8e-10;
hes 0;
 DB 3; Length 388;
 DB 3;
 Length 424;
 Indels
 Indels
 0,
 0;
 Gaps
 0;
 0
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US-09-820-843A-31
 밁
; OTHER INFORMATION: gi|4493889
US-09-820-843A-31
 US-07-727-636-5
 Sequence 31, Application US/09820843A
GENERAL INFORMATION:
APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENT:
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: 063915
 TELEPHONE: 202-861-3067
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: AMINO ACID
 CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.0
SEQ ID NO 31
LENGTH: 396
 Sequence 5, Application US/07727636 GENERAL INFORMATION:
 Matches
 APPLICATION NUMBER: US/07/
FILING DATE: 19910710
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,58
 NAME/KEY: misc_feature
OTHER INFORMATION: Circumsporozoite (CS) protein
NAME/KEY: misc_feature
 TYPE: PRT
ORGANISM: Plasmodium falciparum
 FEATURE:
 IMERAL INFORMATION: ALTAF A.

APPLICANT: LAL, ALTAF A.

APPLICANT: GOLDMAN, IRA F.

TITLE OF INVENTION: CIRCUMSPOROZOITE PROTEIN OF PLASMODIUM

TITLE OF INVENTION: REICHENOWI AND VACCINE FOR HUMAN MALARIA
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 TELECOMMUNICATION INFORMATION: TELEPHONE: 202-861-3067
 COMPUTER READABLE FORM:
 NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
 MOLECULE TYPE:
 344 KPKDQLDYENDLEKKICKMEKCS 366
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
 TOPOLOGY: li
 STREET: 1615 L S
CITY: WASHINGTON
 Local
 REFERENCE/DOCKET NUMBER:
 COUNTRY: USA
 ADDRESSEE:
 1 KPKDELDYENDIEKKICKMEKCS 23
 h 96.1%;
Similarity 91.3%;
21; Conservative
 20036
 D.C.
 E: CUSHMAN, DARBY & CUSHMAN 1615 L STREET, .N.W.
 s: single
linear
 peptide
 US/07/727,636
 26,581
 ?
 Score 122;
Pred. No. 4
 5683/91540
 Mismatches
 4.3e-09;
 DB 3;
 Length 388;
 IDENTIFICATION OF CANDIDATE PRO
 Indels
 0;
 0
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Qy
 В
 US-08-760-797-3
 В
 RESULT 13
US-08-760-797-1
 Sequence 1, Application US/08766
GENERAL INFORMATION:
APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
 Sequence 3, Applicati
GENERAL INFORMATION:
 Matches
 Best Local Similarity
 Query Match
 Matches
 Query Match
Best Local
 TELEFAX: 610 270-5090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 2IP: 1940 LE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
PC-DOS/MS-DOS
PC-DOS/MS-DOS
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
 REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: B4
TELECOMMUNICATION INFORMATION:
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
APPLICANT:
 MOLECULE TYPE: protein
 TITLE OF INVENTION:
 ATTORNEY/AGENT INFORMATION:
 159
 APPLICATION NUMBER: 08/4.
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: US
FILING DATE: 21-OCT-1994
 APPLICATION NUMBER: US/08 FILING DATE: 04-DEC-1996
 COUNTRY:
 STRANDEDNESS:
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 ADDRESSEE:
 TOPOLOGY:
 LENGTH:
 1 KPKDELDYENDIEKKICKMEKCS 23
 KPKDELDYANDIEKKICKMEKCS 181
 : King of Prussia
 Similarity
 amino acid
 Baumeister, Kirk
 Application US/08760797
 Application US/08760797
 Pennsylvania
 E: Intellectual Property P.O. Box 1539 - UW2220
 424 amino acids
 USA
 Conservative
De Wilde, Michel
 Conservative
 linear
 SmithKline Beecham Corp./Corporate
 610 270-5096
 single
 HYBRID PROTEIN BETWEEN CS
PLASMODIUM AND HBSAG
 95.3%;
95.7%;
 95.3e;
95.7e;
 us/08/760,797
 08/442,612
 08/244,085
 B45015C1
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 Score 121; DB 22;
Pred. No. 6.1e-09;
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Pred. No. 6.6e-09;
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 γ
 US-08-903-084-
 RESULT 15
 US-08-760-797-3
 Sequence 1, Application GENERAL INFORMATION:
 Matches
 Query Match
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 TELEFAX: 610 270-5090 INFORMATION FOR SEQ ID NO:
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/760,797 FILLING DATE: 04-DEC-1996 CLASSIFICATION: 435 PRIOR APPLICATION DATA: 00/1/47 617
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
 CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION: HYBRID PROTEIN BETWEEN CS FROM TITLE OF INVENTION: PLASMODIUM AND HBSAG
 TELEPHONE: 610 270-5096
 NUMBER OF SEQUENCES:
 CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
 TITLE OF INVENTION: VACCINE FORMULATIONS CONTAINING TITLE OF INVENTION: 3-O-DEACYLATED MONOPHOSPHORYL L
 APPLICANT: Kummert, Suzanne
APPLICANT: Slaoui, Moncef
APPLICANT: Wijendale, Frans
 APPLICANT:
 MOLECULE TYPE:
 SEQUENCE CHARACTERISTICS:
 APPLICANT:
 APPLICANT:
 NUMBER OF SEQUENCES:
 159 KPKDELDYANDIEKKICKMEKCS 181
 APPLICATION NUMBER: 08/44
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: US
FILING DATE: 21-OCT-1994
 COUNTRY:
 COUNTRY:
 STATE:
 CITY: King of Prussia
 TOPOLOGY: lin
 REFERENCE/DOCKET NUMBER: 33
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 1 KPKDELDYENDIEKKICKMEKCS 23
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 19406-0939
 King of Prussia
19046
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 Application US/08903084
 PA
 Pennsylvania
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 424 amino acids
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 610 270-5090
 Cohen, Joseph
 Francotte, Myriam
 Bruck, Claudine
 USA
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O. Box 1539 - UW2220
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 08/244,085
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 Score 121;
Pred. No. 6.
 B45015C1
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APPLICATION NUMBER: US/08/903,084
FILING DATE: 17-JUL1997
CLASSIFICATION NUMBER: 08/741,575
FILING DATE: 30-OCT-1996
APPLICATION NUMBER: 09/303,542
FILING DATE: 09-SEP-1994
ATTORNEY/AGENT INFORMATION:
COPERATION NUMBER: 09-SEP-1994
ATTORNEY/AGENT INFORMATION:
CREEK COPOCKET NUMBER: 38,938
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TELEFAX: 610-720-7202
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Minimum DB
Maximum DB
 Run
 Result
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 Title:
Perfect score:
 Database
 Total number of
 Searched:
 Scoring table:
 Sequence:
 OM protein - protein search, using sw model
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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 seq length: 0
seq length: 2000000000
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Match
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7: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
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 US-09-763-397A-6
127
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 BLOSUM62
Gapop 10.0 , Gapext 0.5
 173191 seqs, 36597120 residues
 January 29, 2002, 10:58:09;
 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
 KPKDELDYENDIEKKICKMEKCS
 Length
 867
920
1124
922
416
416
5533
5533
5533
5533
5533
5533
607
607
607
607
607
607
133
804
819
829
133
1361
131
 BB
US-09-708-427-5053

US-09-708-427-5052

US-09-708-427-5051

US-09-897-516-6570

US-10-1018-105-4

US-09-708-427-7358

US-09-708-427-7358

US-09-708-427-19153

US-09-708-427-19151

US-09-708-427-19151

US-09-708-427-19151

US-09-708-427-11307

US-09-708-427-11307

US-09-708-427-11307

US-09-708-427-11307

US-09-708-427-11307

US-09-708-427-11302

US-09-708-427-11302

US-09-708-427-35294

US-09-708-427-35293

US-09-708-427-35293

US-09-708-427-35293

US-09-708-427-35293

US-09-708-427-33266

US-09-708-427-33266
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 23
 Search time 120.95 Seconds (without alignments) 6.959 Million cell updates/sec
 173191
 Description
sequence
seq
 5053, Ap
5053, Ap
5051, Ap
6570, Ap
7358, Appli
7357, Ap
735153, Ap
119152, Ap
119153, Ap
119153, Ap
119154, Ap
119155, Ap
119155, Ap
119156, A
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| 43 33.9 30.9 5 US-09-708-427-56476 43 33.9 34.2 5 US-09-708-427-56475 42 33.1 32 7 US-60-323-991-30 42 33.1 150 5 US-09-708-427-39156 42 33.1 150 5 US-09-708-427-39156 42 33.1 163 5 US-09-620-3948-5279 42 33.1 254 5 US-09-611-526-3265 41.5 32.7 1244 5 US-09-708-427-11575 41.5 32.7 1244 5 US-09-708-427-11573 41.5 32.7 1244 5 US-09-708-427-11573 41.5 32.7 1245 5 US-09-708-427-11573 41.5 32.7 1245 5 US-09-708-427-11573 41.5 32.7 1245 5 US-09-815-242-5560 41.3 32.3 232 5 US-09-815-242-5560 41.3 2.3 232 5 US-09-815-242-11666 41.3 2.3 232 5 US-09-815-242-11666 41.3 2.3 270 5 US-09-815-242-1169 41.3 2.3 270 5 US-09-620-3948-1049 41.3 2.3 336 5 US-09-620-3948-1048 41.3 2.3 340 5 US-09-708-427-5893                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 45                 | 44       | 43                  | 42       | 41                  | 40                  | 39       | 38                 | 37       | 36                  | 35                  | 34       | ω<br>u              | 32                  | 31                  | 30               | 29                  | 28       |  |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------|----------|---------------------|----------|---------------------|---------------------|----------|--------------------|----------|---------------------|---------------------|----------|---------------------|---------------------|---------------------|------------------|---------------------|----------|--|
| 309 5 US 312 7 US 150 5 US 150 5 US 163 5 US 164 5 US 1244 5 US 1245 5 US 1249 5 US 232 5 US 232 5 US 272 5 US 273 5 US 274 5 US 275 5 US | 41                 | 41       | 41                  | 41       | 41                  | 41                  | 41       | 41                 | 41.5     | 41.5                | 41.5                | 42       | 42                  | 42                  | 42                  | 42               | 43                  | 43       |  |
| 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 32.3               | 32.3     | 32.3                | 32.3     | 32.3                | 32.3                | 32.3     | 32.3               | 32.7     | 32.7                | 32.7                | 33.1     | 33.1                | 33.1                | 33.1                | 33.1             | 33.9                | 33.9     |  |
| SSO                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 420                | 402      | 336                 | 272      | 270                 | 232                 | 232      | 232                | 1249     | 1245                | 1204                | 467      | 254                 | 163                 | 150                 | 32               | 342                 | 309      |  |
| US-09-708-427-56475 US-09-708-427-56475 US-60-323-991-30 US-09-708-427-39156 US-09-620-3948-5279 US-09-611-526-3265 US-09-708-427-11575 US-09-708-427-11573 US-09-815-242-5560 US-09-815-242-1566 US-09-815-242-1566 US-09-815-242-11666 US-09-815-242-11666 US-09-815-242-11666 US-09-815-342-11666 US-09-815-342-11666 US-09-815-342-11666 US-09-815-342-11666 US-09-815-342-11669 US-09-620-3948-1049 US-09-620-3948-1049 US-09-620-3948-1049 US-09-620-3948-1049 US-09-708-427-5893                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | u                  | u        | u                   | 5        | ഗ                   | S                   | u        | 5                  | σ        | თ                   | u                   | IJ       | ഗ                   | տ                   | υ                   | 7                | տ                   | თ        |  |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | US-09-708-427-5892 | -09      | US-09-620-394B-1047 | -09      | US-09-620-394B-1049 | US-09-815-242-12569 |          | US-09-815-242-5560 | -09      | US-09-708-427-11574 | US-09-708-427-11575 | -09-611  | US-09-815-242-11461 | US-09-620-394B-5279 | US-09-708-427-39156 | US-60-323-991-30 | US-09-708-427-56475 |          |  |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 5892, Ap           | 5893, Ap | 1047, Ap            | 1048, Ap | 1049, Ap            | 12569, A            | 11666, A | 5560, Ap           | 11573, A | 11574, A            | 11575, A            | 3265, Ap | 11461, A            | 5279, Ap            | 39156, A            | 30, Appl         | 56475, A            | 56476, A |  |

## ALIGNMENTS

| RESULT 2 US-09-708-427-5052 US-09-708-427-5052 Sequence 5052, Application US/09708427 GENERAL INFORMATION: APPLICANT: N. ALEXANDROV et al. TITLE OF INVENTION: SEQUENCE-DETERMINED D TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P CURRENT APPLICATION NUMBER: US/09/708,427 CURRENT FILING DATE: 2000-11-09 NUMBER OF SEQ ID NOS: 85364 SOFTWARE: Patentin version 3.1 SEQ ID NO 5052 LENGTH: 872                                          | KDELDYI<br>:   <br>RDTDSY | US-09-708-427-5053  Query Match Best Local Similarity 50. Matches 9; Conservative | FEATURE:  NAME/KEY: misc_feature  LOCATION: 1867  OTHER INFORMATION: Xaa i:  NAME/KEY: misc_feature  LOCATION: 1867  OTHER INFORMATION: Ceres | FILE REFERENCE: 2750-1243P CURRENT APPLICATION NUMBER: US/09/708,427 CURRENT FILING DATE: 2000-11-09 NUMBER OF SEQ ID NOS: 85364 SOFTWARE: Patentin version 3.1 SEQ ID NO. 5053 LENGTH: 867 TYPE: PRT ORGANISM: Arabidopsis thaliana | RESULT 1 US-09-708-427-5053 ; Sequence 5053, Application US/09708427 ; GENERAL INFORMATION: ; APPLICANT: N. ALEXANDROV et al. ; TITLE OF INVENTION: THEFERY : TITLE OF INVENTION: THEFERY                                                   |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------|-----------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 09-708-427-5052 09-708-427-5052 equence 5052, Application US/09708427 eneral information: Alexandrov et al. APPLICANT: N. ALEXANDROV et al. TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243p CURRENT APPLICATION NUMBER: US/09/708,427 CURRENT FILING DATE: 2000-11-09 NUMBER OF SEQ ID NOS: 85364 SOFTWARE: Patentin version 3.1 EQ ID NO 5052 LENGTH: 872 | 20                        | .2%; Scc<br>.0%; Pre                                                              | a is any amino acid<br>a seq. ID 1813621                                                                                                      | 1243P<br>1243P<br>2000-11-09<br>85364<br>s thaliana                                                                                                                                                                                  | ULT 1 09-708-427-5053 equence 5053, Application US/09708427 EQUENCE 5053, Application US/09708427 ENERAL INFORMATION: APPLICANT: N. ALEXANDROV et al. APPLICANT: N. ALEXANDROV et al. TITLE OF INVENTION: THEORY TITLE OF INVENTION: THEORY |

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 US-09-708-427-5052
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 US-09-708-427-5051
 US-09-708-427-5051
 us-09-897-516-6570
 SOFTWARE: PatentIn version 3.1
SEQ ID NO 5051
LENGTH: 920
 Sequence 5051, Appli GENERAL INFORMATION:
 Query Match
Best Local
 Sequence 6570, Application US/09897516
 Best Local Similarity Matches 9; Conserv
 Query Match
 Matches
 APPLICANT:
APPLICANT:
 CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
 APPLICANT: Malvar, Thomas M.
APPLICANT: Slater, Steven C.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome
FILE REFERENCE: 38-21(51847)B
CURRENT APPLICATION NUMBER: US/09/897,516
CURRENT FILING DATE: 2001-06-29
 APPLICANT: Corbin, David R. APPLICANT: Goldman, Barry
 APPLICANT: N. ALEXANDROV et al.
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 NAME/KEY: misc_feature
LOCATION: 1..920
OTHER INFORMATION: Ceres Seq.
 NAME/KEY: misc_feature
LOCATION: 1..920
OTHER INFORMATION: Xaa is
 OTHER INFORMATION: Ceres Seq.
 NAME/KEY: misc_feature LOCATION: 1..872
 OTHER INFORMATION: Xaa is any amino acid
 NAME/KEY: misc_feature LOCATION: 1..872
 FEATURE:
 ORGANISM: Arabidopsis thaliana
 ORGANISM: Arabidopsis thaliana
 TYPE: PRT
 TYPE: PRT
 FEATURE:
 821 RDTDSYINDIEKCLCSQE 838
 869 RDTDSYINDIEKCLCSQE 886
 w
 3 KDELDYENDIEKKICKME 20
APPLICATION NUMBER:
 KDELDYENDIEKKICKME 20
 INFORMATION:
 Similarity 50.0
9; Conservative
 Goldman, Barry S.
Hinkle, Gregory J.
Huesing, Joseph E.
Krasomil-Osterfeld, Karina C.
 Application US/09708427
 Conservative
 36.2%;
 36.2%;
50.0%;
US 60/215, 161
 any
 Score 46; DB 5; Le
Pred. No. 1.2e+02;
2; Mismatches 7;
 Score 46; DB 5;
Pred. No. 1.3e+02;
 ID 1813620
 ID 1813619
 amino acid
 Mismatches
 Sequences
 Length 920;
 Length 872;
 Indels
 Indels
 And Uses Thereof
 0;
 0;
 Gaps
 0;
 0
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 Qy
 US-10-018-105-4
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 δõ
 ; ORGANISM: Xenorhabdus sp. US-09-897-516-6570
 RESULT 6
US-09-708-427-7358
 US-10-018-105-4
 Sequence 7358, Application US/09708427 GENERAL INFORMATION:
 PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
SEQ ID NO 6570
LENGTH: 1124
 SEQ ID NO 4
 GENERAL INFORMATION:
 Matches
 Query Match 35.8%;
Best Local Similarity 50.0%;
 SOFTWARE: Pate
SEQ ID NO 7358
 Sequence 4, Application US/10018105
 Query Match
Best Local
 Matches
 APPLICAME: DAVISON, John
TITLE OF INVENTION: IDENTIFICATION OF CANDIDA ALBICANS ESSENTIAL FUNGAL
TITLE OF INVENTION: SPECIFIC GENES AND USE THEREOF IN ANTIFUNGAL DRUG
TITLE OF INVENTION: DISCOVERY
FILE REFERENCE: 10182-015
CURRENT APPLICATION NUMBER: US/10/018,105
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION UNMER: PCT/CA00/00533
PRIOR PILING DATE: 2000-05-05
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 1999-05-05
 CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY
 APPLICANT:
 SOFTWARE: PatentIn Ver. 2.1
 NUMBER OF SEQ ID NOS:
 APPLICANT: ROEMER, Terry
 FILE REFERENCE: 2750-1243P
 APPLICANT: N. ALEXANDROV et al
 TYPE: PRT
 TYPE: PRT
 ORGANISM: Candida albicans
 NAME/KEY: misc_feature LOCATION: 1..416
 ORGANISM: Arabidopsis thaliana
 LENGTH: 922
OTHER INFORMATION: Xaa is
 FEATURE:
 LENGTH:
 208 EMDAENIAAEIRKKLCYQEK 227
 41 EDELELKSELESEVVKSEK 59
 Local Similarity 36.8 nes 7; Conservative
 5 ELDYEN---DIEKKICKMEK
 3 KDELDYENDIEKKICKMEK 21
 10;
 416
 BUSSEY, Howard
 Conservative
 35.4%;
any amino
 21
 8
 Score 45; DB 6;
Pred. No. 1.8e+02;
 Score 45.5;
Pred. No. 1
 Mismatches
 Mismatches
acid
 1.8e+02;
 DВ
 <u>ن</u>
 Length 922;
 Length 1124;
 Indels
 Indels
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 0;
 Gaps
 1;
 0
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Query Match
Best Local Similarity
""" hes 8; Conserve
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 δ
 ; NAME/KEY: misc_feature
; LOCATION: 1..416
; OTHER INFORMATION: Ceres
US-09-708-427-7358
 ; OTHER INFORMATION: Ceres Seq. US-09-708-427-7357
 US-09-708-427-7357
 밁
 RESULT 8
US-09-708-427-19153
 Sequence 7357, Application US/09 GENERAL INFORMATION: APPLICANT: N. ALEXANDROV et al.
 CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19153
LENGTH: 550
TYPE: PRT
 CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7357
LENGTH: 533
 Sequence 19153, Appl GENERAL INFORMATION:
 Query Match
Best Local Similarity
Matches 8; Conserv
 APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY , FILE REFERENCE: 2750-1243P
 FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..550
OTHER INFORMATION: Xaa is any amino acid
 NAME/KEY: misc_feature
LOCATION: 1..533
OTHER INFORMATION: Xaa is any amino acid
 ORGANISM: Arabidopsis thaliana
 ORGANISM: Arabidopsis thaliana
 NAME/KEY: misc_feature LOCATION: 1..533
 FEATURE:
 NAME/KEY: misc_feature LOCATION: 1..550
OTHER INFORMATION: Ceres Seq. ID 1835494
 388 DDPDLQNTFFYKLCKVEK 405
 271 DDPDLQNTFFYKLCKVEK 288
 4 DELDYENDIEKKICKMEK 21
 4 DELDYENDIEKKICKMEK 21
 Conservative
 Conservative
 Application US/09708427
 Application US/09708427
 34.6%;
44.4%;
 34.68;
 Seq.
 4.
 Score 44; DB 5; Length 533; Pred. No. 1.4e+02; Mismatches 6; Indels
 ID 1816974
 Score 44; DB 5;
Pred. No. 1.1e+02;
 ID 1816975
 Mismatches
 6
 Length 416
 Indels
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 Gaps
 Gaps
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 0;
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US-09-708-427-19152
; Sequence 19152, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID;
; TITLE OF INVENTION: THEREBY
; FILE REFERENCE: 2750-1243P
 ; NAME/KEY: misc_feature
; LCCATION: 1..553
; OTHER INFORMATION: Ceres Seq. ID 1816973
US-09-708-427-7356
 밁
 Query Match
Best Local Similarity
"he's 8; Conserv
 뮹
 US-09-708-427-19153
; OTHER INFORMATION: Ceres Seq. US-09-708-427-19152
 RESULT
 US-09-708-427-7356
 CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 19152
LENGTH: 558
TYPE: PRT
 Sequence 7356, Application US/09 GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
 SOFTWARE: PatentIn version 3.1
SEQ ID NO 7356
LENGTH: 553
 Matches
 Query Match
 CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
 NAME/KEY: misc_feature
LOCATION: 1..558
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..558
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NAME/KEY: misc_feature
LOCATION: 1..553
OTHER INFORMATION: Xaa
 ORGANISM: Arabidopsis thaliana
 ORGANISM: Arabidopsis thaliana
 FEATURE:
 259 KPKKELDLDQDKAAKVNGEEK
 408 DDPDLQNTFFYKLCKVEK 425
 Local Similarity nes 10; Conserv
 1 KPKDELDYENDIEKKICKMEK 21
 4 DELDYENDIEKKICKMEK 21
 Application US/09708427
 Conservative
 Conservative
 34.68;
47.68;
 34.68;
 is any
 279
 2;
 4.
 Score 44;
Pred. No.
 Score 44;
Pred. No.
 ID 1835493
 amino
 Mismatches
 Mismatches
 1.4e+02;
 DB 5;
 .5e+02;
 6
 Length 553;
 Length 550
 Indels
 Indels
 0;
 0;
 Gaps
 Gaps
 0
 0
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В
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 US-09-815-242-13379; Sequence 13379, Application US/09815242
 US-09-708-427-19151
 US-09-708-427-19151
 Best Loc
Matches
 CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 19151
 Sequence 19151, Application US/09708427

Sequence 19151, Application US/09708427

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P

FILE REFERENCE: 2750-1243P
 Query Match
Best Local
 Query Match
 GENERAL INFORMATION:
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 APPLICANT:
 APPLICANT: Xu, H: Howard
TITLE OF INVENTION: Identification of Essential
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
 PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/253,625 PRIOR FILING DATE: 2000-11-27 PRIOR APPLICATION NUMBER: 60/257,931 PRIOR FILING DATE: 2000-12-22
 APPLICANT:
 APPLICANT:
 APPLICANT: Haselbeck, Robert
 NAME/KEY: misc_feature
LOCATION: 1..577
OTHER INFORMATION: Ceres Seq. ID 1835492
 NAME/KEY: misc_feature
LOCATION: 1..577
OTHER INFORMATION: Xaa is any amino acid
 TYPE: PRT ORGANISM: Arabidopsis thaliana FEATURE:
 ENGTH: 577
 267 KPKKELDLDQDKAAKVNGEEK 287
 286 KPKKELDLDQDKAAKVNGEEK 306
 Local Similarity 47.6 nes 10; Conservative
 Local Similarity
 1 KPKDELDYENDIEKKICKMEK 21
 1 KPKDELDYENDIEKKICKMEK 21
 Carr, Grant J.
Yamamoto, Robert T.
 Zyskind, Judith W. Wall, Daniel
 Ohlsen, Kari
 Trawick, John D.
 Conservative
 34.6%;
47.6%;
 34.6%;
47.6%;
 Score 44; DB 5; Le
Pred. No. 1.5e+02;
"''matches 9;
 Score 44; DB 5; Le
Pred. No. 1.5e+02;
"'Amatches 9;
 Length 577;
 Length 558;
 Indels
 Indels
 0;
 0;
 0
 0;
 B
RESULT 14
US-09-708-427-14304
S-09-ence 14304, Application US/09708427
; GENERAL INFORMATION:
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; TYPE: PRT ; ORGANISM: Streptococcus pneumoniae US-09-815-242-13379
 US-09-815-242-13682
 ; ORGANISM: Streptococcus pneumoniae US-09-815-242-13682
 NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 13379
LENGTH: 607
 GENERAL
 Sequence 13682,
 Matches
 Query Match
Best Local :
 Query Match
Best Local Similarity
Matches 8; Conserv
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 APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
 APPLICANT:
 APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
 PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
 TITLE OF INVENTION: Identification TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
 APPLICANT:
 NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
 PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
 PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
 TYPE: PRT
 LENGTH: 607
 498 KRKEEVDLRNEVDQAIFATEK 518
498 KRKEEVDLRNEVDQAIFATEK 518
 y Match
Local Similarity 38.1%; Pred. No.
hes 8; Conservative 6; Mismatch
 1 KPKDELDYENDIEKKICKMEK 21
 1 KPKDELDYENDIEKKICKMEK 21
 APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
 INFORMATION
 Xu, H. Howard
 Zyskind, Judith W. Wall, Daniel
 Carr, Grant J.
 Trawick, John D.
 Yamamoto, Robert T.
 Conservative
 Application US/09815242
 34.6%;
 6
 Score 44;
Pred. No. 1
 Mismatches
 Mismatches
 of Essential Genes
 DB 5;
1.6e+02;
 DB 5;
 Length 607;
 Length 607;
 Indels
 Indels
 0;
 0;
 Gaps
 Gaps
 0
 0;
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APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: THEREBY

FILE REFERENCE: 2750-1243P

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SOFTMARE: Patentin version 3.1

SEQ ID NO 14304

LENGTH: 772

TYPE: PRT

ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1.772

COTHER INFORMATION: Ceres Seq. ID 1827597

US-09-708-427-14304
 FEATURE:
NAME/KEY: misc_feature
LOCATION: 1.803
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1.803
OTHER INFORMATION: Ceres Seq. ID 1827596
US-09-708-427-14303
 US-09-708-427-14303
US-09-708-427-14303
Sequence 14303, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-12439
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: US/09/708,427
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 14303
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Search completed: January 29, 2002, 10:58:09 Job time: 2505 sec
 В
 Query Match 34.6%;
Best Local Similarity 44.4%;
Matches 8; Conservative
 Query Match 34.6%;
Best Local Similarity 44.4%;
Matches 8; Conservative
 TYPE: PRT
ORGANISM: Arabidopsis thaliana
 ENGTH: 803
 647 DDPDLQNTFFYKLCKVEK 664
 616 DDPDLQNTFFYKLCKVEK 633
 4 DELDYENDIEKKICKMEK 21
 4 DELDYENDIEKKICKMEK 21
 Score 44; DB 5;
Pred. No. 2e+02;
4; Mismatches
 Score 44; DB 5;
Pred. No. 2.1e+02;
 Mismatches
 6,
 6,
 Length 803;
 Length 772;
 Indels
 Indels
 0;
 0,
 Gaps
 Gaps
 0;
 0;
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Result
No.
 Database
 Minimum DB seq
Maximum DB seq
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 Post-processing:
 Total number of hits satisfying chosen parameters:
 Searched:
 Scoring table:
 Perfect score:
Sequence:
 Title:
 protein -
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and is derived
 Score
 ..
 NO.
 protein search, using sw
 length: 0
length: 2000000000
 Query
Match
 is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
 US-09-763-397A-5
75
1 KHKKLKQPGDGNP 1
 Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 January 29, 2002, 10:56:00; Search time 1760.55 Seconds (without alignments) 2.050 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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: //cgn2_6/ptodatta/2/paa/US05_COMB.pep:*
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: //cgn2_6/ptodatta/2/paa/US090_COMB.pep:*
 3148936 seqs, 277657034 residues
 Copyright
 KHKKLKQPGDGNP 13
 Length
 GenCore version (c) 1993 - 2000
 DВ
 IJ
 SUMMARIES
 model
 Compugen
 Ltd
Description
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987654821

75 75 75 75 75 69 69

100.0 100.0 100.0 100.0 92.0 92.0 92.0 92.0

13 350 412 412 412 20 20 396

21 US-09-763-397A-5 21 US-09-763-397A-2 3 US-07-677-539B-6 3 US-07-727-636-6 3 US-08-948-885-18 3 US-07-947-033-21 5 US-08-119-694-21 22 US-09-820-843A-31

Sequence 5, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 18, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 31, Appl

25 5 3 13 3 3

| Query Match 100.0%; Score 75; DB 21; Length 13; Best Local Similarity 100.0%; Pred. No. 4.6e-05; Matches 13; Conservative 0; Mismatches 0; Indels 0; Qy 1 KHKKLKQPGDGNP 13 | RESULT 1  US-09-763-397A-5  Sequence 5, Application US/09763397A  GENERAL INFORMATION: APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Control and Prevention APPLICANT: Secretary of the Department of Health and Human Services, Centers for APPLICANT: Control and Prevention APPLICANT: Lal, Altaf A.  APPLICANT: Ping Shi, Ya APPLICANT: Hasnain, Seyed E. TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium FILE REFERENCE: 6395-57049  CURRENT APPLICATION NUMBER: US/09/763,397A  CURRENT APPLICATION NUMBER: US/09/763,397A  CURRENT FILING DATE: 2001-02-16  PRIOR APPLICATION NUMBER: US 60/097,703  PRIOR FILING DATE: 1998-08-21  PRIOR APPLICATION NUMBER: PCT / US99/18869  PRIOR APPLICATION NUMBER: WS 60/097,703  PRIOR FILING DATE: 1999-08-19  NUMBER OF SEQ ID NOS: 26  SEQ ID NO 5  LENGTH: 13  LENGTH: 13  TYPE: PRT ORGANISM: Plasmodium falciparum  US-09-763-397A-5 | ALIGNMENTS | 10 51 68.0 388 3 US-07-675-59B-5 Sequence 5, App 12 47 62.7 102 1 PCT-US01-14826-22 Sequence 2.3, App 13 47 62.7 102 1 PCT-US01-2861-2 Sequence 2.3, App 14 47 62.7 102 1 PCT-US01-2861-2 Sequence 2.3, App 14 47 62.7 102 1 PCT-US99-09970-2 Sequence 2.614 47 62.7 102 21 US-09-306-111-2 Sequence 2.614 47 62.7 102 22 US-09-84-566-24564 Sequence 2.614 19 47 62.7 102 24 US-60-197-873-24564 Sequence 2.6264 19 47 62.7 102 24 US-60-197-873-24564 Sequence 2.6264 19 47 62.7 102 24 US-60-197-873-24564 Sequence 2.6264 19 47 62.7 118 12 US-09-704-08-68 Sequence 2.6264 19 41 54.7 119 11 US-09-704-08-68 Sequence 6.65, App 14 14 14 14 14 14 14 14 14 14 14 14 14                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Gaps 0;                                                                                                                                                                    | represented by the<br>ervices, Centers for<br>gainst Plasmodium Fa                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |            | 223 Appli 223 Appli 223 Appli 223 Appli 22 Appli 23 Appli 24 Appli 26 Appli 26 Appli 27 Appli 28 Appli 29 Appli 20 Appli |

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 В
 US-09-763-397A-2
 ; OTHER INFORMATION: Recombinant DNA/Protein US-09-763-397A-2
 Query Match
Best Local Similarity
Matches 13; Conser
 Sequence 6, Applicati
GENERAL INFORMATION:
 SEQ ID NO 2
 GENERAL INFORMATION:
 Sequence 2, Application US/09763397A
 -07-677-539B-6
 CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR EILING DATE: 1998-08-21
PRIOR APPLICATION NUMBER: PCT / US99/18869
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
 FILE REFERENCE: 6395-57049
CURRENT APPLICATION NUMBER: US/09/763,397A
CURRENT FILING DATE: 2001-02-16
 APPLICANT: Ping Shi, Ya
APPLICANT: Hasnain, Seyed E.
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Falc.
 APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for APPLICANT: Control and Prevention
 LENGTH: 35
TYPE: PRT
 APPLICANT:
 FEATURE:
 ORGANISM: Artificial Sequence
 ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 56
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
TELECOMMUNICATION INFORMATION: TELEPHONE: 202-861-3067
 NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
 APPLICANT: GOLDMAN, IRA F.
TITLE OF INVENTION: REICHE
 APPLICANT: LAL, ALTAF A.
APPLICANT: GOLDMAN, IRA
 APPLICATION NUMBER: US
FILING DATE: 19911205
CLASSIFICATION: 424
 COUNTRY:
 29 KHKKLKQPGDGNP 41
 STREET:
 ADDRESSEE:
 1 KHKKLKQPGDGNP 13
 1 KHKKLKQPGDGNP 13
 350
 WASHINGTON
 20036
 D.C
 Application US/07677539B
 Lal, Altaf A.
 E: CUSHMAN, DARBY & CUSHMAN 1615 L STREET, N.W.
 USA
 Conservative
 CIRCUMSPOROZOITE PROTEIN OF PLASMODIUM REICHENOWI AND VACCINE FOR HUMAN MALARIA 54
 100.0%;
 US/07/677,539B
 5683/91540
 0,
 Score 75; DB 21;
Pred. No. 0.0021;
 Version #1.25
 Length 350;
 Indels
 0;
 0;
 for Di
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В
 QY
 RESULT 4
US-07-727-636-6
 밁
 QΥ
 MOLECULE TYPE: US-07-727-636-6
 Sequence 6, Applicati
GENERAL INFORMATION:
 Matches
 Query Match
Best Local
 Query Match
Best Local Similarity
 Matches
 TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 APPLICATION NUMBER: US/07/
FILING DATE: 19910710
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION UNMBER: 26,58
REFERENCE/DOCKET NUMBER: 5
 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
 NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION:
 MOLECULE TYPE: peptide
 TELECOMMUNICATION INFORMATION: TELEPHONE: 202-861-3067
 APPLICANT:
109 KHKKLKQPGDGNP 121
 109 KHKKLKQPGDGNP 121
 COMPUTER: IBM PC
OPERATING SYSTEM:
 TOPOLOGY:
 STRANDEDNESS:
 MEDIUM TYPE:
 COUNTRY:
 STATE:
 STREET:
 TOPOLOGY:
 STRANDEDNESS:
 LENGTH:
 ADDRESSEE:
 1 KHKKLKQPGDGNP 13
 1 KHKKLKQPGDGNP 13
 ENGTH:
 13;
 Similarity
 WASHINGTON
 AMINO ACID
 20036
 AMINO ACID
 Application US/07727636
 D.C
 E: CUSHMAN, DARBY & CUSHMAN 1615 L STREET, N.W.
 USA
 GOLDMAN,
 Conservative
 Conservative
 LAL, ALTAF A.
 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
 linear
 linear
 Floppy disk
 peptide
 single
 single
 CIRCUMSPOROZOITE PROTEIN OF PLASMODIUM REICHENOWI AND VACCINE FOR HUMAN MALARIA
 100.0%;
 100.0%;
 IRA F
 US/07/727,636
 26,581
 0;
 0;
 5683/91540
 Score 75;
Pred. No.
 Score 75;
Pred. No.
 Mismatches
 Mismatches
 Version #1.25
 0.0026;
 0.0026
 Length 412;
 Length 412;
 Indels
 Indels
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 Gaps
 Gaps
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; MOLECULE TYPE: peptide US-08-948-885-18
 US-07-947-033-21
 Sequence 21, Application US/07947033 GENERAL INFORMATION:
 Matches
 Query Match
Best Local Similarity
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/313,288
FILING DATE: January 5, 1995
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
 Sequence 18, Application US/08948885 GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO:
 APPLICANT: Jessell, Thomas M. and Avihu Klar
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
 APPLICANT: Cerami, Carla
APPLICANT: Frevert, Ute
APPLICANT: Sinnis, Photini
APPLICANT: Sinnis, Photini
APPLICANT: Sinnis, Photini
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING
TITLE OF INVENTION: HEPATOCYTE INVASION BY MALARIAL SPOROZOITES
NUMBER OF SEQUENCES: 27
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby, P.C.
COMPUTER READABLE FORM:
 109 KHKKLKQPGDGNP 121
 TOPOLOGY:
 STREET: 1185 A:
CITY: New York
STATE: New Yor
 TYPE: amino acid
STRANDEDNESS: sir
 APPLICATION NUMBER: US/08/948,885 FILING DATE:
 TELEFAX: (212) 391-0526
 COUNTRY:
 COUNTRY:
 STREET:
 1 KHKKLKQPGDGNP 13
 ADDRESSEE:
 New York
 10022
 New York
 New York
 E: Cooper & Dunham LLP
1185 Avenue of the Americas
 805 Third Avenue
 USA
 United States of America
 Conservative
 linear
 single
 100.0%;
 18:
 0
 Score 75; DB 13;
Pred. No. 0.0026;
 Mismatches
 DB 13;
 Length 412;
 Indels
 0;
 Gaps
 0;
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В
 US-08-119-694-21
 TOPOLOGY: US-07-947-033-21
 Query Match 92.0
Best Local Similarity 92.0
Matches 12; Conservative
 Sequence
 APPLICATION UMBER: US/08/119,694
EFILING DATE: 10-Sept-1993
ATTORNEY/AGENT INFORMATION:
NAME: Adda C. Gogoris, Esq.
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986/17607-US1
TELECOMMUNICATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
 Sequence 21, Application US/08119694 GENERAL INFORMATION:
 TELEFAX: (212) 753-62: TELEX: 236687 INFORMATION FOR SEQ ID NO:
 INFORMATION FOR SEQ ID NO:
 ATTORNEY/AGENT INFORMATION:
NAME: Adda C. Gogoris, Esq.
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
 APPLICANT: Frevert, Ute
APPLICANT: Sinnis, Photini
APPLICANT: Nussenzweig, Victor
 SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
 COMPUTER: AST Premium II 386/33
OPERATING SYSTEM: DOS 3.3
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING TITLE OF INVENTION: HEPATOCYTE INVASION BY MALARIAL TITLE OF INVENTION: SPOROZOITES
 APPLICANT:
 SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
 CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS
 NUMBER OF SEQUENCES:
 TELLEFAX: (44)
TELLEFAX: 236687
 LENGTH: 20 amino TYPE: 'AMINO ACID
 FILING DATE: 19 CLASSIFICATION:
 COUNTRY:
 STATE:
 STREET:
 SOFTWARE:
 OPERATING SYSTEM:
 ADDRESSEE:
 APPLICATION NUMBER: US/07/947,033
 MEDIUM TYPE:
TOPOLOGY:
 3 KHKKLKQPADGNP 15
 1 KHKKLKQPGDGNP 13
 10022
 New York

New York

United States of America
 amino acid
 805 Third Avenue
 Cerami, Carla
 Word Perfect 5.1
 unknown
 E: Diskette, 5, inch, 1.2 MB storage AST Premium II 386/33
SYSTEM: DOS 3.3
 Darby & Darby, P.C.
 Diskette,
 19920917
 92.0%;
 5, inch, 1.2 MB storage
 21:
 5986/07607
 0,:
 Score 69; DB 3;
Pred. No. 0.00071;
 Mismatches
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 Gaps
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RESULT 9
US-09-820-843A-31
; Sequence 31, Application US/09820843A
; Sequence 31, Application US/09820843A
; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
; TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
; FILE REFERENCE: Q63915
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 US-08-119-694-21
 US-08-119-694B-21
 Query Match
Best Local :
 Sequence 21, Application US/08119694B GENERAL INFORMATION:
 Matches
 Matches
 APPLICATION NUMBER: US/08/119,694B
FILING DATE: 10-Sept-193
ATTORNEY/AGENT INFORMATION:
NAME: Adda C. Gogoris, Esq.
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986/17607-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEPAN: (212) 753-6237
CURRENT APPLICATION NUMBER: US/09/820,843A
 APPLICANT: Cerami, Carla
APPLICANT: Frevert, Ute
APPLICANT: Sinnis, Photini
APPLICANT: Nussenzweig, Victor
TITLE OF INVENTION: INHIBITING H
 SEQUENCE CHARACTERISTICS:
 SOFTWARE: Word Perfect CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5, inch, 31
COMPUTER: COMPAQ PROLINEA MT 4/66
OPERATING SYSTEM: DOS 3.3
 CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES:
 TITLE OF INVENTION:
 TELLEFAX: (-
TELEFAX: (-
Tex: 236687
 Local Similarity hes 12; Conserv
 TYPE: amino acid
 CITY: New York
STATE: New York
 Local Similarity hes 12; Conser
 TOPOLOGY:
 COUNTRY:
 STREET:
 ADDRESSEE:
 1 KHKKLKQPGDGNP 13
 LENGTH:
 1 KHKKLKQPGDGNP 13
 3 KHKKLKQPADGNP 15
 New York
 805 Third Avenue
 20 amino acids
 Conservative
 United States of Ameri8ca
 Conservative
 Word Perfect 5.2
 unknown
 Darby & Darby, P.C
 92.0%;
 BY MALARIAL SPOROZOITES
 92.0%;
92.3%;
 COMPOSITIONS AND METHODS FOR INHIBITING HEPATOCYTE INVASION
 Score 69; I
Pred. No. 0.
 Score 69; DB 5;
Pred. No. 0.00071;
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 Mismatches
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 .00071;
 1; Indels
 Length 20;
 Length 20;
 Indels
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 0;
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; LENGTH: 396; TYPE: PRT
; OTGANISM: Plasmodium falciparum
; FEATURE:
; NAME/KEY: misc_feature
OTHER INFORMATION: Circumsporozoite (CS) protein
; NAME/KEY: misc_feature
OTHER INFORMATION: g1|4493889
US-09-820-843A-31
 Query Match
Best Local Similarity
""" 9; Conserv
δÃ
 RESULT 10
US-07-677-539B-5
 δÃ
 Query Match
Best Local Similarity
*~*ches 12; Conserva
 US-07-677-539B-5
 밁
 Sequence 5, Application US/07677539B GENERAL INFORMATION:
 SEQ ID NO 31
LENGTH: 396
 TELEPHONE: 202-861-301
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
 CURRENT FILING DATE: 2001-03-30 NUMBER OF SEQ ID NOS: 118 SOFTWARE: PatentIn version 3.0
 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,5
REFERENCE/DOCKET NUMBER:
 TOPOLOGY: 1. MOLECULE TYPE:
 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 APPLICANT: LAL, ALTAF A.

APPLICANT: GOLDMAN, IRA F.

TITLE OF INVENTION: CICCUMSPOROZOITE PROTEIN OF PLASMODIUM
TITLE OF INVENTION: REICHENOWI AND VACCINE FOR HUMAN MALARIA
 SEQUENCE CHARACTERISTICS:
 TELECOMMUNICATION INFORMATION: TELEPHONE: 202-861-3067
 NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
 LENGTH: 300
TENGTH: 300
TYDE: AMINO ACID
TYDE: Sin(
 MADJUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palana
 APPLICATION NUMBER: UPFILING DATE: 19911205
 COUNTRY: USA
ZIP: 20036
 STATE:
 STREET: 1615 L S
CITY: WASHINGTON
 89 KHKKLKQPADGNP 101
 ADDRESSEE:
 1 KHKKLKQPGDGNP 13
 1 KHKKLKQPGDGN 12
 D.C.
 E: CUSHMAN, DARBY & CUSHMAN
 388 amino acids
 Conservative
 Conservative
 linear
 peptide
 single
 92.0%;
92.3%;
 68.0%;
75.0%;
 us/07/677,539B
 26,581
 1; Mismatches
 0;
 Score 51; DB Pred. No. 17;
 Pred. No. 0.023;
 Score 69; DB 22;
 Mismatches
 ω
 1; Indels
 Length 388;
 Length 396;
 Indels
 0;
 0,
 Gaps
 Gaps
 0;
 0;
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109 KHNKLKQPGNDN 120

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RESULT 12
PCT-US01-14826-223
Sequence 223, Application PC/TUS0114826
Sequence 223, Application PC/TUS0114826
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-103
CURRENT APPLICATION NUMBER: PCT/US01/14826
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/577,408
PRIOR APPLICATION NUMBER: 09/577,288

PRIOR APPLICATION NUMBER: 09/677,288
2000-09-22

PRIOR APPLICATION NUMBER: 09/677,288
2000-10-24

PRIOR APPLICATION NUMBER: 09/715,869
2000-11-17

PRIOR APPLICATION NUMBER: 09/775,330
2000-10-20

 , MOLECULE TYPE: peptide US-07-727-636-5
 В
 ş
 US-07-727-636-5
 Sequence 5, Application US/07727636 GENERAL INFORMATION:
 Matches
 Query Match
Best Local :
 TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
 NUMBER OF SEQ ID NOS: 864
 REFERENCE/DOCKET NUMBER: 56
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067
TELEPHAX: 202-822-0944
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/727,636
FILING DATE: 19910710
CLASSIFICATION: 424
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
 SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acid
 TITLE OF INVENTION: CIRCUMSPOROZOITE PROTEIN OF PLASMODIUM TITLE OF INVENTION: REICHENOWI AND VACCINE FOR HUMAN MALARIA NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1615 L STREET, N.W.
 ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,
 TYPE: AMINO AGENTANDEDNESS:
TOPOLOGY: lin
 APPLICANT: LAL,
APPLICANT: GOLDM
 109 KHNKLKQPGNDN 120
 STREET: 1615 L STREET: WASHINGTON STATE: D.C.
 ZIP: 20036
 Local Similarity es 9; Conserv
 1 KHKKLKOPGDGN 12
Custom
 H: 388 amino acids
AMINO ACID
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 USA
 GOLDMAN, IRA F.
 Conservative
 ALTAF A.
 68.0%;
75.0%;
 26,581
 <u>ب</u>
 Score 51;
Pred. No.
 5683/91540
 Mismatches
 DB 3;
 Length 388;
 Indels
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 Query Match
Best Local Similarity
Watches 8; Conserva
 PCT-US99-09970-2
 RESULT
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 PCT-US01-23861-2
 PRIOR APPLICATION NUMBER: 2001-07-31;
PRIOR ETLING DATE: 2001-07-31;
PRIOR ETLING DATE: 2000-07-31;
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH.
 PCT-US01-23861-2
 PCT-US01-14826-223
 Sequence 2, Applicat GENERAL INFORMATION:
 Sequence 2, Application PC/TUS0123861 GENERAL INFORMATION:
CURRENT APPLICATION NUMBER: PCT/US99/09970
CURRENT FILING DATE: 199-05-07
NUMBER OF SEQ ID NOS: 180
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENCTH: 102
TYPE: PRT
 Query Match
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Matches 8; Conserv
 APPLICANT: Munger, William E. APPLICANT: Kulkarni, Prakash APPLICANT: Kulkarni, Prakash APPLICANT: Getzenberg, Robert R. TITLE OF INVENTION: Expression of a GAGE/PAGE-like Protein in Benign Prostatic TITLE OF INVENTION: Hyperplasia
 FILE REFERENCE: 44921-5031-WO CURRENT APPLICATION NUMBER: PO CURRENT FILING DATE: 2001-07
 APPLICANT: Bowman, Michael R.
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Widom, Angel
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING
FILE REFERENCE: GI 6069-74A
 APPLICANT: Merberg, David APPLICANT: Treacy, Maurice
 APPLICANT: Agostino, Michael J. APPLICANT: Steininger II, Robert J.
 APPLICANT: LaVallie, Edward R. APPLICANT: Collins-Racie, Lisa
 APPLICANT: McCoy, John
 APPLICANT: Evans, Cheryl
 APPLICANT: Jacobs, Kenneth
 ORGANISM: Homo sapiens
 LENGTH: 102
TYPE: PRT
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TYPE: PRT
 ORGANISM: Homo sapiens
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 2, Application PC/TUS9909970
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61.5%;
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61.5%;
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 PCT/US01/23861
 Score 47;
Pred. No.
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APPLICANT: Jacobs, Kenneth
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Werberg, David
APPLICANT: Merberg, David
APPLICANT: Steininger II, Robert J.
APPLICANT: Bowman, Michael J.
APPLICANT: Bowman, Michael R.
APPLICANT: Bowman, Michael R.
APPLICANT: Widom, Angela
APPLICANT: Genetics Institute, Inc.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: GI 6069-74A
CURRENT APPLICATION NUMBER: US/09/306,111
CURRENT APPLICANT DATE: 199-05-06
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 102
TYPE: PRT
US-09-306-111-2
Search completed: January 29, 2002, 10:56:01 Job time: 2397 sec
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US-09-306-111-2
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Best Local Similarity 61.5%;
Matches 8; Conservative
 Sequence 2, Application US/09306111 GENERAL INFORMATION:
 Query Match 62.7%;
Best Local Similarity 61.5%;
Matches 8; Conservative
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Pred. No. 16;
1; Mismatches 4; Indels
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 Gaps
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Result
No.
 Title:
Perfect score:
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 Total number of hits satisfying chosen parameters:
 Run
 웆
 Database
 Minimum
 Sequence:
 Maximum
 Searched:
 Scoring table:
 protein -
 9
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 DB
BB
 Score
 seq
 protein search, using sw model
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length: 2000000000
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2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
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Gapop 10.0 , Gapext 0.5
 US-09-763-397A-5
 January 29, 2002, 10:58:08;
 173191 seqs, 36597120 residues
 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
 KHKKLKQPGDGNP 13
 Length
 DΒ
US-09-897-516-4572
US-09-708-427-11248
US-09-708-427-11246
US-09-708-427-6245
US-09-708-427-6245
US-09-708-427-6245
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US-09-708-427-16308
US-09-708-427-16308
US-09-708-427-4589
US-09-708-427-4589
US-09-708-427-61433
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 SUMMARIES
 Search time 120.95 Seconds (without alignments)
3.934 Million cell updates/sec
 173191
 Description
 sequence
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4689,
61433,
49591,
1794,
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| RESULT 2 US-09-708-427-11248 ; Sequence 11248, Application US/09708427 ; GENERAL INFORMATION: APPLICANT: N. ALEXANDROV et al. TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING; TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P ; CURRENT APPLICATION NUMBER: US/09/708,427 ; CURRENT FILING DATE: 2000-11-09 ; NUMBER OF SEQ ID NOS: 85364 ; SOFTWARE: Patentin version 3.1 ; SEQ ID NO 11248 ; LENGTH: 597 | Query Match Best Local Similarity 60.0%; Pred. No. 7.4; Matches 6; Conservative 3; Mismatches 1; Indels 0; Garante 3; Mismatches 1; Indels 0; Mismatches 1; Mismatc | 516<br>rina C.<br>. Genome Sequences And Uses<br>897,516 | 27 36 48.0 227 5 US-09-969-730-136 Sequence 128 36 48.0 257 5 US-09-74-639-155 Sequence 129 36 48.0 252 5 US-09-74-639-155 Sequence 159 30 36 48.0 261 5 US-09-708-427-59039 Sequence 269 31 36 48.0 261 1 PCT-US01-27760-554 Sequence 270 31 36 48.0 291 1 PCT-US01-27760-554 Sequence 270 31 36 48.0 423 5 US-09-708-427-19308 Sequence 270 31 36 48.0 423 5 US-09-708-427-24191 Sequence 270 31 35 46.7 21 5 US-09-708-427-24191 Sequence 270 31 32 46.7 21 5 US-09-708-427-4370 Sequence 270 31 32 46.7 21 5 US-09-708-427-74370 Sequence 270 31 32 46.7 42 5 US-09-821-726-6 Sequence 270 31 32 46.7 42 5 US-09-821-726-6 Sequence 270 31 32 46.7 42 5 US-09-89-723-211 Sequence 270 31 32 46.7 185 5 US-09-989-730-211 Sequence 270 31 32 46.7 185 5 US-09-989-730-211 Sequence 270 31 32 46.7 185 5 US-09-990-444-211 Sequence 270 31 32 32 33 34 34 35 34 34 34 34 35 34 34 34 34 34 34 34 34 34 34 34 34 34                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
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| RESPONDING POL                                                                                                                                                                                                                                                                                                                                                                                                                             | 0; Gaps .                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Thereof                                                  | ance 136, Appance 59040, Appance 59040, Appance 554, Appance 554, Appance 24191, Appance 10, Appliance 10, Appliance 211, Appance 211, |

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US-09-708-427-11247

Sequence 11247, Application US/09708427

Sequence 11247, Application US/09708427

Sequence 11247, Application US/09708427

APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: THEREBY

FILE REFERENCE: 2750-1243

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SOFTWARE: Patentin version 3.1

SEQ ID NO 11247

LENGTH: 628
 US-09-708-427-11246
, Sequence 11246, Application US/09708427
; GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
 Query Match
Best Local Similarity
"---hes 8; Conserv
 밁
 Ş
 ; NAME/KEY: misc_feature; LOCATION: 1.628; OTHER INFORMATION: Ceres Seq. ID 1822796 US-09-708-427-11247
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 ; OTHER INFORMATION: Ceres Seq. ID 1822797 US-09-708-427-11248
 FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11246
 Query Match
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 TYPE: PRT
 LOCATION: 1..628
OTHER INFORMATION: Xaa is any amino acid
 FEATURE:
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ORGANISM: Arabidopsis thaliana
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 NAME/KEY: misc_feature
LOCATION: 1.597
 LENGTH: 633
 NAME/KEY: misc_feature
 FEATURE:
 ORGANISM: Arabidopsis thaliana
 87 KNKKLQQRGDTN
 Local Similarity
les 8; Conserv
 56 KNKKLOORGDIN 67
 1 KHKKLKQPGDGN 12
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 53.3%;
 53.3%;
 2;
 Score 40; DB
Pred. No. 44;
 Score 40; DB
Pred. No. 42;
 amino acid
 Mismatches
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 <u>ن</u>
 5
 Length 628;
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 Indels
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 0;
 Gaps
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 0
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US-09-708-427-6245
; Sequence 6245, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
 망
 Qγ
 US-09-708-427-6246
 RESULT 5
US-09-708-427-6246
 В
 QУ
 US-09-708-427-11246
 GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
APPLICANTE et al.
APPLICANT: N. ALEXANDROV et al.
APPLICANTE et al.
APPLICANTE et al.
APPLICANTE et al.
A
 NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 6245
LENGTH: 454
 Query Match 52.0%;
Best Local Similarity 58.3%;
Matches 7; Conservative
 SOFTWARE: Pat
SEQ ID NO 6246
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 Sequence 6246, Application US/09708427
 Query Match 53.3%;
Best Local Similarity 66.7%;
 CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY
 CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
 FILE REFERENCE: 2750-1243P
 NAME/KEY: misc_feature
LOCATION: 1..425
OTHER INFORMATION: Ceres Seq.
 LENGTH: 425
TYPE: PRT
ORGANISM: Arabidopsis thaliana
 TYPE: PRT
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 NAME/KEY: misc_feature LOCATION: 1..454
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 92 KNKKLOORGDIN 103
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 1 KHKKLKQPGDGN 12
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 PatentIn version 3.1
 Conservative
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 is any amino acid
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 Score 39; DB Pred. No. 44;
 Score 40; DB
Pred. No. 45;
 ID 1815598
 ID 1822795
 Mismatches
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 5.
 5
 Length 425
 Length 633;
 Indels
 Indels
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 0
 Gaps
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Query Match
Best Local Similarity
""trhes 7; Conserve
 Query Match
Best Local Similarity
"hehes 7; Conserva
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LOCATION: 1..454
; OTHER INFORMATION: Ceres Seq.
US-09-708-427-6245
 US-09-708-427-43901
Sequence 43901, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
 밁
 ; OTHER INFORMATION: Ceres Seq. US-09-708-427-6244
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 S
 US-09-708-427-6244
 FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 43901
LENGTH: 122
 CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6244
LENGTH: 558
 Sequence 6244, Application US/09 GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY
 NAME/KEY: misc_feature
LOCATION: 1.58
OTHER INFORMATION: Xaa is any
NAME/KEY: misc_feature
LOCATION: 1.558
 NAME/KEY: misc_feature
LOCATION: 1..122
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..122
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 ORGANISM: Zea mays subsp. mays
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 ORGANISM: Arabidopsis thaliana
 TYPE: PRT
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 227 KEKALKEKGEGN 238
 123 KEKALKEKGEGN 134
 1 KHKKLKQPGDGN 12
 1 KHKKLKQPGDGN 12
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 Application US/09708427
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 52.0%;
58.3%;
 52.0%;
58.3%;
 Mismatches
 ID 1848537
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 Score 39; DB Pred. No. 58;
 Score 39; DB
Pred. No. 47;
 ID 1815597
 ID 1815596
 Mismatches
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 Length 558
 Length 454
 Indels
 Indels
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 Gaps
 0;
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NAME/KEY: misc_feature
LOCATION: 1..126
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..126
OTHER INFORMATION: Ceres Seq. ID 1848536
US-09-708-427-43900
; OTHER INFORMATION: Ceres Seq. ID 1848535 US-09-708-427-43899
 US-09-708-427-43899
 ₽
 В
 US-09-708-427-43900
 US-09-708-427-43901
 Sequence 43899, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
 Query Match
Best Local Similarity //..
Thes 7; Conservative
 Sequence 43900, Application US/09708427 GENERAL INFORMATION:
 SEQ ID NO 43899
LENGTH: 152
TYPE: PRT
 SEQ ID NO 43900
LENGTH: 126
TYPE: PRT
 Query Match
Best Local Similarity
Matches 7; Conserv
 FEATURE:

NAME/KEY: misc_feature
LOCATION: 1..152

OTHER INFORMATION: Xaa i.

NAME/KEY: misc_feature
LOCATION: 1..152
 CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
 CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
 SOFTWARE: PatentIn version 3.1
 APPLICANT: N. ALEXANDROV et al.
 ORGANISM: Zea mays subsp. mays FEATURE:
 ORGANISM:
 42 KRLKQSGDG
 1:111 |||
38 KRLKQSGDG
 3 KKLKQPGDG 11
 3 KKLKQPGDG 11
 Zea mays subsp.
 Conservative
 50
 46
 50.7%;
77.8%;
 50.78;
77.88;
 is any amino acid
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 1; Mismatches
 Score 38; DB
Pred. No. 19;
 Score 38; DB
Pred. No. 18;
 5·
 5
 Length 126;
 Length 122;
 Indels
 Indels
 0,
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 Gaps
 Gaps
 0
 0
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APPLICANT: Bower, Stanley G.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

ITILE OF INVENTION: Sphingomonas elodea genome sequences and use

FILE REFERENCE: 38-10(15806)B

CURRENT APPLICATION NUMBER: US/10/015,127

CURRENT FILING DATE: 2001-10-29

PRIOR APPLICATION NUMBER: US 60/252,455

PRIOR APPLICATION NUMBER: US 60/252,455

INUMBER OF SEQ ID NOS: 14357

SEQ ID NO 13035

LENGTH: 252

TWOND: DEMONSTRANCE OF SEQ ID NOS: 14357
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US-10-015-127-13035
; Sequence 13035, Application US/10015127
; GENERAL INFORMATION:
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 ; OTHER INFORMATION: Ceres Seq. US-09-708-427-32720
 RESULT 12
US-09-708-427-32720
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 B
 ; ORGANISM: Sphingomonas elodea US-10-015-127-13035
 δÃ
 Sequence 32720, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-11439
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 32720
LENGTH: 287
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LOCATION: 1..287
OTHER INFORMATION: Xaa is any amino acid
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LOCATION: 1..287
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 1 KHKKLKQPGDG 11
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 Score 38; DB 5;
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 Score 38; DB 6; Pred. No. 38;
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; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
; TITLE OF INVENTION: THEREBY
; FILE REFERENCE: 2750-1243P
; CURRENT STAING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 85364
; SOFTWARE: Patentin version 3.1
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; APPLICANT: N. ALEXANDROV et al.
 ; NAME/KEY: misc_feature
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US-09-708-427-32718
 ; NAME/KEY: misc_feature
; LCCATION: 1..342
; OTHER INFORMATION: Ceres Seq. ID 1834863
US-09-708-427-32719
 밁
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 Ωy
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Best Local Similarity
Matches 7; Conserv
 SEQ ID NO 32718
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Best Local Similarity
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY ELLE REFERENCE: 2750-1243P CURRENT APPLICATION NUMBER: US/09/708,427 CURRENT FILING DATE: 2000-11-09 NUMBER OF SEQ 1D NOS: 8354 NOS: 8754 NOS: 87
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RESULT 15 US-60-337-358-600

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Yang, Chunzhi

Zeng, Xiaoping

APPLICANT: Zhao, Yajuan

APPLICANT: Zhao, Yajuan

APPLICANT: Zhao, Yajuan

APPLICANT: Zhao, Yajuan

FILE REFERENCE: 38-15(52796)A

CURRENT APPLICATION NUMBER: US/60/337,358

CURRENT FILING DATE: 2001-12-04

NUMBER OF SEQ ID NOS: 745

SEQ ID NO 600

LENGTH: 856

TYPE: PRT

ORGANISM: Zea mays

US-60-337-358-600
Search completed: January 29, 2002, 10:58:09 Job time: 2505 sec
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 APPLICANT: Agarwal, Ameeta K.
APPLICANT: Ahrens, Jeffrey E.
APPLICANT: Ball, James A.
APPLICANT: Banu, G.
APPLICANT: Bell, Erin
APPLICANT: Boddupalli, Raghava
APPLICANT: Chomet, Paul S.
APPLICANT: Daly, Mackenzie
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Dong, Jinzhuo
Duff, Stephen M.
Edgerton, Michael D
Galligan, Meghan M.
Hinchey, Brenda S.
Huang, Shihshieh
Johnson, Richard G.
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Malloy, Kathleen A.
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Lund, Adrian
 Lai, Chao-Qiang
 Jung, Vincent
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Maximum Match 100%
Listing first 45 summaries
 Total number of hits satisfying chosen parameters:
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Sequence:
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 Database
 Maximum
 Searched:
 Scoring table:
 Title:
 OM protein -
 Minimum
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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US-07-958-321-9
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1 US-08-773-675-8
1 US-08-998-335-1
3 US-08-998-335-1
4 US-09-060-450-1
4 US-09-074-410-34
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 SUMMARIES
 Compugen Ltd
 3148936
Sequence 105, Appli
Sequence 9, Appli
Sequence 11, Appli
Sequence 4, Appli
Sequence 8, Appli
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Sequence 34, Appli
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| 69                | 69       | 69      | 69    | 69              | 69              | 69              | 69                | 69                | 69               | 69                | 69                | 69                  | 69                  | 69               | 69              | 69       | 69               | 69                | 69              | 69                | 69               | 69               | 69               | 69               | 69              | 69               | 69               | 69                | 69   | 69               | 69    | 69           | 69               | 69               | 69               |  |
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| 229               | 164      | 164     | 164   | 163             | 163             | 130             | 68                | 83                | 48               | 36                | 36                | 36                  | 36                  | 28               | 28              | 28       | 20               | 16                | 16              | 16                | 16               | 16               | 16               | 16               | 16              | 16               | 13               | 13                | 13   | 13               | 13    | 13           | 13               | 12               | 12               |  |
| 18                | 22       | 7       | ω     | 7               | w               | æ               | 13                | 4                 | 14               | 21                | 21                | Ь                   | -                   | 14               | 13              | 13       | 13               | 18                | 17              | 17                | 17               | 11               | 11               | 11               | œ               | ω                | 17               | 11                | 1    | 11               | 7     | S            | w                | 21               | 17               |  |
| US-09-454-204A-41 | -09-826- | 97-128- | 554 - | US-08-397-128-2 | US-07-941-654-2 | US-08-466-755-7 | US-08-982-965-13  | US-08-029-666A-12 | US-09-060-450-11 | US-09-701-588-105 | US-09-701-588-104 | PCT-US99-13975B-105 | PCT-US99-13975B-104 | US-09-060-450-10 | US-08-998-335-4 | -866-80- | US-08-944-147-19 | US-09-454-204A-26 | US-09-389-482-9 | US-09-310-462A-18 | US-09-310-462-18 | US-08-773-675B-9 | US-08-773-675A-9 | US-08-773-675-10 | US-08-466-755-6 | US-07-958-321-12 | US-09-389-482-10 | US-08-773-675B-10 | 675A | US-08-773-675-11 | 932-  | -08-138-514- | US-07-958-321-13 | US-09-763-397A-4 | us-09-300-959-39 |  |
| Sequence 41, Appl | e 1,     | 1, 2    | 1,    | 2               | ,2              | 7, A            | Sequence 13, Appl | 12, /             | 11, 4            | 105,              | e 104,            | 105,                | 104,                | 10               | 4               | 4, 2     | 19,              | 26,               | 9,              | 18,               | 18,              | 9                | 9                | e 10             | 6,              | 12, ,            | 10,              | 10,               | 10,  | e<br>11          | ω     | 8            | 13,              | e 4, A           | е 39,            |  |

## ALIGNMENTS

```
APPLICANT: Birkett, Ashley J.

APPLICANT: Birkett, Ashley J.

TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and TITLE OF INVENTION: their Derivatives

FILE REFERENCE: Syn-101 4564/69529

CURRENT APPLICATION NUMBER: PCT/US99/03055

CURRENT FILING DATE: 1999-02-11

EARLIER APPLICATION NUMBER: 60/074537

EARLIER FILING DATE: 1998-02-12

NUMBER OF SEQ ID NOS: 113

SOFTMARE: Patentin Ver. 2.0

SEQ ID NO 105

LENGTH: 12

TYPE: PAT

ORGANISM: Artificial Sequence
FEATURE:

COMMENT OF SEQ ID NOS: 131

SOFTMARE: PATENTIAL Sequence
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PCT-US99-03055-105

; Sequence 105, Application PC/TUS9903055

; GENERAL INFORMATION:
 PCT-US99-03055-105
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Best Local Similarity
Matches 12; Conserv
 PUBLICATION INFORMATION:
JOURNAL: Science
VOLUME: 228
 PAGES: 1436-1440
DATE: 1985
 OTHER INFORMATION: Description of Artificial Sequence: Cytochrome OTHER INFORMATION: P-450 fragment
100.0%; silarity 100.0%; silarity 100.0%; sometime of the conservative of the conserva
Score 69; DB 1; 1
Pred. No. 0.00064;
); Mismatches 0;
 Length 12;
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Indels

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Gaps

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 US-07-958-321-11 ; Sequence 11, Application US/07958321
 В
 US-07-958-321-9
 RESULT 2
US-07-958-321-9
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 Sequence 9, Applicati
GENERAL INFORMATION:
 CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: GB 9022190.4

FILING DATE: 12-CCT-1990

PRIOR APPLICATION NUMBER: PCT/GB91/01785

FILING DATE: 14-CCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: MacLean, Kurt A.

REGISTRATION NUMBER: 31,118

REGISTRATION NUMBER: 31,118
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 GENERAL INFORMATION:
 TELEFAX: 714-263-8260 INFORMATION FOR SEQ ID NO:
APPLICANT: Perham, nace....
APPLICANT: Willis, Anne E.
APPLICANT: Greenwood, Judith
TITLE OF INVENTION: ENGINEERED BACTERIOPHAGES AND VACCINES
TITLE OF INVENTION: CONTAINING THEM
 REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 APPLICANT: Greenwood, Judith
TITLE OF INVENTION: ENGINEERE
TITLE OF INVENTION: CONTAININ
NUMBER OF SEQUENCES: 21
 SEQUENCE CHARACTERISTICS:
 CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 APPLICANT: Willis,
 APPLICANT:
 COUNTRY: U
ZIP: 90067
 STREET: 2121 Aver
CITY: Los Angles
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 TOPOLOGY:
 APPLICATION NUMBER: US FILING DATE: 19921222
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 TELEPHONE:
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 ADDRESSEE: POMS, SMITH, LANDE & ROSE STREET: 2121 Avenue of the Stars
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 Application US/07958321
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 714-263-8250
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US-08-387-932-4
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INFORMATION FOR SEQ ID NO:
 COMPUTER: IBM PC compatible
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CURRENT APPLICATION DATA:
 NAME: MacLean, Kurt A.
REGISTION NUMBER: 31,118
REFERENCE/DOCKET NUMBER: 89
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ATTORNEY/AGENT INFORMATION:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9022190.4
FILING DATE: 12-OCT-1990
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 ZIP: 19477
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MEDIUM TYPE: Floppy
 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
 APPLICANT: FISCHER, PETER
APPLICANT: TYLER, MARGARET I
TITLE OF INVENTION: Retro-, Inverso-, and Retro-Inverso
TITLE OF INVENTION: Synthetic Peptide Analogues
 CORRESPONDENCE ADDRESS:
 APPLICANT:
 MOLECULE TYPE: protein
 STREET: 2121 Avenue CITY: Los Angles STATE: CA
 STREET: Spring House Corporate Cntr., P.O. Box 457 CITY: Spring House
 FILING DATE: 19
CLASSIFICATION:
 APPLICATION NUMBER: US FILING DATE: 19921222
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 TYPE: amino acid TOPOLOGY: linear
 COUNTRY:
 ADDRESSEE: POMS, SMITH, LANDE & ROSE STREET: 2121 Avenue of the Stars
CLASSIFICATION: 424
 FILING DATE:
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 100.0%; Score 69; DB 3; 100.0%; Pred. No. 0.00064; or Mismatches 0;
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT// FILING DATE: 27-AUG-1993

PCT/AU93/00441

PRIOR APPLICATION DATA:

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 US-08-387-932-4
 US-08-773-675-8
 Sequence 8, Applicati
GENERAL INFORMATION:
 Query Match
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 INFORMATION FOR SEQ ID NO:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
 PUBLICATION INFORMATION:
DOCUMENT NUMBER: AU PL4374
FILING DATE: 27-AUG-1992
 CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
 REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
 FILING DATE: 03-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: MITCHARD, LEONARD
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/604,958
FILING DATE: 03-JUN-1996
 APPLICANT: PERHAM, RICHARD N. APPLICANT: WILLIS, ANNE APPLICANT: GREENWOOD, JUDITH
 FRAGMENT TYPE:
ORIGINAL SOURCE:
 SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
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 APPLICANT: NUSSENZWeig, Ruth S.
APPLICANT: NUSSENZWeig, Ruth S.
APPLICANT: ROSE, Keith
TITLE OF INVENTION: POLYOXIME-BASED ANTI-MALARIAL VACCINES
FILE REFERENCE: 5986/IC599-US1
CURRENT FILING DATE: 1997-12-24
EARLIER APPLICATION NUMBER: 60/034,506
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EARLIER FILING DATE: 1996-12-24
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
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EARLIER FILING DATE: 1996-12-24
NUMBER OF SEQ ID NOS: 4
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 Sequence 1, Application US/08998335A GENERAL INFORMATION:
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 TITLE OF INVENTION: POLYOXIME-BASED ANTI-MALARIAL VACCINES FILE REFERENCE: 5986/1C599USI CURRENT APPLICATION NUMBER: US/08/998,335
CURRENT FILING DATE: 1997-12-24
 APPLICANT: Nussenzweig, Ruth S. APPLICANT: Rose, Keith
 APPLICANT: Nardin, Elizabeth
 APPLICANT: Nardin, Elizabeth
 INFORMATION FOR SEQ ID NO:
 TYPE: PRT
 TYPE: PRT
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Pred. No. 0.00064;
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 Length 12;
 Indels
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 0
 Gaps
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 US-09-074-410-34
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 SEQ ID NO 1
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 Sequence 34, Application US/09074410 GENERAL INFORMATION:
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 APPLICANT: Nardin, Elizabeth
APPLICANT: Moreno, Alberto
TITLE OF INVENTION: UNIVERSAL T-CELL EPITOPES FOR ANTI-MALARIAL VACCINES
FILE REFERENCE: 5986/18615-US1
CURRENT APPLICATION NUMBER: US/09/060,450
CURRENT FILING DATE: 1998-01-21
EARLIER APPLICATION UMMER: 60/033,916
EARLIER FILING DATE: 1997-01-21
 NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 3.0
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/045,949
APPLICATION NUMBER: 08-MAY-1997
TITME DATE: 08-MAY-1997
 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/074,410 FILING DATE: 08-MAY-1998
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
 APPLICANT: REDDISH, Mark A. APPLICANT: LONGENECKER, B. Michael TITLE OF INVENTION: METHOD FOR GENERATING ACTIVATED T-CELLS TITLE OF INVENTION: AND ANTIGEN-PULSED ANTIGEN-PRESENTING CELLS NUMBER OF SEQUENCES: 34
ATTORNEY/AGENT INFORMATION: NAME: Saxe, Bernhard D.
 APPLICANT: AGRAWAL, Babita APPLICANT: KRANTZ, Mark J.
 STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
 Local Similarity
nes 12; Conserv
 CITY: Washington
 1 NANPNANPNANP 12
 1 NANPNANPNANP 12
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 1 NANPNANPNANP 12
 Similarity
 100.0%; ilarity 100.0%; Conservative 0
 Conservative
 100.0%;
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 0;
 Score 69; DB 14;
Pred. No. 0.00064;
 Score 69;
Pred. No.
 Mismatches
 0.00064;
 DB 13;
 Length 12;
 Length 12;
 Indels
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 0;
 0;
 Gaps
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US-09-300-959-39
; Sequence 39, Applica
; GENERAL INFORMATION:
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Best Local Similarity
Watches 12; Conserve
 В
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 US-09-763-397A-4
 Query Match
Best Local Similarity 100.
 Sequence 4, Application US/09763397A GENERAL INFORMATION:
 SOFTWARE: 1
SEQ ID NO 39
 CURRENT APPLICATION NUMBER: US/09/300,959
CURRENT FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: US 60/083,154
PRIOR FILING DATE: 1998-04-27
 APPLICANT: Zanetti, Maurizio
TITLE OF INVENTION: Somatic :
FILE REFERENCE: P-ZA 3519
 TELEFAX: (202) 672-539 INFORMATION FOR SEQ ID NO:
 APPLICANT: Control and Prevention
APPLICANT: Lal, Altaf A.
APPLICANT: Lal, Altaf A.
APPLICANT: Ping Shi, Ya
APPLICANT: Hasnain, Seyed E.
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium
FILE REFERENCE: 6395-57049
CURRENT APPLICATION NUMBER: US/09/763,397A
CURRENT FILING DATE: 2001-62-16
 CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR FILING DATE: 1998-08-21
 APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for
 NUMBER OF SEQ ID NOS:
 LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
PRIOR APPLICATION NUMBER: PCT / US99/18869
 SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
 REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEPAX: (202) 672-539
 STRANDEDNESS:
TOPOLOGY: li
 TYPE:
 REGISTRATION NUMBER:
 1 NANPNANPNANP 12
 1 NANPNANPNANP 12
 1 NANPNANPNANP 12
 1 NANPNANPNANP 12
 amino acid
 PatentIn Ver. 2.1
 Application US/09300959
 Conservative
 linear
 peptide
 Somatic Transgene Immunization and Related Methods
 42
 100.0%; Score 69;
100.0%; Pred. No.
tive 0; Mismatcl
 100.0%; Score 69; DB 17; 100.0%; Pred. No. 0.00064; o. Mismatches 0;
 28,665
 042881/0114
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US-07-958-321-13
 ; ORGANISM: Plasmodium falciparum US-09-763-397A-4
 Sequence 13, Application US/07958321 GENERAL INFORMATION:
 Query Match
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 PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 26
 TELEPHONE: 714-263-8260
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INFORMATION FOR SEQ ID NO:
 SOFTWARE: PatentIn version 3.1
 LENGTH: 12
TYPE: PRT
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/G
FILING DATE: 14-OCT-1991
ATTORNEY/AGENT INFORMATION:
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9022190.4
FILING DATE: 12-OCT-1990
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 APPLICANT: Perham, APPLICANT: Willis, APPLICANT: Greenwoo
 SEQUENCE CHARACTERISTICS
 TELECOMMUNICATION INFORMATION: TELEPHONE: 714-263-8250
 TITLE OF INVENTION: CONUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
 MOLECULE TYPE: peptide
HYPOTHETICAL: NO
 NAME/KEY: Peptide LOCATION: 1..13 OTHER INFORMATION: OTHER INFORMATION:
 FITLE OF INVENTION:
 NAME: MacLean, Kurt A.
REGISTRATION NUMBER: 31,118
REFERENCE/DOCKET NUMBER: 89-208
 FILING DATE:
 APPLICATION NUMBER: US
FILING DATE: 19921222
 STREET: 2121 Aver
 ORGANISM:
 TOPOLOGY:
 ADDRESSEE:
 LENGTH:
 1 NANPNANPNANP 12
 NANPNANPNANP 12
 12;
 90067
 INFORMATION:
 CA
 amino acid
 SOURCE:
 13 amino acids
 3: POMS, SMITH, LANDE & 2121 Avenue of the Stars
 USA
 Conservative
 Willis, Anne E. Greenwood, Judith
 Perham, Richard N.
 linear
 P. falciparum
 ENGINEERED BACTERIOPHAGES AND VACCINES CONTAINING THEM
 100.0%;
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peptide used to check reactivity of antibodies
raised against fdMal."
 PCT/GB91/01785
 US/07/958,321
 LANDE & ROSE
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Pred. No.
 Mismatches
 0.00064;
 DB 21;
 Length 12;
 Indels
 0;
 Gaps
 0;
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RESULT 13
US-08-138-514-8
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 Query Match
Best Local Similarity
Matches 12; Conserv
 Query Match
Best Local (
 Sequence 8
 GENERAL INFORMATION:
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3901
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 8:
 ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: YSTEM: PC-DOS/MS-DOS
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,514
FILING DATE: 15-OCT-1993
CLASSIFICATION: 424
 MOLECULL NO
 SEQUENCE CHARACTERISTICS LENGTH: 13 amino acid
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 FEATURE
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 FEATURE:
 TOPOLOGY: li
 ATTORNEY/AGENT INFORMATION:
 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION:
 APPLICANT:
 FRAGMENT TYPE:
 NAME/KEY:
LOCATION:
 NAME: Bencen, Gerard
REGISTRATION NUMBER:
 OTHER INFORMATION: /label- amide
 LOCATION:
 NAME/KEY:
 LOCATION:
 REFERENCE/DOCKET NUMBER:
 COUNTRY:
 CITY: Rahway
 STREET:
 NAME/KEY:
 NAME/KEY:
 ADDRESSEE: Merck & Co., Inc.
 LOCATION:
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 , Application US/08138514
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 New Jersey
 P.O. Box 2000
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 Cross-links
2..4
 United States
 Cunningham, Barry
 Conservative
 Cross-links 6..8
 Tolman, Richard L
 Linear
 Modified-site
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 internal
 NFU.... 35,746
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 Score 69; DB 3;
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 0.0007
 DB 5;
 Length 13;
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Matches

Mismatches

Indels

<u>0</u>

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NANPNANPNANP 12

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; FILING DATE: US-08-387-932-3
 Sequence 3, Application us/vuring GENERAL INFORMATION:

APPLICANT: COMIS, ALFIO
APPLICANT: TISCHER, PETER
APPLICANT: TYLER, MARGARET I

TITLE OF INVENTION: Retro-, Inverso-, and Retro-Inverso;
TITLE OF INVENTION: Synthetic Peptide Analogues
Query Match
Best Local Similarity
Matches 12; Conserv
 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/AU93/
FILING DATE: 27-AUG-1993
PRIOR APPLICATION UDATA:
APPLICATION NUMBER: AU 4374
FILING DATE: 27-AUG-1992
ATTORNEY/AGENT INFORMATION:
 INFORMATION FOR SEQ ID NO:
 LOCATION: 1..2
LOCATION: 1..2
COTHER INFORMATION: /note= "RESIDUE 1 IS AN EXTRA CYSTEINE OTHER INFORMATION: RESIDUE ADDED TO THE N-TERMINUS OF THE OTHER INFORMATION: REPTIDE"
PUBLICATION INFORMATION: PEPTIDE"
PUBLICATION INFORMATION: DOCUMENT NUMBER: AU PL4374
FILING DATE: 27-AUG-1992
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWMARE: Patentin Release #1.0, Vers. #1.25
CURRENT APPLICATION DATA:
 MOLECULE NO ANTI-SENSE: NO ANTI-SENSE: NO Internal
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
 FRAGMENT TYPE: 1
ORIGINAL SOURCE:
 MOLECULE TYPE: pe
 SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
 COUNTRY: UZIP: 19477
 STREET: Spring House Corporate Cntr., CITY: Spring House
 TELEFAX: 215-540-5818
 REGISTRATION NUMBER: 31,215
 FILING DATE:
 APPLICATION NUMBER:
 ADDRESSEE:
 DEVELOPMENTAL STAGE:
 NAME/KEY: Modified-site
 ORGANISM:
 amino acid
Y: linear
 Bak, Mary E
 Pennsylvania
 13 amino acids
 United States of America
 Conservative
 Plasmodium falciparum TAL STAGE: SPOROZOITE
 Howson and Howson
 Floppy disk
 peptide
100.0%; S
100.0%; F
ative 0;
 US/08/387,932
 PCT/AU93/00441
 ω..
 GHC2USA
 Score 69;
Pred. No.
 Mismatches
 DB 7;
0.0007;
 P.O. Box 457
 Length 13;
 Indels
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 Gaps
 0;
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 ; MOLECULE TYPE: US-08-773-675-11
 US-08-773-675-11
search completed: January 29, 2002, 10:56:00
Job time: 2396 sec
 Sequence 11, Application US/08773675
GENERAL INFORMATION:
APPLICANT: PERHAM, RICHARD N.
 Query Match
Best Local S
Matches 12
 TELEFAX: (703) 816-41 INFORMATION FOR SEQ ID NO:
 FILING DATE: 24-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 03-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: MITCHIERD 1FORMATION:
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
 TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 816-4000
 CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION: ENGINEERED BACTERIOPHAGES AND VACCINES TITLE OF INVENTION: CONTAINING THEM
 APPLICANT: WILLIS, ANNE APPLICANT: GREENWOOD, JUDITH
 NUMBER OF SEQUENCES:
 STRANDEDNESS:
TOPOLOGY: 1i
 NAME: MITCHARD, LEONARD C. REGISTRATION NUMBER: 29,00
 APPLICATION NUMBER: US/01
FILING DATE: 24-DEC-1996
 COUNTRY: U.S.A.
 STATE:
 CITY: ARLINGTON
 STREET:
 REFERENCE/DOCKET NUMBER:
 ADDRESSEE:
 1 NANPNANPNANP 12
 2 NANPNANPNANP 13
 1 NANPNANPNANP
 NANPNANPNANP
 l Similarity
12; Conserv
 22201-4714
 amino acid
 VIRGINIA
 1100 NORTH GLEBE ROAD
 100.0%; ilarity 100.0%; Conservative C
 peptide
 3) 612

3 816-4100

NO: 11:
 12
 12
 US 08/604,958
 US/08/773,675
 29,009
 179-13
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 Score 69; DB 11
Pred. No. 0.0007
 Mismatches
 Version #1.30
 Length 13;
 Indels
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 0;
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US-09-543-696B-23
Sequence 23, Application US/09543696B
Sequence 23, Application US/09543696B
GENERAL INFORMATION:
APPLICANT: Potempa, Jan S.
APPLICANT: Travis, James
APPLICANT: Genco, Caroline A.
TITLE OF INVERTION: GINGIVALIS PEPTIDES AND METHODS
TITLE OF INVERTION: GINGIVALIS PEPTIDES AND METHODS
FILE REFERENCE: 235.00120120
FILE REFERENCE: 235.00120120
CURRENT APPLICATION NUMBER: US/09/543,696B
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 08/822,324
 NANPNANPNANP 12
 Ouery Match
Best Local Similarity
Matches 12; Conserv
 <u>ជជល់ស្លេសស្រេសស្រេសស្រេស</u>នេធនេ
 US-09-938-406-5
a
 Sequence 26420, A
Sequence 26419, A
Sequence 78694, A
Sequence 31468, A
Sequence 3419, A
Sequence 3419, A
Sequence 3419, A
Sequence 3411, A
Sequence 10155, A
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Sequence 2211, A
Sequence 2210, A
 Sequence 5, Appli
Sequence 23, Appl
Sequence 5117, Ap
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Compugen Ltd
 US-09-938-406-5
US-09-643-696B-23
US-09-842-500-1
US-09-482-500-1
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 Total number of hits satisfying chosen parameters:
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Copyright (c) 1993 - 2000
 January 29, 2002, 10:58:07
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 1 NANPNANPNANP 12
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Match Length
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Perfect score:
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2223, A
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11804, AP
1204, AP
1418, AP
1416, AP
1895, AP
 Sequence 4718, A Sequence 1896, A Sequence 1896, A Sequence 4717, A Sequence 1895, A Sequence 1894, A Sequence 19136, Sequence 2109, A Sequenc
 Gaps
 Sequence
Sequence
Sequence
 Sequence
 Sequence
 Sequence
 ;
 Length 68;
 Indels
 Sequence 5, Application US/09938406
GENERAL INFORMATION:
APPLICANT: LOWell, George
APPLICANT: LOWell, George
APPLICANT: Vancott, Thomas
APPLICANT: Howell, George
TITLE OF INVENTION: PROTEIN AND PEPTIDE VACCINES FOR
TITLE OF INVENTION: PROTEIN AND PEPTIDE VACCINES
CURRENT APPLICATION UNDER: US/09/938,406
CURRENT APPLICATION NUMBER: US/09/938,406
CURRENT FILING DATE: 1999-09-30
PRIOR FILING DATE: 1999-09-30
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: US 60/021,687
PRIOR FILING DATE: 1996-07-10
PRIOR FILING DATE: 1996-07-10
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 68
 US-09-708-427-53325
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US-09-760-446A-1187
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Conservative 0; Mismatches 0;
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236
303
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303
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402
431
4431
465
571
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446
 ; TYPE: PRT
; ORGANISM: P. falciparum
US-09-938-406-5
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1 NANPNANPNANP 12
 1 NANPNANPNANP 12
 SEQ ID NO 6
LENGTH: 1704
 LENGTH: 1477
 US-09-482-500A-1
 TYPE: PRT
 SEQ ID NO 1
 TYPE: PRT
 Query Match
 Op
 qq
 ŏλ
 APPLICANT: Imamura, Takahisa
APPLICANT: Potempa, Jan
APPLICANT: Potempa, Jan
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROL OF BLOOD COAGULATION
FILE REPERENCE: 235.00160101
CURRENT APPLICATION NUMBER: US/09/482,500
CURRENT FILING DATE: 2000-01-13
PRIOR APPLICATION NUMBER: US 60/115,869
PRIOR FILING DATE: 1999-01-13
 ö
 ó;
 APPLICANT: Corbin, David R.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Haseling, Joseph B.
APPLICANT: Malvar, Thomas M.
APPLICANT: Malvar, Thomas M.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
FILE REFERENCE: 38-21(51847)B.
CURRENT APPLICATION NUMBER: US/09/897,516
CURRENT APPLICATION NUMBER: US 60/215, 161
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
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0; Mismatches
 Pred. No. 2.4;; Mismatches
 Score 49;
 Sequence 5117, Application US/09897516 GENERAL INFORMATION:
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: 60/013,945
PRIOR FILING DATE: 1996-03-22
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 23
LENGTH: 28
 Sequence 1, Application US/09482500
GENERAL INFORMATION:
APPLICANT: Travis, James
 78.3%;
75.0%;
 71.0%;
80.0%;
 SEQ ID NOS: 4
PatentIn version 3.0
 ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 75.u.
 Query Match
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Matches 8; Conservative
 ; TYPE: PRT
; ORGANISM: Xenorhabdus sp.
US-09-897-516-5117
 1 NANPNANPNANP 12
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 3 NPNANPNANP 12
 RESULT 3
US-09-897-516-5117
 US-09-482-500-1
 TYPE: PRT
 NUMBER OF
SOFTWARE:
 qq
 δλ
 qq
 δ
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APPLICANT: Travis, James
APPLICANT: Travis, James
APPLICANT: Travis, James
APPLICANT: Imamura, Takahisa
APPLICANT: Dotempa, Jan
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROL OF BLOOD COAGULATION
FILE REFERENCE: 235.00160101
CURRENT PILLING DATE: 2001-12-17
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PRIOR PILING DATE: 1999-01-13
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S-08-543-696B-7
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S-08-543-696B-8
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SOFTWARE: Patentin version 3.0
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Best Local Similarity 66.7
Matches 8; Conservative
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Sequence 26419, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT APPLICATION NUMBER: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PALEALIN VETSION 3.1
 GENERAL INFORMATION:
GENERAL INFORMATION:
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GENERAL INFORMATION:
TAPLICANT: N. ALEXANDROVCE tal.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APLLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOUTHWARE: PatentIn version 3.1
SEQ ID NO 78695
LENGTH: 424
 ö
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 Gaps
 Gaps
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0
 Length 424;
 Length 953;
 Indels
 Indels
 Score 46; DB 5;
Pred. No. 7.9;
0; Mismatches
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Pred. No. 4.9;
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LOCATION: 1..953

OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature

LOCATION: 1..953

OTHER INFORMATION: Ceres Seq. ID 1818047
US-09-708-427-26419
 LOCATION: 1..424
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..424
COTHER INFORMATION: Ceres Seq. ID 1963464
US-09-708-427-78695
 TYPE: PRT ORGANISM: Arabidopsis thaliana
 mays
 Query Match 66.7%;
Best Local Similarity 66.7%;
Matches 8; Conservative (
 Query Match
Best Local Similarity 80.0%;
Matches 8; Conservative
 TYPE: PRT
ORGANISM: Zea mays subsp.
 1 || || || || || 202 NENPYPNPNQNP 213
 NAME/KEY: misc_feature
 1 NANPNANPNANP 12
 106 NANPNANSNS 115
 1 NANPNANPNA 10
 US-09-708-427-26419
 US-09-708-427-78695
 SEQ ID NO 26419
LENGTH: 953
 FEATURE
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 RESULT
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 APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION UNDBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SEQ ID NO 26420
LENGTH: 757
LENGTH: 757
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 Length 367;
 Length 757;
 3; Indels
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 Score 47; DB 5;
Pred. No. 2.1;
 DB 5;
 Score 46; DB 5
Pred. No. 6.3;
0; Mismatches
 Pred. No. 5.1;
 Sequence 2. Application US/09971118
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VOGANATHAN, THILLAINATHAN
APPLICANT: VOGANATHAN, THILLAINATHAN
TITLE OF INVENTION: SGK2 AND ITS USES
FILE REFERENCE: KINE025CIP
CURRENT APPLICATION NUMBER: US/09/971,118
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: PCT/US01/21479
PRIOR APPLICATION NUMBER: 60/237,419
PRIOR APPLICATION NUMBER: 60/237,419
PRIOR APPLICATION NUMBER: 60/237,419
PRIOR FILING DATE: 2000-10-02
SOFTWARE: PSSCI ID NOS: 8
SOFTWARE: PSSCI FOR WINGOWS VERSION 4.0
SEQ ID NO 2
LENGTH: 367
 0; Mismatches
 1; Mismatches
 NAME/KEY: misc_feature
: LOCATION: 1.757
: UCCATION: 1.757
: NAME/KEY: misc_feature
: LOCATION: 1.757
: LOCATION: 1.757
: OTHER INFORMATION: Ceres Seq. ID 1818048
US-09-708-427-26420
 ; Sequence 26420, Application US/09708427
; GENERAL INFORMATION:
 ORGANISM: Arabidopsis thaliana
 66.7%;
66.7%;
66.78;
 Ouery Match
Best Local Similarity 66.7
ماست 8; Conservative
Best Local Similarity 66.7
Matches 8; Conservative
 Best Local Similarity 66.7
Matches 8; Conservative
 TYPE: PRT ORGANISM: Homp sapiens US-09-971-118-2
 | || || || || || 947 NGTPNPNPNPNP 958
 1 NANPNANPNANP 12
 1 |:|||| |
21 NLGPSANPNAQP 32
 6 NENPYPNPNONP 17
 1 NANPNANPNANP 12
 1 NANPNANPNANP 12
 RESULT 8
US-09-708-427-26420
 RESULT 7
US-09-971-118-2
 Query Match
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APPLICANT: N. ALEXBADROV et al.
APPLICANT: N. ALEXBADROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REPERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 86364
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 3418
LENGTH: 343
TITLE OF INVENTION: SEQUENCE-BETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: SEQUENCE-BETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOCTHANRE: Patentin version 3.1
SEQ ID NO 3419
LENGTH: 342
 ; Sequence 3417, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID; TITLE OF INVENTION: THEREBY
 1;
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 14;
 14;
 Length 343;
 Length 342;
 Indels
 Indels
 DB 5;
 DB 5;
 Score 43; DB
Pred. No. 7.8;
 3; Mismatches
 3; Mismatches
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 62.3%; Score 43; 34.6%; Pred. No.
 ; OTHER INFORMATION: Ceres Seq. ID 1810473
US-09-708-427-3418
 ID 1810474
 US-09-708-427-3418; Sequence 3418, Application US/09708427; GENERAL INFORMATION:
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 ORGANISM: Arabidopsis thaliana
 ORGANISM: Arabidopsis thaliana
 COTATION: 1...342
COTHER INFORMATION: Xaa is any
NAME/KEY: misc_feature
LOCATION: 1...342
COTHER INFORMATION: Ceres Seq.
US-09-708-427-3419
 62.3%;
 Query Match
Best Local Similarity 34.0.
 Ouery Match
Best Local Similarity 34.0.
 NAME/KEY: misc_feature LOCATION: 1..343
 NAME/KEY: misc_feature
 1 NANPN----
 US-09-708-427-3417
 LOCATION:
 TYPE: PRT
 TYPE: PRT
 FEATURE
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 Sequence 78694, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROW et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 78694
 APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1248
FILE REFERENCE: 2750-1249
CURRENT APPLICATION WUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATCHIN VERSION 3.1
SEQ ID NO 31468
LENGTH: 346
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 Gaps
 Gaps
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 Length 346;
 Length 521;
 2; Indels
 1; Indels
 DB 5;
 DB 5;
 Score 45; DB 5
Pred. No. 6;
1; Mismatches
 Pred. No. 5.6;
 1; Mismatches
 COCATION: 1..346
COTHER INFORMATION: Xaa is any amino acid
NAME/RET: misc_feature
LOCATION: 1..346
COTHER INFORMATION: Ceres Seq. ID 1832153
US-09-708-427-31468
 NAME/KEY: misc_feature
1.521
DOCATION: 1..521
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..521
CCATION: 1..521
OTHER INFORMATION: Ceres Seq. ID 1963463
US-09-708-427-78694
 Score 44;
 Sequence 31468, Application US/09708427 GENERAL, INFORMATION:
 ; Sequence 3419, Application US/09708427 ; GENERAL INFORMATION:
 TYPE: PRT
ORGANISM: Arabidopsis thaliana
 ORGANISM: Zea mays subsp. mays
 63.8%;
70.0%;
 65.2%;
80.0%;
 Query Match 65.2
Best Local Similarity 80.0
Matches 8; Conservative
 7; Conservative
 NAME/KEY: misc_feature
 203 NANPNANSNS 212
 1. NANPNANPNA 10
 Best Local Similarity
Matches 7; Conserv
 3 NPNANPNANP 12
 :|| ||| ||
5 DPNPNPNPNP 14
 US-09-708-427-31468
 RESULT 13
US-09-708-427-3419
 US-09-708-427-78694
 Query Match
 TYPE: PRT
 QQ
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Search completed: January 29, 2002, 10:58:08 Job time: 2504 sec

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